

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
9831	40199	A	9892	121	2320	EMAFQKAVKGTILVGGGALAT VLGLSQFAHYRRKQMNLA YVK AADCSIEPVNREPPSRE AQLTL QNTSEFDILVIGGGATGSGCAL DAVTRGLKTALVERDDFSSGTS SRSTKLIHGVRVYLQKAIMKLD IEQYRMVKEALHERANLLEIAP HLSAPLPIMLPVYKWWQLPYY WVGKILYDLVARKANCLKSSY VLSKSRAL EHFPM LQKDKLVG AIVYYDQGHND A RMNLAIALT AAIRYGAATANYMEVVS L LKK TDPQTGKIVHVS GARCKGCPST GQEFDRVAKCVINATGPFTDSV RKMDDDKAAANCOP SAGVHIV MPGYSPESMGLLD PATSDGR VIFFLPWQKMTIAGTTDTPTDV THHPIPSEEDINFILNEV RNYLS CDVEVRRGDVLA AWSGIRPLV TDPKSADTQSISRNVHVDISESG LITIAAGKWT TYRSM AEDTINA AVKTHNLKAGPSRTVGLFLQG GKDWSPTLYIRLVQDYGLESEV AQHLAATYGDKA FEVAKMAS VTGKRWPVGVHLVSEFPYIEA EVKYGIKEYACTA VDMISRRT LAFNLVQAAEEALPRIVELMGR ELNWDDYKKQEQL ETARK/FL YYEMGYKSRSEQLTDRSEISLL PSDIDRYKKRFHKFDADQKGFI TIVDVQRVLESIN VQMDENTLH EILNEVDLNKNGQVELNEFLQL

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9832	40200	A	9893	1	2020	MLKPLMGGGAHRRAAAGARK WDGTAAHASTSGLEVLWVTTSR SKTVESVGLAKPGQHNDARMN LAIALTAARYGAATANYMEVV SLLKKTDPPQTKGVRVSGARCK DVLTTGQEFVRAKCVINATGPF TDSVRKMDDKDAAA/CQA/SA GVHIVMPGYSPESMGLLDPAT SDGRVIFFLPWQKMTIAGTTDT PTDVTHHIPSEEDINFILNEVR NYLSCDVEVRRGDVLAAWSGI RPLVTDPKSADTQSISSRNHVVDI SESGLTIAGGKWTTYRSMAD TINAAVKTHNLKAGPSRTVGLF LQGGKDWSPPLYRLVQDYG ESEVAQHLLAATYGDKAFAVEAK MASVTGKRV/WPIVGVRVLSDF PYIEAEVKYGIKEYACTAVDMT SRRTRLAFLNLQAAEEALPRLL ELMGRELNWDDYKKQEQLT ARKFLYYEMGYKSRSEQLTDR SEISLLPSDIDRYKRRCHKFDAD QRGFMTVVVEVQVRVLESINVQM DENTLHEILNEVDLNKNGQVEL NEFLQLMSAIQKGRVSGRLAI LMKTAENLDRRVPIPVDRSCG GLYFCVRNWWVLGLTDFKNE AADPSGVKLQTTFTVSVTLAKV ARLELFVSPGGLVVLGSGVKL QIFAPNMAMHNKAAPPQIPDTR RELAEVLKRRQELAAATLAKFG
9833	40201	A	9894	2	593	ISSAVEFETSQSLGWTEQSAA RSRGENIVCGPQGPRG/GPWVP AEPTGSPVVSSEPLDLLPTDLDR QEMPPPRVFKSFLSLFQGLSVL LSLAGDVLVSMYREVCSIRFLF TVVSLNLNLSAFWLGLLYLVS PLENEPKEMTLSEYHERVRSQ GQQLQQLQAELDKLHKEVSTV RAANSERGAKLVFQRLNEGFV

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9834	40202	A	9895	1	1105	MRRSSRPGSASSSRKHTPNFFSE NSSMSITSEDSKGLRSAEPGPGE PEGRRRARGPSCGLLFQGLSVLL SLAGDVLVSMYREVCSIRFLT AVSLLSLFLSAFWLGLLYLVSP LENPKEMLTLSYHERVRSQG QQLQQLQAELDKLHKEVSTVR AANSERVAKLVFQRLNEDFVR KPDYALSSVGASIDLQKTSHDY ADRNTAYFWNRFSFWNYARPP TVILEPHVFPNCWAFEGVQGG VVIQLPG/HECTLSIDLQHPPPS VEHTGGANSAPRDFAVFLLSF FTHQGLQVYDETEVSLGKFTFD VEKSEIQT FHLQNDPPAAFPKV KIQILSNWGHPRFTCLYRVRAH GVRTSEGAEGSAQGP
9835	40203	A	9896	10	395	VEPGKRLIDRIVETICSCFOGPO TDEGVQLQIIKALLTAVTSPHIEI HEGTILQTVRTCYNILASKNLI NQTTAKATLTQML/NHARSDSG KVSTENGDA PRERGSSLSGTN DGAQEVVKDILEDVVT

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9836	40204	A	9897	1	1698	MLGTSVEDIAQFLHQEERLDST QVGDFLGDSARFNKEVMYAYV DQLDFCEKEFVSALRTFLEGFR LPGEAQKIDRLMEKFAARYIEC NQQTFLFASADTAYVLAYSIM LTTDLHSP/PDLEMHQAPAGARS ADRNRCEDALPVWIA*KRRE PEGPHIGRRRVHGPWPR*FGEW RSG*KTDGQLPRIGW*DQLAEC GCSCGQDFYVVYQTGWKNS* LCPLAVCCVHG*TGFPSSHV QLAEDCGDILQHESDPTIVVS NMACDWRSLQ*DKL*MLGTSV EDIAQFLHQEERLDSTQVGDFL GDSARFNKEVMYAYVDQLDFC FKEFVSALRTFLEGFRLPGEAQ KIDRLMEKFAARYIECNQQTFL FASADTAYVLAYSIMLTTDLH SPQILKCISQLELAQLIGTVKT RYLSGSGREREGSLKGHTLAGE EFMGLGLGNLVSGGVDKRQM ASFQESVGETSSQSVVAVDRI FTGSTRLDGNAIVDFVRWLCA VSMDELASPHHPRMFSLQKIVE ISYYNMNRIRLQWSRIWHVIGD HFNKTSCDRLRELHVSEVFTVI TETRETKGPRDTPIFIETLVKVK DAEDQLGARVGYIELDLNSGKI LESFRPEERFPMSTFKVLLCG AVLSRIDAGQEQLGRRHYSQN DLVEYSPVTEKHLTDGMTVRE LCSAAITMSDNTAANLLTTIG
9837	40205	A	9898	1	492	
9838	40206	A	9899	1	3555	
9839	40207	A	9900	1	4145	MFVLKVGCSLLLRDPRRSLLH YTCFTSVPLVQVGCNPNEVDV AIFAVDSLRLQSMKFLEKGELA NFRFQKDFLRPFEHIMKKNRSP TIRDMAIRCAQMVNSQAANIR SATIFQHHPAIDSFQDAVKCL SEFACNAAFPDTSMEARLIRF CGNYLISERPRVLLYEYTSDDMN VAPGDRVWVRGWFPILFELSCL NRCKLDVTRTGLTVMFEIMKS YGHITFEKHWQDLFRIVFRIFD NMKLEPELSEKS

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9840	40208	A	9901	1	5477	MQESQTKSMFVSRALEKILADK EVKRPQHSQLRACQVALAWK LLLIAPLAVGKATPVKMWSNK VEQLTVMNMHSAEQETDEIKA EIEKQRLGTAAPPKANFIEADK YFLPFELACQSKSPRVVSTSLDC LQKLIAYGHITGNAPDSGAPGK RLIDRIVETICSFCFGPQTDEGV QLQIIKALLTAVTSPHIEHGTI LQTVRTCYNIYLASKNLINQTT AKATLTQMLNVIFTRMENQVL QEARELEKPIQSK
9841	40209	A	9902	2	740	TGWEGRAAEAEVPQDDRRREPRH S/IEVEEEDQKLVSASLEPIGG/P PDCPQKQ/PQCPLSPSKKWGC DLCL*QHKLAQKWRREISTSVP SQPLGPGRTADTGPSLPT/TPA GQEAGRTPAPPAWSAFDL.DST VVKMEKGWICS*KYTRSQASC SELPRRLGRAPTTELGMPTQE VAPLPARG*GPESLPL/ASRQEF LSGRTVRVKLGLPLPLETGKIV LPGEGGSPHVCPSPWIIERRTA DQGVVAE
9842	40210	A	9903	1	1376	MPSSSVGPAPPSLRGSSEQLAW LRGIFSYRSSPPSPQOSSPNQTR SRQHYAPSVFEKYTASVTVGSK EVTNLNYDTAALAGPWPALHS WRPLRGAGCGALEAKPYTKQ WAALGPPMVPGLRLRYLLWSLQ TLATPGQRPREGPHAHTPRAEA TAGQEPARDPKGSARNPEPQRP RGKGVRAAPKQGVGRGMSIPAQ PHASTRAGSERSE/QRRLSSF TGSCDSDLKFNQLKFRKKKLLK FCKSHIHDWGLFAMEPSGDPLE SAWIHARNAPTTTPSQTPHPPPR EAGNPNNPPRAPEARGPGHDKA AQKACVHGGPNTQHPRPQPEP AVPPAALAPPPKHQLSSQASSPS RLGRAAERPHKTQQRQTPTHT GPRAAATAEHAPQALPPAPAP HYNRTRPAQLRNPPTPKKGSEE PAQPTKHTPATPAKRDPKGGG ARRRPAPRLQPHSGGEEDKES

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9843	40211	A	9904	724	2076	KLCPCLYHFFHTNVQRHAPFVA NPFLLTHIQISTKHPAIVGTTELL LCVGGVQRVLQLAPQRLQLLA QVPALLRLGPGHTLRLQVLLG LGQGCLSLPQGFQQLGPGPTLV FCPLPELLEEDAVGEALATDAD ALQDPVAAKL VQHQPWLQLPG LGKQPPPLPVSQLLEVGRAVPLH HPQGALLLALLEGLQSLPRV HSPFLHDTFRHRPVPASQLN SFEQLCITTPQKLQQLFNHTMF VSPPAVNQANPAGLLALDEE CWFPKATDKSFVEKVAQEQQG HPKFQRPRLHRDQADFSLHY AGKVDYKANEWLMKNMDPLN DNVAALLHQSTDRLTAEIWKD VEGIVGLEQVSSLDGPPGGR RRGMFRTVGQLYKESLSRLMA TLSTNTNPSFVRCIVPNEKRAG KLEPRLVLDQLRCNGVLEGIRI CRQGFNRLFFQEFRQ
9844	40212	A	9905	2	480	VGCMGCSKGPWRQAFQVDVH VSDALPQCRQLQTGMRGAFGK PQGTVARVHIGQVIMSIRTKLQ NKEHVIEALRRAKFKFPGRQKV CSAAAPFSHLCPRPDSVLSIAP *IHISKKWGFTKFNADEFEDMV AEKRLIPDGGGVKYIPSRGLD KWRALHS
9845	40213	A	9906	1	485	SDEYDQLCSEALVGAQICAKK YIVKCCGKNGFHIRVRLHPFHV ICINRMLACAGTDRLQTGMGG AIGKPQGTVARILIGQVIMSIRT KLQNKHEHVIEALRRAKFKFPGR QKIHISKKWGFTKFNADEFEDM VAEKRLIPDGGGVKYIPSRGLD DKWRALHS
9846	40214	A	9907	198	452	DYYLEGLNHIVVHHDHFLNLQN HSSNLPVAEICYR*RYRKKVQQ RIIAKDYTTLEFSNR*LFN

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9847	40215	A	9908	2	1968	SYLHCKWATMEELEKDPRIAQ KIKRFRNKQAQMKHIFTEPDED LFNPDYVEVDRILEVAAHTKDAE TGEEVTHYLVKWCSLPYEEST WELEEDVDPKVKEFESLQVLP EIKHVERPASDSWQKLEKSREY KNSNQLREYQLEGMNWLLFN WYNRKNCILADEMGLGKTIQSI TFLSEIFLRGIHGPFLIAPLSTIT NWEREFRTWTEMNAIVYHGSQ ISRQMIQQYEMVYRDAQGNPL SGVFKFHVVITTFEMILADCP ELKKIHWSCVIIDEAHRKKNRNC KLLLEGLKLMALAHKVLTTGTPLQ NSVEELFSLNLFLEPSQFPSETA FLEEFGDLKTEEQVKKLQSILKP MMLRRLKDDVEKNLAPKQETII EVELTNIQKKYYRAILEKNFSFL TKGANQHNMPLINTMMELRK CCNHPLYLINGAEEKILED FRKTHSPDAPDFQLQGMIAQVAGKL VLIDKLLPKLIAGGHKVLIFSQM VRCLDILEDYLIQRRYTYERIDG RVRGNLRQAIDRFCKPDSDRF VFLLCTRAGGLGINLTAADTCII FDSOWNPQNDLQVPEGRIQKV WEQMSWPRAQPDNAAAACL QDFGSQLGVQSEETGPFHNRQK QDSGNSHTAPRGRESFIKPPSSR DLLPLKIQKEGPATNYNS
9848	40216	C	9909	223	402	

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9849	40217	A	9910	1	1710	MFEKAARQEWIQVAKSVTRVA MSSYTFQKNPDLISVGEDVEKK LELSYAAVTMAWQQYGDYGY PYQQYHDYSDDGWVNLNRQG FSYQCPQGGVIVAVRSIFSKE ADSVSRASATGPDGQFFLLER VGCTKTTAEAQPORDDPYLVLT RTVEGLSRTVEGVGRGLTQAA AGEGAGAVEAAWNSLCGPFSS TPMASDEETEAIIRGHETRPDDT AKNSGAIQHQSCSWPLY/RA PHSVKRYQTCSNNGLVAGFQS RYFESVLDREWQFYCCRYSKR CPYSCW/LSLAADQTLMTPGVG EAPRKCSSFRKGNRTIEPALTGP KSPTYSVGMPSLKLRPNDSHPS AVLLLPNFWLTTEYPGHYGE MDMISYNYDYYIRGATTTFSAV ERKEERRERKIGDKKHTEPTV LVWAAIPHYLRLGNLRTIEYFH SSGSWKVQDQVDPPEEPARQN HRDRVPCHTTPPLGGQEGDSQPV VMRAKDHYELEKQKALGQVE DEEDLCQQQLPEQTYGSEEP QEAKKNLGSPEPNSQAGAQQPI SMATNRAVFDVTCNFSPHWLQ CLQSRSLSPEDPGL
9850	40218	B	9911	101	1237	
9851	40219	A	9912	1	622	NLSDRHRGSHLESQHFORLKQE DLLSPRIQDQPGQHWETLSHINI VVIGHVDSGKSTTGHLYKCG GIDKRTIEKFEKEAAEMGKGSF KYAWVLDKLKAER/ERGITIDIS LWKFETSKYYVTIIDAPGHRDFI KNMITGTSQADCAVLIVAAGV GEFEAGISKNGQTRHALPG/ YSQKRYEEIVKEVSTYIKKIGYT PDTVACVP
9852	40220	A	9913	1	762	VVQTQISKTADELISYWGTSFPP PFAASLTLYELCYCITIDISLWK FETSKYYATVIDAPGHRDFIKN MITGTSQADCAVLIFAAGVGEF EAVTFAPVNVTTTEVKSVMHH EVLSEALPGDNVDFDVKNVSV KEVHHGNVAGQISAGCAPVLID CHMAHIACKFAKLKKKTGSTS GKKLEDGPTFLKSGDAAIIVDM VPGKPMCVESFVYPLSRFAV CDMRQTVAVGVIEAMDKMAA\ GAGKVTMSAQKAHNAK

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9853	40221	A	9914	1	618	MVQARPGAHP TLLPGPTAAWV SGFSGGSDLTGAREAQERGR WSPTESSASVSPVAKVSKFTLS SELEGGDYPKERERTGGGPRGP PDWTPHGTGA\ LQSPHPRTAPA PHPTPCGPRPDAGQSPGAPPA WSPRVHRPTPSLLPPRRWTA LWAAWQRP LPASQPGRGTS NPGPGRTPSPQEVGSPGHHIS LRTGFPPTL
9854	40222	C	9915	3	406	
9855	40223	A	9916	1379	2096	NGGGCGAARGGAAPGEGTRRG ACWATRG LPTGRSAAAPARR GERQQLAMDVFLMIRRHKTTF TDAKESSTVFR/ELKRIRRGQSS KRPPDEQRL\YK\DDQLLD\DG\ KTLGECGF TSNRHRPQAPAT VGSLPASSAASSTDDTFEALCI EPFSS\PEL\PDVDGRPGGFGEG SAQLNKAVQVETPQEGPIFPQL KGDGLSLPGCCLFFPPLPGMGP TPCGLLLGLVLGSSCAVLSPRS
9856	40224	A	9917	1	695	MAHAGRTGYDNREIVMKYIHY KLSQRGYEWDAGDVGAAPPG AAPAPGIFSSQPGHTPHPAASRD PVARTSPLQTPAAPGAAAGPAL SPVPPVVH LALRQAGDDFSRRY RGDFAEMSSQLHLTPFTARGRF ATVVEELFRDGSVNREMSPL\V DNIALWMTEY\LNRLDHTWQD NGGWPWDFLIGATTPTVTIPYLP YHSTEECLINVKGTAEFKIPFA KPDEMIQA KIIDGC
9857	40225	A	9918	3	422	CSLKNWREVLALLTYSGTEKF PELC\DLMEKVMVNLNRSLEQLR GPH/GGS AVLGGQSPFPFPRI VGATLHSEKTSYRLGSQPSHQ VPTSPRPRVFTPQSSPAMPLAP SHPSYPQGPRTQNISDYRAGP QAIQPLPL
9858	40226	A	9919	1	849	

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9859	40227	A	9920	3	868	NSSPPFPFRIVVGATLHKSSETS SYRLGSPQSHQVPTSPRPRVFT PQSSPAMPLAPSHSPYQGPRT QNISDYRAPGPQAIQPLPLSPGV RPGPQDSWKEAPAPRGNLQRN KLPETFMPPAPITGPS/IM/RPHP* ATRDSSLTAPLSPV*VMLPQEF QENSPAGDKDNVFPGLGKPPSP PCVQVMVDGPHSSR/PCAEGD WVQVPGVLTAEKGRLLISPILL *WEQCDCESLGTS*GSHEKDS LPLWPFSLLLYQQLQHLPEKLM ERKELPPEHQLKSSFEALLQRC
9860	40228	A	9921	1	307	MKLKELERPAVQAWSPASQYP LYLATGTSAAQQLDSSFSTNGTL EIFEVDFRDPSLDLKHGVLISA LSRFHKLWVGSPGSGLLSSGV IVGGDNGMLILYNVTHILSSG KEPVIAQKQKHTGAVRALDLN PFQPPEDIKALSNNRQAQHILSS AHPSGKAVVWDLRKNEPIKVS DHSNRMHCSGLAWHPDIATQL VLCSEDDRLPVIQLWDLRFASS PLKVLESHSRGILSVSWQADA ELLLTSAKDSQILCRNLGSSEPC PRLVFISQVTTESEFLMRSaelQ EALGSGNLLNYCQNKSSQALL QSEKMLWQFLKVTLEQDSRMK FLKLLGYSKDELQKKVATWLK SDVGLGESPPQKGNLNSDRQ QAFCSQASKHTTKEASASSAFF DELVPQNMTPEIPITKDIDGLL SQALLLGELGPAVELCKEERF ADAILAQAGGTDLKQTQERY LAKKKTKISSLLACVVQKNWK DVVCTCSLKNWREALALLTY SGTEKFPCLCDMLGTRMEQEGS RALTSEARLCYVCSGSVERLVE CWAQKCHQALSPMALQDLMEK VMVLNRSLEQLRGPHGVSPGP ATTYRVQYANLLAAQGSLAT AMSFLPRDCA/PAARDIYAPSTN YCSSYEPHP*ATRDSSLTAPCLQ SASAPAT*EDGKEGAAPRASVL EEQL*GASPTLLPVCN*LKDKK

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9861	40229	A	9922	3	2751	SVSWSQADAELLTSAKDSQIL CRNLGSSEVVYKLPQTSSWCDF VQWCPDRPSVFSAAAFNGWISL YSVMGRSWEVQHMROADKISS SFSKGGQPLPPLQVPEQVAQAPLI PPLKKPKWIRRPITGVSFAGGG KLVTFTGLPSTPAHLVPQPCPRL VFISQVTTSEFLMRSaelQEAL GSGNLLNYCQNKSSQALLQSE KMLWQFLKVTLEQDSRMKFLK LLGYSKDELQKKVATWLKSDV GLGESPOPKGNDLNS
9862	40230	A	9923	363	543	
9863	40231	A	9924	2	737	EAETEYFVRICKHMTNHNIVFQ LFHLLTFQFDCNTLNDQLEK VTVQMPESSEYEVLSICIPAPSLP YNQPGICYTLVRLPDDPTAVA GSFSCMTMKFTVRDCDPNTGVPD EDGNDDEYVLEDELVTVSDHIQ KVLKPNFAAAWEEVGDTFEK EETFALSSSTKLEEA VNNITFL GMQPCERSDKVPENQD/SHSL YLAGIFRGGYDL/LVRARLALA DGVTMQVTVRCKHRTFVDIILA
9864	40232	A	9925	327	464	GSPTTRPAKPLTLSSGHLRSRPR WAEGPQYHLP*ISAPRAKLG MM
9865	40233	A	9926	2	1179	WQPDIGPYGGLLNvvvdGLFI GWMYLPHPDHPVDDPMRFKPL FRHILMERKAATVECMYGHKG PHHGHIIQVKKDEFSTKCNQTD HHRMSGGRQEEFRTWLREEWG RTLEDIFHEHMQELILMKFIYTS QYDNCLTYRRIYLPSPRPDDLK PGLFKGTGSGHGLEIVMLSFHG RRARGTKITGDPNIPAGQQTVEI DLRIIRIQLPDLENQRNFELSRI VLEVRERVRQEQEGGHEAGE GRGRQGPRESQPSAPQAEAP SKGPDGTPGEDGGEPGDAAVAA AEQPAQCGGQPFVLPVGVSSR NEDYPRTCRMCFYGTGLIAGH GFTSPERTPGVFILFDEDRFGFV WLELKSFSLYSRVQATFRNAD APSPQAFDEMLKNIQSLTS
9866	40234	A	9927	287	537	TGKFPSC/CLLSFYGTGLIAGHG FTSPERTPGVFILFDEDRFGFV LELKSFSLYSRVQATFRNADAP SPQAFDEMLKNIQSLTS
9867	40235	A	9928	1	3651	

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9868	40236	A	9929	1	3720	MEEMFGGGAADDYKAGPPE DEGDPKAGAGPPGPPAYDPY GPYCPGRASGAGPETPGLGLDP NKPPELPSTVNAEPLGLIQSGPH QAAPPPPPPPPPAPASEPKGG LTSPIFCSTKPKKLLKTSSFHLL RRRDPPFQTPKKLYAQEYEFEA DEDKADVADIRLNPRLPDV SSCRSRPALSPGLDIDFCPPNPG PDGPRRRGRKPTAKARDGPPRP RGRPRIRPLEVPTTAGPASASTP TDGAKKPRGRG
9869	40237	A	9930	503	739	QGWRRRRPISKISESRNMQNFL HALSNCLPEGGA*DRCSSRLEE GRQLPPLLLGSLQVAKKSGGTG WMVRCSCQLFLG
9870	40238	A	9931	1	1148	MGGKGGDSWVISATPLGKCCA AVPLGGNPTLRVDQLWRKQRP PLQQCTASAPGGWVTSMLGAG THAANTGFQLVWSSKRPMYKV LQAFFGVQRSDRSAMNGQGS KCVGMPITHTRQQADLGRGPE ETEDKKQQSRGSDRLRSEGE EPYLLRTSKVKDKERILKAARE MKQIIYNGAPIHLAADFVETL QAKKEWCDIFKVLKKKTFYPK MVLTAGPSHPQSVISVSFTGLA NAASLTMSPDHLHGQPGFAGLSS VAAVDWQWALLRPSPPQGRM GLLPICQATQGPQLCVASPSDK EGFLLLFGEIARLTNKGGARL YKCDIVQGVCCEDPLATLDWE LRPDLEQGERPTPERHKPFLG KSFSAPLIKICRYEQWFMF
9871	40239	A	9932	333	689	NSFLTCLPPVSI*TDLLQPSAQ WKQLSLARRNVHSTRLAGARR CAASGPSVVAACHYHPVSGHSR LLHGCGHGWGSWQVPEVPPG SPFSLAPVWKKRQTALPAILHL PVEHYYPEL

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9872	40240	A	9933	84	933	PLTSPEAFSNRCGLRGPP/PCVP VGRLLQFNDVSSSLGICLPDSSCC SSWHGPHSLHH/HVQACKASIR ASGTAASANCAFSRYHVHCSIA FQIKVLHNLIVLTVIIPAAEHMA WGPGLAQPNPPHRSAGSHSSWGP EVGPKLSTTALVGTYPQVPPV GLETGPPSLFQPLPISTHTAWNT ENCPANATVIAHPTLAAQGTKN PPTLLVHHCHYQHLKDDGT RRENSLKLGEKVLQTEGIQK GMDPTMEYATNYWKKLQWLK RRQTALPAIHLPEVHYYPEL
9873	40241	A	9934	1	627	MESLDTETSTWGECHRKIRGM VPQVKELAEAAAAPPDGA VAE YRREKQKYEALRKQSKKCTS REDQQIIKNLPCTNHCIWQSTH EHIPALSDLSGKRAKQVIPVKG GEHYERTLALLNQFKSKLTQAI AETPENDIPETEVEDDEGWMS HVLQFEQKSRKSGKVPMSQDS DTEIYDPRNP/LVNRKREGKK AKSLMREKKERRLK
9874	40242	A	9935	1	371	PMRPAFTRVEMARVLMERNQY KERLMELQEA VRWTE MIRASR EHP SVQEKKKSTIWQFFSR LFSS SSSLPRKRPYPSPVNIHYKSPTE GCSVAAGFSPPPCHLHCDVCPL PRLFPQDLEVTGP
9875	40243	A	9936	2	186	
9876	40244	C	9937	109	408	
9877	40245	C	9938	161	341	
9878	40246	C	9939	303	439	
9879	40247	C	9940	201	419	
9880	40248	C	9941	122	307	
9881	40249	A	9942	3	80	YNPAPYKEKTITL/PCPRKLGP QGS/S*NGPPSSSSSQCSVSFND PHLPEGQVQAAR*WAPPGL
9882	40250	C	9943	249	427	
9883	40251	A	9944	90	244	TVVPHDPCGTD AHCETHMD MCPSHSVMLCGWLTF AEF RGA MGEGG RESFLLNQASFCY*CSQ AGFSSNLWRCSRAGRGN TADE LWCHMTLV AQMPYV KHTWT CVPATVLC SVAGSP LSSGVQW GREGGKASS
9884	40252	C	9945	4	204	
9885	40253	C	9946	340	497	
9886	40254	C	9947	158	184	

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9887	40255	A	9948	200	386	LFYTM*IMAFLLSSSSSPGRPF* RILGGAKVYAGMQRYSFLLIGS RIITYLGIFGRELYFC
9888	40256	B	9949	47	622	
9889	40257	A	9950	1	630	
9890	40258	A	9951	1	782	
9891	40259	A	9952	1	677	MHGLGRWDACPDDEMSESGQ SSAAATPSTTGTKSNTPTSSVPS AAVTPLNESLQPLGDYGVGSK NSKRAREKRDNRNMEVQVTQE MRNVSIIGMGSSDEWSDVQDIID STPELDMCPETRLDRTGSSPTQ GIVNKAFGINTDSLYHELSTAG\ S*VIGDVDEGADLLGNNDKCK VYTSVQTRPPQACTFSVRLVES THAELVGIEGRLYHKIHLPLRVH GAVGVSVLT
9892	40260	C	9953	202	366	
9893	40261	A	9954	1	2429	MKEGGWGDPCVGRGVTSGHV LQMKLLPFRQKKAHIMEIQLNG GTVAEKVAWAQARLEKQVPV HSVFSQSEVIDVAVTKGRGVK GVTSRWHTKKLPRKTHKGLRK VACIGAWHPARVGCISARAGQ KGYHHRTELNKKIFRIGRGPHM EDGKLVKNNASTSYDVTAKSIT PLGGFFPHYGEVNNDFVMLKGC IAGTKKRVTILRKSLLVHHSRQ AVENIELKFIDTTSKFGHGRFQT AQEKRAFMDGLSLSPAASDS DYPGEMFLDSDVNPEDPGAD GVLAGITLVGCATRCNVPRSN SSRGDTPVLDKGGQGEVATIANG KVNPSQSTEEATEVDPGPG SEPETATLRPGPLTEHVFTDPAP TPSSGPQPGSENGPEPDSSSTRP EPEPSGDPTGAGSSAAPTMLWG AQNGWL YVHSAVANWKKCLH SIKLKDSVLSLVHVKGRLVAL ADGTLAIFHRGEDGQWDLNLY HLMDLGHPHHSIRCMV VYDR VWCGYKKNKVHVIQPKTMQIEA SAGQGPGEGRLLASSPASSI RKSTRPTHDSKSFDAHPRES QVRQLAWIGDGVVVSIRLDST LRLYHAHTHQHLQDVVDIEPVVS KMLGTGKLGFSFVRITALLVAG SRLWVGTVGNGVVISIPLTETVV LHRGQLLGLRANKTSPTSGEGA RPGGIHVYGGDSSDRAASSFIP

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9894	40262	A	9955	9	452	KIKVLSKNSQVTFDFPVPTLLND GQCLGYNSTPYKEKAITL/PCPR KLGPQGSFKTA/APSSSSPSFNF FNGSQNSVTNFWSSCFH*KVLI LKTNNLKLPHAKKKTkvv/LQ NILLSF*RFYDALLSLTLLLN LNGQLKQTVMRPFHH
9895	40263	A	9956	1	3223	ATATPSTTGKSNTPTSSVPSAA VTPLNESLQPLGDYGVVSKNSK RAREKRDSR/NMEVQVTQEMR NVSIGMGSSDEWSDVQDIIDST PELDMCPETRLDRTGSSPTQGI VNKAFIGINTDSLYHELSTAGS\ EVIGDVDEGADLLGEFSGMGK EVGNLLENSQLLETKNALNV VKNDLIAKVDQLSGEQEVLRG ELEAAKQAKVKLENRIKELEE LKRVKSEAIARREPKEEAEDVS SYLCTESDKIPMAQ
9896	40264	B	9957	176	658	
9897	40265	A	9958	2	5671	AGGPCVRSSRELWTILLGRSAL RELSQIEAELNKHWRRLLEGLS YYKPPSPSSAEKVANKDVASPL LKELGLRISKFLGLDEEQSVQLL QCYLQEDYRGTRDSVKTVLQD ERQSQALILKIADYYYEERTCIL RCVLHLLTYFQDERHPYRVEY ADCVDKLEKELVSKYRQFEE LYKTEAPTWETHGNLMTERQV SRWFVQCLREQSMLEIIFLYY AYFEMAPSDLLVLTKMFKEQG FGSRQTNRHLVDETFMD
9898	40266	A	9959	1	404	MVDQEAIFGCKNRNNCSHLEPP VSRLEGGAFVRDLLSPQTQYLLA SCPYYDGSFVIQIPSSNLFMV VVDSSCLCESAPITMAPIEIRYI LLCEVHSLPRKPENARECGGA PSL\QAQTVLLLLPLLLMLFSR
9899	40267	A	9960	1	1374	
9900	40268	A	9961	102	205	

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9901	40269	A	9962	1	1527	MVPDAAVLAQLAIRARVNRWR PTGLSAPHLCGAACSRCHAAI AKYFGDALPACAGKGDHCQNP TAVRRRLLEALERSSSWSKTCIG PSQGNQFDPPELYEGGRKGYGG FSRYDEGSGSGDEGRDEAHK REWNLFYQKQMLRKGDPKI EEFVPPDENCLKEASSRRIPRL TVKAREHCLRLLEALSSNRQS TRTADADAFRAKAVELEHETF RNAKVANLYKASVLKKVADIIH RASKDGQPYDMGGSAKSCSAQ AEPPEPNEYDIPPAHVYSLKPK RVGAGFPKGSCFPQTATELMET TRIREQAPQPERGGEHEPPSRPC GLLDEGSEPLPGPRGEVPGGS AHYGGSPPEKKAKSSSGGSSLA KGRASKKQQLATAAHKDSQS IARFFCRRVESPALLASAPAEAG ACPSCEGVSGTPDWQQRSTQGR KMEPGDIRLPLRLRSASGRGQ APARPETRAPLKSSPPLQRTHG KGKRPFRPARRTQASLRRGHA PQPIPPS
9902	40270	A	9963	2	99	
9903	40271	A	9964	115	1360	ENGQLHMVNALDGVRSLSLQK PRPFRLLFPKGFSELCMNREDD TARKEKTDHFIFTYTREGNLR YSAKSLFSLVLGFISDNVDHIDSLI GFPEQIAEKLFSAAEARQKFTPE GAGUARALQKFTGGLWEVWVL CSLCFLWLKLPDICCKLGDEHE LLEHLTNEALSRY*PVTTCT*IV SVLF*RLIQDYRVVMKRGLENL TLDDLCKFSKSL*ILMLEEWP *RSCSSFSGTGLKVRLLVPSLIFL DSTI*YFACANWEFDHSNCKTE GWADQVLQIFLPCG*CSFSS*FQ VSYPTSRETAESCFRSTLSLVQN MHDEAAQRFCEKFPFL*SFLPFI CILKAVRLF*KLQFYKEKAPDC HGPVLKHEAISSQESKSKKRP FEESETEQNNSQPSKQKYVCL AVEDWDLNLSY

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9904	40272	A	9965	3	1026	DNVDHIDSLIGFPEQIAEKLFFA AEARQKFTEPGAGLRALQKFTF AYGSLVLCSLCLRNRYLVISEK LEEIKSFRELTCLDLSCCKLGDE HELLEHLTNEALSSVTQLHLKD NCLSDAGVRKMTAPVVRMKR GLENLTLADLSCNPEITGGRA LGYPFLFRGNLNCFRDISGDR GSRDIKTLKHKLQTHIGLVHSH VPLKEFDHSNCKTEGWADQIV LQWERTVAEAVKPRETSEPIAA AQRFGKRSRAEAPL/CPLAD THMNSSVKLQFYKEKAP/DCH GPVLKHEAISKPRSPKSKSRP FEESETEQNNSQPSKQKYVCL AVEDWDLNSY
9905	40273	A	9966	1	289	VKCHLHRPILWDPWKTSGIQQ VLTPL*KAMEKLEAILLICSLE AIGLITLPSLSMTQFLQLHVECC YVSPDQTPYFIDVETAMKDEV TVHNPHG
9906	40274	A	9967	1	1413	MVVPPIAELKNLEVLNLFNNQ IEKLPTQISRLQKLKHLNLGFLS PCNSMNRNLNISPQGFSLPALE VLDTYNNLNENYLPGNFFYLT TLCALYLSNDNFILPPDQKLT KLQILSNRDNLISLPKEIRVLT QLKELHIQGNRLTVLPPELGSR GGSGSRFSAETA TGGAQNAPP VLSAGTIFKQRRNPSPALRG GSVAA*PSPAAAKYGKDQREH LPTAAGDGVGWEPTRDIQVGS ATAQALSQANAARGRLSTAQA AGSLHVECCYVSPGQTLFYTDV EIEAMKDESRGISILYKHRHLK VPLDQKLPKSGHQPDGYGQH DHKPMQMTSLRNATLR
9907	40275	A	9968	1	619	MNRLNISPQGFGLSPALEVLDL TYNNLNENYLPGNFFYLTLCAL LYLSNDNFILPPDQKLTQLQ LSNRDNLISLPKEIRVLTQLKE LHIQGNRLTVLPPELASSRCGP LSHPYAGKRIPRNAVFKFEQNT PWHTPPKKAGREMLLDVGTGP EAATSKPPAFLHRRRGSGWNP RSRSSSLQRTWPFGSREAEYPP ASGA

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9908	40276	A	9969	810	1672	GLPSVTMSKSLKKLVESREKN QPEVDMSDRGISNMLDVNGLF TLSHITQLVLSHNKLTMVPPNIA ELKNLEVLNFFNNQIEELPTQIS SLQKLKHLNLGMNRLNLTLPRG FGSLPALEVLDTYNNLSNSL PGNFFYLVTTLRALYLSDNDF EILPPDIGKLVTKLQILSLRDNDL ISLPKEIGELTQIKELHIQGNRL TVVPPPELGNLGF*LGQKQVFK AENNPVWVTPIADQFQLGVSHVF EYIRSETYKLYLGRHMQANPEP PKKNNDKSKKISRPLAANNR
9909	40277	C	9970	120	347	
9910	40278	A	9971	2	10018	LCVSPVTAGRPASRLREMEVEQ EQRRRKVEAGRTKLAHFQRQK TKGDSHSEKKTAKRKGSAYD ASVQEEPSPTVKEDSALCGGGDI CKSTSCDDTPDGAGGAFAAQF EDCDGEKREDLEQLQKQVND HPPEQCGMFTVSDHPPEQGHM FTVGDHPPEQGRGMFTVSDHPPE QHGGMFTVSDHPPEQGRGMFTISD HQPEQGRGMFTVSDHTPEQRGIF TISDHPAEQGRGMFTKECEQECE LAITDLESGREDEAGLHQ
9911	40279	A	9972	2	5196	APLDGEVELLQKLEKLDEFN ELAIQKESADQVLMQEEIKR LEEMNINIRKKVAQLQEEVEKQ KNIVKGLEQDKEVLKQKMSS LLLASTLQSTLDAGRCPEPPSGS PPEGPEIQLEVTQRALLRRESEV LDLKEQLEKMKGDLESKNEIL HLNLKLDMQNSQTAVSLRELE EENTSLKVIYTRSSEIEELKAIE NLQENQKRLQKEKAEIEQLHE VIEKLQHELSLMGPVVHEVSDS QAGSLQSELLC
9912	40280	A	9973	1	8277	GEFGSEKKTALHEKEETLRQS AQAQPFHQEEKESLSQLQKKN HQVQQLKDQVLSLSHEIECRS ELEVLQRRRERENREGANLLS MLKADVNLSHSERGALQDALR RLGLGFGETLRAAVTLRSRIGE RVGLCLDDAGAGALSTAPAL EETWSDVALPELDRTLSECAEM SSVAEISSHMRESFLMSPESVRE CEQPIRRVFQSLAVDGLMEM ALDSSRQLEEARQIHSRFEKEFS FKNEETAQVVRKHQ
9913	40281	A	9974	1	393	

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9914	40282	A	9975	2	153	
9915	40283	A	9976	184	790	KFTKHISMNQEDLDPDSTTDVG DVTNTEELIRECEEMWVKDME ECQNKLSLIGTETLTDNAQLSL LIMQVKCLTAELSQQWKKTPPE TIPLTEDVLITLGKEEFQKIRGQ DLEMVLSTKESKNEKLKEDLER EQRWLDEQQIMESLNLVHSE LKNKVETFSERIFNELKTKML NIKEYKEKLLSTLGEFLEDHFL
9916	40284	C	9977	23	217	
9917	40285	A	9978	25	100	
9918	40286	A	9979	1	2850	
9919	40287	A	9980	108	1132	HPHQVETSRDVAGEQSHAVAF MSTGISQADVCRLEWFSAPNLK GRPRKKKPCPQRDSFSGVKDS NNNSDGKAVAKVKCEARSALT KPKNNHNCKKVSNEEKPKVAI GEECRADQAFVLVALYKYVMK ERKTRIERIPYLGFNQINLWTMF QAAQKLGGYETITARRQWKHI YDELGGNPGSTSAATCTRRHYE RLILPYERFIKGEEDKPLPIPK RKQENSQENENKTKVFGTKRI KHEIPKSKKEKENAPKQDAAE VSSEQEKEQETLISQKSIPEPLPA ADMKKKIEGYQEFSAPLASR VDPEKDNETDQGSNSEKVAEE AGEKGPTPLPSAPL
9920	40288	B	9981	177	3543	
9921	40289	B	9982	63	374	

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9922	40290	A	9983	1	2023	MGGGSWAPTGLCPQLSLLAMS PEKRKLA AQEGQFTPEPRPEEP KEKLHTEEFSEYFFRAPEKDM VSM AVLPLARARGHLWAYSC PLRQPLLKR VHANVDLWDIAC QIFVDILPHQACTSAVVGVS YQSVSAWSCPSTVLDSTHIL RYMGDYP SRQAWPTLELTDQIF TLALQHPALQDEVYCQILKHLT HNSDRHSEERGWQLLWCTGL FPSPKGLLPHAQKFIDTRRGKLL APDCSRRIQKVLRTGPRKQPPH HVEVEAAEQNVSRICHKIYFPN DTSEMELVVANTRVRDVCDSI ATRLQLASWEGCSLFIKISDKVI SQKEGDFFFDSLREVS DWVK NKPQKEGEASVELGEGVAGW VEGALAASVRPMPIHPSIRSRVS LGC GNQALGPGGAPVTLPYQ VYFMRKLLWNISPGKDVNADT ILHYHQELPKYLRGFHKCSRED AIHLA GLIYKAQFNND RSQLAS VPKILREL VPENLTRLMSSEEW KKSILLAYDKHKDKTVEEAKV AFLKWICRWPTFGSAFF/EGEG KPCPTGPGPTQAASAQSPSRPS VNQHTSWQTSEPSYPDVILIAIN RHGVLLIHPKTKDLLTTPFTK ISSWSSGSTYFHMALGSLGRGS RLLSETSLGYKMDDLTSYVQ QLLSAMNKQRGSKAPALAST

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9923	40291	A	9984	428	2502	VSKEIVYNKLLPYAERLDAESD LQLAQIKCNLGRAVQLQELWP GGLFWTRKLS/TRAGPLALSSLE LSPSGDPRVVTPEVKYSSRPPCH FPTGLPGSLPSLYVLRICFSRSV RVVVFPPGGPWVAQGP RPGR ETWGFTMLLRIRLYGRKFSKE DHVLFKLLYELVSIPKLEISMM QG FARLLINLLKYFPADATAEM LEEWRPLMCPFDVTMQKAITY FEIFLPTSLPPELHHKGFKLWFD ELIGLWVSQNL PQWEGQLVN LFARLATDNIGYIDWDYPYV PKG GPSKLVQKHLA GLFNSITSFYH PSNNGRWLNKLMKLLQRLPNS VVRRLHRERYKKPSWLT PVPDS HKLTDQDVTDFVQCIQPVLLA MFSKTGSLEAAQALQNALMR PELVIPPVLERTYPAETLTTEPH QLTATLSCVIGVARSLVSGGRW FPEGTHMLPLL MRALPGVDPN DFSKCMITFQFIATFSTLVPLVD CSSVLQERNDLTEVERELCSAT AEFEDFVLQFMDRCFGLIESSTL EQTRETEETEKMTHELSVELG LSSTFSTLTQCSKEIFMV ALQK VFNFSTSHIFETRVAGRMVADM CRAAVKDWGKPGDLWNLGIQ WHVPSSEEVSAFYLLDSFLQP ELVKLQHC GDGKLEMSRDDIL QSLTIVHNCLIGSGNLLPPLKGE
9924	40292	A	9985	2	5396	AESDLQLAQIKCNLGRAVQLQEL LWPGGLFWTRKLSYIRLYGR KFSKEDHVLFIKLLYELVSIPKL EISM MQFARLLINLLKKKELL SRADLELPWRPLYDMVERILYS KTEHLGLNWFPNSVENILKTLV KSCRYPFPADATAEMLEEW RP LMCPFDVTMQKAITYFEIFLPTS LPPELHHKGFKLWFD ELIGLWV SVQNL PQWEGQLVNLFARLAT DNIGYIDWDYPYVPKIFTRILRSL NLPVGS SQVLVPR
9925	40293	A	9986	1	477	VREFFGRRFRGCCGALRPYKR LVDNIFPEDP/GYVCIAMEALDQ LLMACHCQSINLFVESFLKMVA KLESEKSNLQILGTNSFVKFA NIEEDTPSYHRSYDFVSRFSEM CHSSHDDLEIKTKIRMSGIKSLQ GVVRKTVNDELQANWDPQH

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9926	40294	A	9987	1	2371	AGGARLRPARGRPPRLPPRP PCRPPVPAPTVNERRAPPRAG WERKSDAGLSRGARPAEMYGV CGCCGALRPYKRLVDNIFPED PEDGLVKTNMEKLTIFYALSAPE KLDRI GAYLSERLIRDVGRHRY GYVCIAMEALDQLLMACHCQS INLFVESFLKMVAKLLESEKPN LQILGTNSFVKFANIEEDTPSYH RSYDFFVSRFSEMCSSHDDLEI KTKIRMSGIKLQGVVRKTVN DELQANIWDQHM DKIVPSLLF NLQHVEEAESRSPSLQAPEKE KESPAELAERCLRELLGRAAFG NIKNAIKPVLHLDNHSLEWPK VFAIRC FKIMYSIQPQHSHLVQ QLLGHLDANSR SAATVRAGIVE VLSEAAVIAATGSVGPVLEMF NVTLLRQLRLSIDYALTGSYDGA VSLGTKIIEHEERM FQEAVIKT VGSFASTLPTYQRSEVILFIMSK VPRPSLHQAVDTGRTGENRNR LTQIMLLKSLQVSTGFQCNNM MSALPSNFDRLSTALMEDAE IRLFVLEILISFIDRHGNRHKFTI STLSDISVLKLVDKCSRQDTV FMKKHSQQLYRHIYLSCKEETN VQKH YEALYGLLALISIELANE EVVVDLIRLVLA VQDV AQVNE ENLPVYNRCALYALGAAYLNLI SQLTTVP AFCQHHIEVIETRKKE APYMLPEDVFVERPRLSQNLDG
9927	40295	A	9988	1	662	IPGSTISWSPAAARGLSVCRCCR LHPASAMDLFGDLPEPERSRP AAGKEAQKGPLLFDDLPPASST DSG/SSLQALPGSGGPLLFDDL PASSGDSGLATSISQMVKTEG KGAKRKTSEEEKNGSEELVEK KVCKASSVIFGLKGYVAERKGE REEMQDAHVILNDITEECRPPSS LITRVSYFAVFDGHGGIRASKF AAQNLHQNLIRKFKPKGDVISVE

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9928	40296	A	9989	3	1145	KEAQKGPLLFDDLPPASSTDSA VAALGTTTPSPVTLWFLQTRRGS KIWRNSLDYQSKVGAEPWCHE RQQKADRFLGKRGRVPASSVIF GLKGYVAERKGEREEMQDAH VILNDITEECRPPSSLTRVSYFA VFDGHGGIRAKSFAAQNHLQN LVRKFKPGDVISVEKTVKRCLL DTFKHTDEEFKQASSQKPAW KDGSTATCVLAVDNILYIANLG DSRAILCRYNEESQKHAALSLS KEHNPTQYEERMRIQKAGGNV RDGRVLGVLEVSRSIGDGQYK RCGCHLCAPTSSRCQLTPNDR FILVWPCDGLFKVFTPEEAVN FILVSCLEDEKIQTRGKSAADV RLRSSPATRLANKAVAAGARP DNVTVMVVRIGH
9929	40297	A	9990	2	419	
9930	40298	A	9991	2	1842	CLRLIAAAPPI/AIEPATTSLSLAF LLLQRDQSSRTGLPEEKEEVT MDTSENRPENDVPEPPMIADQ VSNDDRPEGSVEDEEKKESSLP KSFKRKISVVSATKGVPAGNSD TEGGQPGRKRRWGASTATTQK KPSISITTESLSLIPDIKPLAQOE AVVDLHADDRISEDETERNGD DGTHDKGLKICRTVTQVVP AE GQENGQREEEEEKEPEAEPPV PPQVSVEVALPPAEHEVKKVT LGDTLTRRSISQKSGVSITIDD PVRTAQVPSPPRGKISINIVHISN LVRPFTLGQLKELLGRTGTLVE EAFWIDKIKSHCFVITYSTVEEA VATRTALHGVKWPQSNPKFLC ADYAEQDELDYHRGLLVDRPS ETKTEEQGIPLRPHPPPPVQPP QHPRAEQREQERAVREQWAER EREMERRERTRSERWDRDKV REGPRSRSRSDRRRKRERAKSK EKKSEKKEKAQEPPAKLLDDL FRKTKAAPCIYWLPLTDSQIVQ KEAERAERAKEREKRRKEQEE EEQKEREKEAERERNRQLEREK RREHSRERDRERERERDRGRD RDRDRERDRERERDRDRDK RHSRSRSRSTPVRDRGGR
9931	40299	A	9992	1400	2959	
9932	40300	C	9993	169	430	

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9933	40301	A	9994	2	199	STSR/KMTELEEVTLNGKPLQALRV/TDLKAALEQRGLAKSGQK SALVKRLKGVRSSRCWGVGGERTR
9934	40302	A	9995	1	4033	MWRRKHPRTSGGTRGVLSGNGR GVEYGSGRGHLGTFEGRWRKL PKMPEAVGTDPTSRKMAELEE VTLDGKPLQALRVTDLKAAL QRGLAKSGQKSALVKRLKGA MLLENLQKHSTPHAAFQPSQIG EEMSQNSFIKQYLEKQQLLRQ RLEREAREAEEEAESAESDE MIHPEGVASLLPPDFQSSLERPE LELSRHSRPRKSSSISEEKGDSD EKPRKGERRSSRVQARAAKLS EGSQPAEEFEEDQETP
9935	40303	A	9996	3	6305	ELEEVTLDGKPLQALRVTDL KAALEQRGLAKSGQKSALVKRL KGALMLLENLQKHSAPHAAPFP NSQIGEEMSQNSFIKQYLEKQ ELLSSRLEREAREA ALEGGKSS SISEEKGDSDDDKPRKGERRSS RVQRARAALAEQSQPAEEEEE DQETPSRNLVRADRNLTETEE EEEEEEEEEDDEEEGDDEGQK SREAPILKEFKEEGEEIPRVKPE EMMDERPKTRSQEQEVLERRGG RFTRSQEEARKSHL
9936	40304	B	9997	99	332	
9937	40305	A	9998	3	236	YIFTILNTLQGVFILLFGCLMDR KIQEALRKRFCRAQAPS/SHHLP GELLPSDPQLCIEHVRHSMAL LLRGHGHSQKL
9938	40306	B	9999	1	3099	
9939	40307	A	10000	355	858	RASSAAGWSRKTSAASSAFSS CWSS*QS*SYSSSSLS/HGQGE RERQEGPEGRPAAPVPHREQRG AERLEHHPG*DAMLWCH*LH RLVPSAGGEHGRPLHGHGELPG LRAQRHHAFVENGLL*KGEDV VR*Q*ARAGHGDDVPHPHADP GHGLLDPLPAHPDPW

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9940	40308	A	10001	3	1478	GRALTSRRRACQGAEEAAGSPA QVTTSTGHHQHRSQHRSPPA QVTTSTGHHQHRSQAATTSTG HHQHRPPPAQVTTSTGHHQHR SPAQATTSTGHHQHRSVHTGH HQHRS/HTSTGHHQHRSQAAT TSTGHHQHRSPPAQVTTSTGHH QI/GIHHQHRSPPA/HGHHQHSSPP A/HGHHQHRSPPA/HGHHQH/H HHQHSSPPA/HGHHQH/HQ/P GHHQHRS/P/HSTAHHQH/HGHHQ HSSPPA/HGHHQH/HGHHQH SSPYQH/HGHHQHRSPPA/HGHH QHRSVHTAHHQHRSQH/HGHH Q/PGHHQHRSQAATTSTGHTS TGHHQHRS/HTSTGHHVHTGHH QHRSQHRSPPAQAATTSTAHH QHSS/HTSTGHHQHRS/P/HSTGH HQHSSPPA/HGHHQHSSPPAQA TTSTGHHQHRSPPA/AAAADPS ALSAARRGSPGA/AAAPQSRGTR GGGAPAKW/GSALGLG/WAGR ARARLGRPLRPILGAMPAPRT PRERREHGEVE
9941	40309	A	10002	5	341	PPRRRGQKRRQK/REEGERERG ERKRPRDRKEERKG/RRTKRQG GTETRESRPNQDGPQAKRKKQ TAGQREEREQGRSSRQGA ERERGRETTHTCLLVPCW/WEP NGRLCL
9942	40310	A	10003	1	582	MLAQRGGRSVVQCIASVSKLSV TQRSFVTLMDEEALGNCGSS GSQTCEKAVCIHNLPLTSHAF QSGFPFHQSPEASLPKMVSQAQ TARLSLESMLRELGFHISEAGFP APVSGYEHNSPSRPGVMPGSGT HWWKORSQKVEDNRTMVKGIO GDTVKHQQLPRINGN*LAYM TAKSRTWL/PVQDQDGPQTI
9943	40311	A	10004	1	332	MEYYAAIKNDFMSFVGTWM KLETILSKLSQGQKTKHHIFSLI EAQAQVSPPPYPAPQELTQPL LQQPRAPEAPAQ/PPGSLLTAT VRLSASPGPLGIFDQLLPRCGF

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9944	40312	A	10005	1	1108	MLAQRGGRSVVQCIASVSKLSV TQRSFVTLMDEEALGNCGGSS GSQTCEKAVCIHNLPLFTSHAF QSGFPPHQSPASLPKMVSDAQ TARLSLESMRELGFHISESAGFP APVSGYEHSNPLSTTNLSGSPSR RRQPPVSPLTLSFGPEAHQGFSR QLSSTSLAPYPTSQMVSSDRS QLSFLPTEAQAVSPPPYPAPQ ELTQPLLQOPRAPEAPAQPPQA ASSLPQSDFQLLPAQGSLLTNFF PDVGFDQQSMRPGCLSSGTAS GATGSRRELQDSFHLRSPYSNC GSLPNTILPEDSSTSLFKDLNSA LAGLPEVSLDVTFFPLEELQI EPLSLDGR/HMLSDSSMGLLDP SVEETFRADRL
9945	40313	A	10006	1	691	MRERARPPRGCLAPPLPPG/E/S GADGQAPPRGRGTAGG/ELAA AGCGARAAMHRGAVPSAEPVP ASP/DGRWQWAGEGRPCNAAG GSR/T/GAGCGWPAPAGWGPAP SSAASCPASGGATHRGASAAPG GGGGGRAP/GPDALQRRAGAP PNAPGTPGSPSESSLRMRRESA AGAPAVGMMAAATSLGQALGPR VPRSPYRTAVVLSRSSAFGYFSL ITLARYTLGCLSHSDITLFECL
9946	40314	A	10007	1	1065	MADKRAGTPEAAARPPPLAR EGDARTVPAARAREAGGRGSL HPAAGPGTAFFSPGRGEAASTA TTPSLENGRVRDEAPETCGAEG LGTRAGASEKAEDANKEEGAIF KKEPAEEVEKQEGEEKQEVA AEAQEGPR/PPEPWCPN/CMDP LEAIQWEAEAVSAQADRAYLP LERRFRGRMHRLYLARRSFIIQNI PGFWVTAFLNHPQLSAMISPRD EDMLCYLMNLEVRELHRSRTG CKFKFRFWSNPYFQNKVIVKEY ECRASGRVVSIAIRIRWHWGQE PPALVHRNRDTVRSFFSWFSQH SLPEADRYAQIHKDDLWPNPLQ YYLLGDRPCRARGGLARWPTE TPSRPYGFQSG
9947	40315	A	10008	2	433	
9948	40316	A	10009	125	289	TRKSGCLKIRFHVFLFLYRNP MDVADAYVTVFVRHSQDVLRD KVNEEMYIERLF
9949	40317	A	10010	1	774	
9950	40318	A	10011	1	1749	

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9951	40319	A	10012	1	1175	MFASCYMRNIPKRVIEFGTCLW RTCKNCLSSLEFKMPFPHPHRSV TYNLKQERCRLSLDASLSCMLS IEDSQIPNTRLECKGLSRCTSV ASTCPLVTFSFCLFSPKMEQYS KDDSEKTLKGWFSFGQVFLD EYCARNGVRGCHRHLCYLRDL LERAENGAMIDPTLLHYFAFC ASHVHGNSQQMHHVYLSGLPPN TDPEGSKTPSPPEAKKDTKK ESKKRKDKTQANQELKRLTS NLP/ICEPTQW*TFPKYQIYQLT SL*ASHKCLLFRHRHG WLLY/D ADNGSGTSEDFLWKLDALQTFI RDLHWPEEEFGKHLEQRKLKLM ASDMIESCVKRTRIAFEVKLQK TSSIQQIFRVQFNMPCFNMV GLMAKGSIQPKLCSMEMMQE
9952	40320	A	10013	1	3951	MLDPSSSEESDEIVEESGKEV LGSAPSGARLSPSRTSEGSAGSA GLGGGGAGAGAGVGAGGGGG SGASSGGGAGGLQPSRAGGG RPSSPSPSVSEKEEELERLQK EEEEERKKRLQLYVFMRCIAYP FNAKQPTDMARRQKQISKQQL QTVKDRFQAFNLNETQIMADE AFMNAVQSYEYFVLKSDRVAR MVQSGGCSANDSREVFKKHIE KRVRSLEIDGLSKETVLSSWM AKFDAIYRGEEDPRKQQ
9953	40321	A	10014	1	457	VAAVAATALKGGGARNARVL RGIFAGATAINKASHNRTRALQ N/HTASPEGKEEPIEPLIPGTGKY IPQKRGAKNPHENCGNLPWAIG FPCGILLDFSPKR/RKLDKDRV KQMKARQNMVSNMTGEYESQ RFRASSQSAPSPDVGSGVSGV QT
9954	40322	A	10015	464	863	TPAAVESSPSIPLAPRLLYTG*PL QP/GRGQGC/PRIVPCCPKP/V CAPRPPWPQRSQRLRSAGLSPL CAAAAAPPVPAGSHGTPGRVWA PLSNSACCTCCRHP* ¹ LHPGTL D PGRWQAR*GPALPRGPIPGSPP
9955	40323	A	10016	1	300	PKILVGASKVLLLSAHLKLGFI DTLSRQAKAVDVASRVTHYSN LL/CDFLQIGIVATTKAALQYP IAFPGPKDMVERVKELGHSITQ QFRRLVGLQAAA

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9956	40324	A	10017	3	291	ARI/VFAISFYFMPCCPLTA/SSFYLLSGLLDAFDGHALALLIKFCVRGSESHKMIDLSGNP/VLRIYYTS/RVGSVGLFR/MGLWVTAPIALLKSLISVIT
9957	40325	A	10018	1	344	VLIRARLSDNPAVRGSESHKMI DLFCYPVLRIYYTSRPAFLTCA GNELFYCLLYLFHFSEGLVGS VGLFRMGLWVTAPIALLKSLIS VIHLTAARNMAIALGRQDRA KKK
9958	40326	A	10019	1	469	MVRSCFVDRRKRCNFNRQAS EVLNEYFYSHVSNPYHSEAKE ELAKKCGITVSQVSNRFGNKKI RYKKNIGEFQEEANIYAVKTAV SVTQGGHSSTSISPTPPSCAGCG GSFNISGSGDMFLGMPGLNGDS YSASQALES GDASPAQSEMPK MGT
9959	40327	A	10020	232	1728	PGGGRGGAGRGPQGGPPAMDE RLLGPPPPGGGRGGLGVSGEP GGPGEPPGGGDPGGSGGVPG GRGKQDIGDILQIMTITDQSLD EAQGQKTPLNCPARKKPVLFSGRGEIKEKTGLSIRSSQEEEPVD PQLMRLDNMLLAEGVAGPEKGGGSAASAAAAASGGGVSPDN SIEHSDYRSKLAQIRHIYHSELE KYEQACNEFTTHVMNLLREQS RTRPVAPKEMERMVSIHRKFS AIQMLKQSTCEAMMLRSRF LDARRKRRNFSRQATEVLNEYF YSHLSNPYPSEEAKKEELAKKCG ITVSQVSNRFGNKKIRYKKNIG KFQEEANIYAVKTAVSVTQGG HSSTSPTPPSSAGSGSFNISGS GDMFLGMPGLNGDSYASQ/V WESLRIISMARGVIGG*TFGG RARCYSPRIMRANGSWQEA VTPSSVTSPTGPGSVHSDTSLI LPLRVTVGVGALTRLEEDAGFQ RTNPNTGEAQDREGPMGSSPP
9960	40328	A	10021	337	830	IPRLPGSIQLSFVGAFGQTSKSLF FLCVFILLFQFFLCVYVPMCT E/RRINIPGPGCGMCLSVKGRC EPVLKEFGFAWPESLNCCKFP QNDHNHMCMEGPGDEEVPLPH KTIQPGEECHSVGTNSDQYIW VKRSLNCVLKC/GYDACLYSRS AQEVTDIWMA

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9961	40329	A	10022	1	1561	MAWRGAGPSVPGAPGGVGLSL GLLLQLLLLLGPARGFQDEEER RCDPIRISMCLNGYNVTKMPN LVGHQLQTDALQLTFTPLIQ YGCSSQLQFFLCGGYVPMGTEK INIPGPGCGMCLSVKRRCEP LKEFGFA/WPESLNCSE/YPHP QNDHNPVHPWKGGDEEVPLP HKTPIQPGEECHSVGTNSDQYI WVKRSLNVLKCGYDAGLYSR SAKEFTDIWMAVWASLCFISTA FTVLFTLIDSCRFSPERPIFLS MCYNIYSIAIYVRLTVGRERISC DFEEAAEPVLIQEGKLNTGCAII FLLMYFFGMASIWVILTLT WFLAAGLKWGHEAIEHSSYF HIAAWAIPPVKITVILIMRLVDA DELTGLCYVGNQNLDAITGFV VAPLFTYLVIGTLFIAAGLVLF KIRSNLQKDGTKTDKLERLMV KIGVFSVLYTVPATCVIACYFY EISNWFALFRYSADDSNMAVEM LKIFMSLLVGITSGMWIWSAKT LHTWQKCSNRLVNYT
9962	40330	A	10023	496	664	FYKAVPSIHQLDVPQTHQP*ST GLVQKVYSRSKHVSL*PKYYY VQLVPKLDHLIFY
9963	40331	A	10024	1	954	
9964	40332	A	10025	127	481	GRTREATWRVYSVAVGVSRSQ IIRIAREFADNADKTHGRSMIIV GAGLNHWYHLDMMNYRGLINM LIFCGCVGQSGQ/GWAHYVGQ EKLRPQTGWQPGVCLDWQRP RHMNSTSYFLLVP
9965	40333	B	10026	161	234	
9966	40334	A	10027	3	199	DDFLDLAESPNASDTESSEIPL KAGPGTLIMATGVQDFNRTEFD RLNAIKGHLEIALEKHFFT
9967	40335	A	10028	37	455	LRTHLLPRLSQSSPVSSLPRALL RPPGQLELWAVPAGPGPLIAA DASQNLQTHMEALASQSRGRV DMSDGHGLAVLSPIEEELRKLRE ETNAEMLRQELDRERQRMEL EQKVQEVLKARTEEQMAQQPP KGQAQASNGA

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9968	40336	A	10029	1	1721	DKIRFRGHKRDDFLDLAESPNA SDTECSDEIPLKVPRTSPRDSEE LRDPAGPGTLMATGVQDFNRT EFDRLNEIKGHLEIALLEKHFLQ EELRKLREETNAEMLRQELDRE RQRRMELEQKVQEVLKARTEE QMAQQPPKQQAQASNGAERRS QGLSSRLQKWYERFGEYVED FRFQPEENTVETEEPLSARRLTE NMRRLKRGAQPVNTFVKNLSA LSDWYSVYTSIAFTVYMNVA WHGWAIFLFLAILRLSLNYLI ARGWRIQWSIVPEVSEPPVPPK EDLTVSEKFLVLDVAQAQON LFGKMADILEKIKNLFMWVQP EITQKLYVALWAAFLASCFFPY RLVGLAVGLYAGIKFLIDIFIK RCPRLRAKYDTPYIIWRSLPTDP QLKERSAAVSRRLQTTSSRSY VPSAPAGLKEEDAGRFHSTKK GNFHEIFNL TENERPLAVCENG WRCCLINRDRKMPPTYIRNGV LYVTENYLCFESSKSGSKRNK VIKLVDTIDIKYKVLVSLPGSG MGIASVTPSTQKPLVFGAMVH RDEAFETILSYIKITSAASAGG
9969	40337	A	10030	18	573	
9970	40338	C	10031	71	205	
9971	40339	C	10032	190	243	
9972	40340	A	10033	18	283	
9973	40341	A	10034	1	190	
9974	40342	A	10035	1	135	
9975	40343	C	10036	90	137	
9976	40344	B	10037	272	560	
9977	40345	A	10038	3	422	
9978	40346	A	10039	205	1090	
9979	40347	A	10040	1	2142	

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9980	40348	A	10041	15	1524	FPGRFRFAEGERTCEAEPPRDEP PADGALKRAELKTQANDYFK AKDYENAIKFYSQAIELNPSNAI YYGNRSLVYLRTCEYGYSL*D ATRAIELDKKIYIMGYRRAVAS NMALGKFRAALRDYETVVVKV KPIIDKDAKMKYQECNKIVKP KAFAEIAAGDEHKRSVVDSLDI ESMTIEDEYS*PKLEDGKVITIS MKELMQWYKQDKKLHRKCAY QILVQVKEVLSKSLTLVETTLK ETEKITVCGDTHGQFYDLLNIFE LNLGPSETNPYIFNGDFVDRGSF SVEVILTLFGFKLLYPDFHILLR GNHETDNMNQIYGFGEVKA KYTAQMYELFSEVFEWLPLAQ CINGKVLIMHGGLFSEDGVTLD DIRKIERNRQPPDSGPMC/DLLW SDPQPQNGRSISKRGVTCQFGP DVTKAFLEENNLDYIIRSHEVK AEGYEVAHGGRCVTVFSAPNY CDQMGNKAS/YIHLQG/SDLRP/ QFHQFATAVPHPNVK/PMAYAN
9981	40349	A	10042	94	188	VIEHLVSDGLDFL/NLVICPPR PPKVLGLQA
9982	40350	A	10043	419	495	EPTNENSPIALSR*VNSQKISMK AV
9983	40351	A	10044	1	265	EMESRSIA/RMECSGSISAHCKL RLPGSHHSPASVSRVAGTTGTC HHARLIFLYF/LETFGHFVSHD GLHLL/NLVICPPRPPKVLGLQA
9984	40352	A	10045	3	706	ADAWAWPHC/CTVLL*CLGFA GVLFGWPSLVFVKNEYFKD LCGPDAGPIGNATGQADCKAQ DERFSLIFTLGSFMNFMFTFTG YIFDRFKTTVARLIAIFFYTTAT LIIAFTSAGSAVLLFLAMPMLTI GGILFLITNLQIGNLFGQHRSTII TLYNGAFDSSSAVFLIKLLYEK GISLR/VLLHLHLCLQYLACSTH FPDPAGAHPIPTAPQLQLWPV PWEVHHKREGNS

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9985	40353	A	10046	1	1413	MKRGNGSRRRRLLENNGVVF HIESFAQIPKDEKSRKLLGPIEH WTFVVEKGKGPETGTVSMV LEDGEVEADIKQGSVVGCCNV PPDAARERAEKAYMDGEQPTLI LLWLWLKKQIPVHKGTHSVGR HQTELLPNNGGGVVRFFYTAT LIIAFTSAGSAVLLFLAMPMLTI GGILFLITNLQIGNLFGQHRSTII TLYNGAFDSSSAVFLIKLLYEK GISLRASFIFISVCTWHVARTF LLMPRGHIPPYPNYSYGLCP GNGTTKEEKETAHENRELQSK EFLSAKEVSTYTNAFAFTQFGV LCAPWNGLLMDRLKQKYQKE ARKTGSSTLAVLCSTVPSLAL TSLCLCGFALCASVPLPLQYL.T FILQVISRSFLYGSNGRFLTAF PSEHFQKLFGLVMALSAVVSL LQPFITLIKGSIQNDPFYVNV MFMLAILLTLPLPSGISGMPYL
9986	40354	B	10047	316	395	
9987	40355	A	10048	1	1614	RMQQQAVMIHYMQQQQQQQQ QQLGGPPTPAINTPVHFQSPPPV PGEVLKVGVPVLCPPCPH*SQ PPLEPLPYLSETYGNKFAAHIS AQALRNPHQPPQGCELDTC PPPLATVLP/ISPMAMLHIGSNPE REVSEELASGHAACRAHCC ASETMPNTVLLARVGVVCKGS REGGTHCGSEPGESGVTSSSCP ADLTQKRELGTASLYPCAF PTPPSFSPSLPAAPLPASFLVLT WAG*KANDL*/VRLRGRVMG LGGQQLTRLALLQKSRELEN HSRRLEMTNKQLWLRQVWS* TWTSVLTLNLAPGPKGQYFR MFCFGNKQSSASLNTYQLEVL FCETLILAPTLAPSSMAHLEL ALKAIVTLKVPHTSVQWAWP MQAHSTSTLTLAQVVKQEL PSEEGPGEALMLGAEPDPEPL PALPPQAPLPLTPQPPFHHLD FSHLSFGGREDEGPGYPEPLA PGHGSPPFSLSKKDLMLLDD SLPLASDPLLTMSPEASKASS RRSSFSMEEGDVL

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9988	40356	A	10049	1	1651	GGVTAGARAPARGSVTAEEAA RAGRGSGRGADGGREGRTGRA SLVARGSRPGAGGGHSLRAR HPNLRQVAGA/GGARAADRLT FRAREPAPAATMASRIGLRMQL MREQAQQEEQRERMQQQAVM HYMQQQQQQQQLGGPPTP AINTPVIHFQSPPPVPGEVLKVS YLENPTS YHLQSQSHQKVREY LSETYGNKF AAAHISPAQALR NPHQPPPGCELDTCPPPLAT VLPISPMAMLHIGSNPERLEDD VIDNIMRLATMSLGYINPEMQM PNTVLLARLPLSSSHLNVYSSDP QVTASLVGVTSSSCPADLTQKR ELTDAESRALAKERQKKDNHN LIERRRRFNINDRIKELGMLIPK ANDLDVRWNKGITLKASVDYI RRMQKDLQKSRELEHNSRRLE MTNKQLWLRIQELMQARVHG LPTTSPSGMMAELAQQVVVKQ ELPSEEGPGEALMLGA/EGP/DP EPLPALHRQAPLPLTPQAPSPFH S/HWDFSHSL/SFGGRVDDWSP GLPRTPGAGAWLPQPQVQEGS GPHAPGRLTATAGL
9989	40357	A	10050	2	76	TPLAPPPKPVRRRLKSRR*IKAR S
9990	40358	A	10051	3	206	
9991	40359	A	10052	1	492	

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9992	40360	A	10053	2	2395	KQTELRSSGSRDVTGALLVAA AVASEAVGSLRVAEGGPNTLL QVLRISWAPWCNKATQTMEERK VKRRSPKSFSAHCTQVVNVQK KMSIPVSKS/TGFSNPASQVNFT SRPKVKKEVMK/VEKTKPQGLEE GQRHSSQLPIQHSFLTQDVSRCS RKMERGLLSLNDFFHSWK/TFK HFGMECS/VEQMEHVSSELQEK LARLNLLEYGELELPEDKRKT ASDS/NDRL/SLDCREMPAFRT FLKRHDKTIVTKMLSLPELLLY PSRRFEYLNLLYAVRLHTPAE HVDRGDLTTAIDQIKKYGYID QTLSEVNRYLIRVQDVAQLHCC DEEISFSLSVACRSVDSASPESL PEMQNSQATLALLNQNLHFNKI TRLYEHIHDL/SLFLNDALLVSS RGTSHTPFERTSKTTYQFIASVA LHRLIENIPDSKYVKNAFILQG PKYKWICATEIEDDKFLWLSVL RNAIKSSMEKACGLVFTGQFMF DTMGMTNILNNQDTAQAALADG LMELSKEDSKCGKKIKDVEGN VIPTKCDPKTTFSLFMKERNVV EDNSWDTKSRLSKNDLNFEALI NLERILQKDSAEKRARVVRELL QSERKYVQILEIVRDVYVAPLK AALSSNRAILSAA/NIQIIFCDILQ ILSLNRQFLDNLRLQEWGPA HCVGEIVTKFGSQNLNTYTNFFN NYPVILKTIEKQWETFSERSSSS
9993	40361	A	10054	2	296	
9994	40362	A	10055	2	369	
9995	40363	B	10056	82	2483	
9996	40364	A	10057	2	3343	YDVVLDAIDTMQRVAWHIND MKRKHEHAVRLQEIQSLLTNW KGPDLTSYGELVLEGTFRIQRA KNERTLFLFDKLLITKKRDDT FTYKAHILCGNMLVEVIPKEP LSFSVFHYKNPKLQHTVQAKSQ QDKRLWVHLKRLILENHAAKI PAKAKQAILEMDAIIHHPGFCYS PEGGTKALFGSKEGSAPYRLRR KSEPPSRSHKVLKTSETAQDIQ KVSREEGSPQLSSARPSPAQRNS QPSSSTMISVLRAAG

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9997	40365	A	10058	32	483	LKGHADAVLAAGTEAVKCHLL LGRHLLRLMASSGIHHKIVN*R QYAKFSHG*IQKF**WQHRQQF RGKETEMASAVDLPVTLTETEA NFPPEYKFWKTVENNPQDFTG WVYLLQYVEQENHLMARKA FDRFFIHPYCYGYWKYADL
9998	40366	A	10059	1	1090	MRQKRKEEKELFHNDCEKKE KNSWERMRTGTTEKMASESET PTGAISQYKERMPSTHSPHIM DLSELRFPSKPEIALTEALRLA DED/WDKQLHALEQLASCYS GTRHTTSSFHCGHQGMWWHPE AWRC/LATAEPQREPGKSTISSH SSLWN*Q/LHSHKLQSVPLKV KNLRSGVSRAAVVCLSDLFTYL KKSMDQELDTTVKVLHLKAGE SNTFIREDVDKALRAMVNNVT PARAVVSLINGGQSHLHIAVRR CTAQLHSDVLEFMEPERILSAA KDMAERILPAAAKFAQSSQET RYYGRKMLFFMMCHPNFEKM LEKYVPSKDLPLYIKDSVRNLQ KVCCKSLFYKQLYKQSLFLHP
9999	40367	A	10060	36	203	
10000	40368	A	10061	1	798	MKFQYKEDHPFEYRKKEGEKI RKKYPRDPVPVIVEKAPKAR/RA *SGQEEVPSAL*PYCCLP/DGAG LGTCS/HAMPEPPTHSMGTCAA RASPTSTTPCSTAPSPIDRE/EQT TQGLRNASARRGTGRQLHLQ/S PVWDPLEASWAPESGNVESI SSSGIVNIPISTLCLAQGFSRFVN APIDTLYLAALVGPWRTFMSSS GIVNTPIGTLYLAQGMVHYHKS PFPTCLVQMSKIESLPKEGAQ GVAAGLPSLAPTCTPPDPMSK LHNN
10001	40369	A	10062	164	605	ALLKQHLRTVHRSAPPIRGHCC VSSSWT*G/AGKLSLEHTEEPSD VPSHLLYRWSISSAITEVFQALA SSNPPRSQ*MSIPRRINESTRHSP GPSIEEVKECMQDDN*YLQGTS YAPAGSQSYAKLCFQVLKRN TCPPEKPNPASER

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10002	40370	A	10063	3	2480	RPITGAEIVAIHNSLPTKKSPGLD GFTAEFYQRYKEELVFPFLKLF QSIEKEGILPNSFYEASIIIPKPG RDTTKKENFRPISLMNIDAKILN KILANRIQQHIKKLIHHDQVGF PGMQGWFNIRKSINVIQHINRT KDKNHMISIDAFAFKIQQ/R LHAKNS/RIN*VLM/ETYFKIIRA IYDKPIANILNGQKLEAFPLKT GTRQGCPLSPLFNIVLEVLR AIRQEKEIKGQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLIS NFSKVSGYKINVQKSQAFLVTN NRQTESQIMSELPFTIASKRIKY LGQLTRDVKDLFKENYKPLLK EIKEDTNKWNIPCSWVGRINI VKMAILPKVIYRFNAIPIKLPMT FFTELEKTTLKFIWNQKRAHIA KSILSQKNKAGGITLPDFKLYY KATITKTAWYWYQNRDIDQW NRTEPSEITPHTYNCLIFDKPEK NKKWGDLSFNKWCWENWLA ICRKLKLDPLTPYTKINSRWIK DLNVRPKTIKLTLEENLGITQNI GMGKDFMSKTPKAMATKDKID KWDLIKLSFCTAKETTIRVNR QPTKWEKIFATYSSDKGLISRIY NELNQIYKKKTNNPIKKWAKD MNRHFSKEDIYAAKHKMKCS SSLAIEMQIKTTMRYHLTPVR MAIHKSGNNRCWRGCGEIGTL LHCW/DCKLVQPLWKS/VRF
10003	40371	A	10064	317	582	STVCCFLRFIGGGFRHPLSVD LWIHYIKILKETLDPGDPETNNT IRGYVEH*Y*NVFYDINNYSDV DNRAHES*AGSLTSIPLKK
10004	40372	A	10065	41	434	GDLQPTAALWEPLSGLAKAGA RSLSLQGGVGGEARARTRAAR GACGPAAAPGGHGLGGHALGA AGR/LLALGRLGTCSLPCLSLP PSPWAPVPPPEPR*VPPIHAGRP VPSATQRLRSAGAQRRTRGRL
10005	40373	A	10066	67	459	LRDCKYTHRHCVSSRFINTPIN TLCLAQGL*VHQSTLCI*LLWV GGLGGNFECVQYSVSN*SDGDV ENLCI*LRDCKCTNQHPVKTG FGSTNQDVGWGGQIKRIKAGLP EPASGNSLGSPTLWELCSLQ

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10006	40374	A	10067	2481	2882	IPQGNRYRVIARNAKTQRGGNLT LTKPS/GIGRRGENSSISSWQRQ QKGGKKTGSQRKRQRGRDKKL ERKRDHRHSQREGKKERKRQR RSQRERWK**RKNSVPIPLKAR VNFSLPTQGNLLDLNPLYPLK QLKK
10007	40375	B	10068	52	5199	
10008	40376	A	10069	1510	2454	
10009	40377	B	10070	97	3414	
10010	40378	A	10071	164	620	PPTGCGTGPIGCSGPGTGPVPVP VAPFPFQEGARTQPGSAGAIPG ARGLRRAETLVALGAVGPGLP TPPPPPPPAPQSQAPGGPEAQPF GSRVVCVLASCCAHRPRPAPSAP PAPPAPPESTVRPAPPTRPGESS YSSISHAFTATNPFPGTA
10011	40379	A	10072	1	513	MATLAGEGRPAGWVPWISLLA VGVLIWKLWPAPPGGELQFA FVCFLGNNVYEAFAHWKRLN LLCRSEAAAMKK/HATRLWINLI SILHHQLGEIPADFFVDIVSQHN FLTSTLQVFSSACSIADVATLR KKAELFQAHLTKKFRWDFAE PEDCAPVVEELPEGIEMG
10012	40380	A	10073	1	1642	MDYIRTDLTAAAPSPRRLGPP PGEQPPSGSGHVRPPGARPPHR GGGRGGGGDPAAPARGGGG GGKARPPGGGAAPCEPGCQR APMVSVSSERHPLYNRVKTGQI ANCALPCHNPFQSDERAFTVF WIGLWSVLCFVSTFATVSTFLID MERFKYPERPIIFLSACYLFVS GYLVRLVAGHEKVACSGGAPG AGGAGGAGGAAAGAGAAAGAG AGGPGGRGEYELGAVEQHVR YETTGPALCTVFLLYVYFGMA SSIWWVILSLTWFLAAGMKWG NEAIAGYQYFHLAAWLVPSV KSIAVLALSSVDGDPVAGICYV GNQSLDNLRGFVLAPLVLYFIG TMFLLAGFVSLFRIRSVIKQD GPTKTHKLEKLMIRLGLFTVLY TVPAVVVACLFEYQHNRP EATHNCPCLRDLPDQARRPD YAVFMLKYFMCLVVGITSGVW VWSGKTLESWRSCLTRCCWAS KGAAVGGGAGATAAGGGGGP GGGGGGPGGGGGPGGGGGSL YSDVS/TGLTWSRGTAASSVYP

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10013	40381	A	10074	3	475	HSSLNSVDKARALEADNGELE VNIRDWYQKQGPASRDYSHY YTTIQDLRDKILGATIENSRIVL QIDNARLAADDFRTKFETEHAL RMSVEADINGLRRVLDLTLAR IDLEMHIEGLKEELAYLKKNHE EEISTLRGQVGGQVTV*VDSAP GTDL
10014	40382	A	10075	39	1323	NGMWSNWNPLIPQRWEEKFQS PSRHRGSSSRGVSLSS\SGGYSGI LSGSNGLLAGNEKLTMHNLNN CLASYLDKVHALEAANSKLEF GLSVVWLDVTLARTDLEAQI KGLKEELAYLKKKHEEEINALR GQVGDQVHILSDRQSQYEIMA KQNWKDAEAWFTSWTEELNQ EVTGHIEQLQISRSEVTDLQCTL QGLEIELHSQSVKAPLEGTLA ETEACFGAQLVQIQALISSIEAQ LGDVRADGEWQNQEYQRLLE QEIATYRSLLEGQEDHYNNLST SKVQIPECTVSNVPVASVCLQT LEPHSLASNPGSSTYSVTFGQYI NLSVSPFLLLEATIAGAKKAAT GNNSTQFSPPAERQLCFTCPRT IPLTTASHAGSYGPKLVKYTSL RPLPMAAPTESNPALPSSRATA HRLLPAPGHFPSGL
10015	40383	B	10076	133	180	

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10016	40384	A	10077	1	2182	MSVDKAEELCGSLTLTWLQTFHV PSPCASPDLSGLAVAYVLNQ IDPSWFNEAWLQGISDPGNW KLKVSNLKMLVRLSLVEYSQDV LAHPVSEELPDVSLIGEFSDPA ELGKLLQLVLGCAISCEKKQDH IQRMITLEESVQHVVMEAIQEL MTKDTVPDSLSPETYGNFDSQS RRYYFLSEEAEEGDELQQRCLD LERQLMLLSEKQSLAQENAGL RERMGRPEGEGTPGLTAKKLLL LQSLEQLQEENFRLESGREDE RLRCAELEREVAELQHRNQAL TSLAQEAQALKDEMDELQSS ERAGQLEATLTSCRRRLGELRE LRRQVRQLEERNAGHAERTQ LEDELRRAGSLRAQLEAQRRO VQELLGQRQEEAMKAELWFE CRNLEEKYESVTEKERLLAER DSLREANEELRCAQLQPRGLTQ ADPSLDPTSTPVDNLAAEILPAE LRETLRLSLLENKRLCRQEAA DRERQE/EKLQRHLEDANRAR HGLETQ/HLRLNQAAAYSELRA QVEDLQKALQEQQGKTEDAISI LLKRKLEEHQLKLEADLELQR KREYIEELPPTDSSTA/RRIEEL QHNLQKKDADLRAMEERYRR YVDKARMVMQTMPEKQRPAA GAPPELHSLRTQLRERDVRIRH LEMDFEKSRSQREQEELLISA WYNNMGMALQQRAGE/EPAPA
10017	40385	A	10078	1	687	
10018	40386	A	10079	1	1104	
10019	40387	A	10080	1	677	MAAAGGGGGGAAAAAGRAYSF KVVLLEGCGVGTSLVLRyce NKFNDKHITTLQASFLTCKLNI GGKRVNLAIWDTAGQERFHAL GPIYYRDSNGAILVYDITDEDSF QKVKNVVKELRKMLGN/ETCL CIVGNKIDLEKERHVSIEAESY AESVGAkHYHTSAKQNGGIEE LFLDLCKRMIETAQVDERAKG NGSSQPGTARRGVQIIDDEPQA QTSGGGCCSSG
10020	40388	A	10081	1	1467	
10021	40389	A	10082	2	244	
10022	40390	A	10083	1	257	
10023	40391	A	10084	1	558	
10024	40392	B	10085	41	618	
10025	40393	A	10086	1	591	

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10026	40394	A	10087	128	851	KMEKEKGNDDGIPDQENSLDFS EHFNQLELLETHGHLIPTGTQSL WVGNSDEDEEQDDKNEEWYR LQEKKMEKDPSRLLWAAEKN RLTIVRRLSEKATHVNTVRDE DEYTPLHRAAYSGHLDIVQELI AQGADVHAIVTDGWTPLHSA CKWNTRVASFLLQHDADINA QTKGLLTPHLAAAGNRDSKDT LELLLMNRVYKPKLKNLEET AFDIARRTSIYHYLFEIVEGCTN
10027	40395	A	10088	2	264	NKQPIWIPSRHLKPYHEPDAKE EIPGGS*GPTSCSHVETDAEDP NCHEQIILSNTATHLGTQEAIVI DGRKKPEESRTTSHICRCRS
10028	40396	A	10089	2	461	
10029	40397	A	10090	2	749	
10030	40398	B	10091	1	1077	
10031	40399	A	10092	1	1114	MPQNSLEECALGLGKSLQEN VNNFPKTKLFQFLKLTNWILPKI TKFKPIEGAENVFTDGSSNGKA SYFGLKGKVFQTPYTAQKVE LVAVIEVLTAFDMPVMSISDST YVVHSTQLTENAQLRLHTDEQ LMTLFSQLQTAVR/CFAVMGIP ASRKTDNVPGYTIQTLATFFSM WNKHITGIPYNSQGGAIIVGRIN LSLKQRLQKQKEGNNREYRTPQ MQLNLALLALIFLSLSKGQMLS AAEQHLQKPPAKTEAEQLIWW RDTKTRSWIEGKIITCGRGYAC VSPGQNZQPIWTPSRHLKPYHE PDAK/KRFREDPEDFPSCSHVKT DAEEDPNCHEQHPNTAIHLRS DQEAVTDGRRKPEESGTTSHNE
10032	40400	A	10093	239	783	RRAPGTAPDAGPELRS/LIHL GPACIFLRKGFAENRQPVQLRE AFREFDKDKDGYINCRDLGNC MRTMGYMPTEMLIELSQQIN MNLGGHVDFFDFVELMGPKLL AETADMIGVKELR/DAFREFTD NGDGEISTSELREAMRKLGLHQ VGHRIEIEIRDVDNLNGDGRVD FEAPFPSSN
10033	40401	A	10094	1	304	
10034	40402	A	10095	3	154	
10035	40403	B	10096	126	251	
10036	40404	B	10097	122	2916	

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10037	40405	A	10098	3	2433	LAELSSLVRLRLSHNSISHIAEG AFKGLRSLRVLDLDHNEISGTIE DTSGAFSLGLDSLKLTLFGNKKIK SVAKRAFSGLEGLEHLNLGNG AIRSVQFDAFVKMKNLKEHIS SDSLFLCDCQLKWLPPWLI GRML QAFVTATCAHPESLKGQSIFSV P PESFVCCDDFLKPQIITQPETTMA MVGKDIRFTCSAASSSSSPMTF AWKKDNEVL TNADMENFVHV HAQDGEVMEYTTILHLRQVTF GHEGRYQCVITNHFGSTYSHKA RLTVNVLPSTFKTPHDITIRTTT MARLECAATGHPNPQIAWQKD GGTDFFPAARERRMHVMPDDD VFFITDVKIDDAAGVYSCTAQNS AGSISANATLTVLETPSLVVPLE DRVVS VGETVALQCKATGNPP PRITWFGDRPLSLTERHHLTP DNQLLVVQNVVAEDAGRYTCE MSNTLGTERRAHSQSLVLPAAAG CRKDGTTVGIFTIAVVSSIVLTS LVWVCIIYQTRKKSEESYVNT DET VVPDVPSYSSQGTLSDR QETVVRTEGGPQANGHIESNGK ASVTVKQSSAVTVSLGAGGGL QVFTGQVPGIRWGKLGEVEGG VCPDRDASHFEPDTHSVACRQP KLCAGSA YHKEPWKAMEKAE GTPGPHKMEHGGRVVCSDCNT EVD CYSRGQAFHPQPVSRDSAQ PSAPNGPEPGSDQEHSPHHQC
10038	40406	A	10099	1	164	
10039	40407	A	10100	368	566	

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10040	40408	A	10101	3	1160	RDQRGYRDDRSPAREPGDVSA RTRSGGGGGRSATTAMPPVPVN GNLHQHDPQDLRHNGNVVVA GRPSCSRGPRRAIQKQPAGGR RSRGPAAGGLCLQPPDGGTC VPEEPPVPPMDWEALEKHLAG LQFREQEVNRNQ/QARTNSTSA QKNERESIRQKLALGSFFDDGP GIYTSCKSKGKPSLSSRLQSGM NLQICFVNDSGSDKSDAADS KTETSLDTPLSPMSKQSSSYSD RDTTNEESES LGWTWDFLYKG KRNLQAEAKMALAMAKPMAK MQVEVEKQNRKKSPVADLLPH MPHISECLMKRSLKPTDLRDLI MGQLQVIVNDFISQIKSLNEEW VQLLLAQDELHTEQDAMLVDIE DLTRHAESQQKHMAEKMPAK
10041	40409	A	10102	1	506	RGRPRTEPDPCCPRAAAGARPS GPG/QDLPRRLPGSPGAPGAG GGAGTAAGRKGPGLPPEEAAD GAWRLGEGWAAASEEPAPPGP HTSQRGASPPQPGWARAAGLS NQPTKDRIFGGSHKAA PQASAD SPTSLQCGAAGHCPKASRRALG DNPETEATSSLSPTEWLQ
10042	40410	A	10103	1	429	MGSRLNWMEVIEQCTYLHLVLI KCMFFWNRQHRGGIQEKAALK QRTPRIFHEKNTPCYLLVQE*H RSNAFGEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEE EETLFSNM
10043	40411	A	10104	4	122	
10044	40412	A	10105	53	619	ILVWSIVPEGKILWGTKQQRD SRTQRLLLKSPWRAKQSVWEE/ ERKKKNKEEKEEKEEKEEKK EKEKEKKRKKRKKKKKKKK KKKKKKKKKKKKKKEEEEEE EDEEEEEEEEEKKKEEKEKV EKKKEKK/QEEKEEN/EEEEK EEEEKEKSSSKYSLDSVPTL LISLVWILNTPELLQPA
10045	40413	A	10106	2821	4680	
10046	40414	A	10107	18	1535	
10047	40415	A	10108	3	1494	
10048	40416	A	10109	3	617	
10049	40417	A	10110	3	1142	
10050	40418	B	10111	1	2151	
10051	40419	B	10112	1	1461	
10052	40420	A	10113	1	1248	
10053	40421	A	10114	2	1624	

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10054	40422	A	10115	1	1416	
10055	40423	A	10116	1	2262	
10056	40424	A	10117	1	1791	
10057	40425	B	10118	1	1497	
10058	40426	B	10119	1	1599	
10059	40427	A	10120	1	1722	
10060	40428	A	10121	1	3168	
10061	40429	A	10122	1	1083	
10062	40430	A	10123	1	589	MGAIFYDKPTANIILNGQKIEAF PLKTGIRQGCPISLILFNIVLEV LARAIRQKEIKVIQVGVKEEVK LSLFADDMMIVYLEDPIISAPNLL KLISNFSKVSQYKINVQKSQAF LYTNNRQTESQIMSELPFTIASK RKYLGIQLTRDVKDLFKENYK PLLKEKEDTNKWKNI PCSWVG RINIVKMAILPKPYVES
10063	40431	A	10124	1	1566	
10064	40432	B	10125	1	2406	
10065	40433	A	10126	1	2478	
10066	40434	B	10127	69	1259	
10067	40435	B	10128	225	997	
10068	40436	A	10129	2	1124	
10069	40437	A	10130	1	2058	
10070	40438	A	10131	258	823	TLMQKSSAKYWQTESSTSKSL STMIKWASSLGCKAGSIYANQ* M*SSI/YTNNRQTESQIMSELPFT IASKRIKYLGIQLTRDVKDLFKE NYKPLLKEIKEDTNKWKNI PCS WVGRINIVKMAILPKVIYRFNAI PIKLPMTFFTELEKTTLKFI RNQ KRACIAKSILSQTKLEASRYLTS NYTTRLQ
10071	40439	A	10132	1	1512	
10072	40440	A	10133	1	992	
10073	40441	B	10134	1	2019	
10074	40442	A	10135	1	1203	
10075	40443	A	10136	1	1578	
10076	40444	A	10137	1	2956	
10077	40445	A	10138	1	1983	
10078	40446	A	10139	1	3156	
10079	40447	A	10140	1	3325	
10080	40448	A	10141	1	1870	
10081	40449	A	10142	1	1446	
10082	40450	A	10143	1	2310	
10083	40451	A	10144	1	1293	
10084	40452	A	10145	1	1038	
10085	40453	A	10146	1	1713	
10086	40454	A	10147	1	2271	
10087	40455	A	10148	1	3654	
10088	40456	A	10149	1090	1647	

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10089	40457	B	10150	1	1248	
10090	40458	A	10151	1	1884	
10091	40459	A	10152	1	1140	
10092	40460	B	10153	1	1545	
10093	40461	A	10154	1	3300	
10094	40462	A	10155	1	1824	
10095	40463	A	10156	1	1023	
10096	40464	A	10157	1	2169	
10097	40465	A	10158	1	2661	
10098	40466	A	10159	1	1104	
10099	40467	A	10160	1	1668	
10100	40468	A	10161	1	1945	
10101	40469	A	10162	1	3303	
10102	40470	A	10163	1	1382	
10103	40471	A	10164	1	399	MPPVDASRDRLRLNPLSSVKAK PNEYLLLVQVLFLNRNTKEGLI RLARYPDLLQQTESQIMSELP FTIASKRIKYPGIQLTKDVEDLF KENYKPLLSKIKEDANKWKNP CSWIGRINIVKMAVLPKKKIIV
10104	40472	A	10165	1	2218	
10105	40473	B	10166	1	2562	
10106	40474	A	10167	1	3169	

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10107	40475	A	10168	1	2105	MKAIEIKMFFETNENKDDTTYQN LWDAFKAVCRGKFIALNAHRR KQERSKIDNLTSQLKELEKQEQ THSKASRRQEITKIRAELEKEIET QKTLQKINESRSWFFERINKIDR PLARLIKKKREKNQIDTIKNDK WDITTDPTETITIREYYKHLA NKLENLEEMDKFLDTYTLPRLN QEEVESLNRPTGSEIVAIINSLP TKKSPGPDGFTAEFYQRYKEEL VPFLLLKLFQSIGKEGILPNSFYE ASIIIPKPGRDTTKKANFRPISL MNIDAKILNKILAKRIQQHIKKL IIHHDQHINKAKDKNHMIISIDAE KAFDKIQQFFMLKTLNKLIDG TYFKIIRAIYDKPTANIILNGQKL EAFPLKTGTGRCPLSPLFNIV LEVLAIRAIQEKEIKGIQLGKEE VKLSLFADDMIVYLENPIVSAQ NLLKLISNFSKVSQYKINVQKS QAFLYTNNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKVE NYKPLLEKEIEDTNKWNIPCS WVGRINIVKMAILPKGFCFRFN HHQTGFSPAGANQRGLAATLS GPGGEGQSAVARLTGEKKNHP GAQYANRLSPRVGRFINAAGTT GFPTGKRAVSATQLMDFADFG TTIKQDFRLLGQTSVDRLLQLS QQQAVKGNQLLPVSLVVRKTT LAPNTQTASPRALADSLMQLA RQVSRLESGQ
10108	40476	A	10169	1	1689	
10109	40477	A	10170	425	1333	
10110	40478	A	10171	1	2274	
10111	40479	A	10172	1	3828	
10112	40480	A	10173	3	3130	
10113	40481	A	10174	1	960	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 50,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, V = possible nucleotide insertion)
10114	40482	A	10175	746	2470	TLMQKSSIKYWQNESSTSKSL STMIKWASSLGGCAWPNIRKSI KVIQHINRAKDNHMIISDAEK AFDKIQQPFMLKTLNKLIGDGT YFKIIRAIYDKPTANILNGQKLE AFPLKTGTRQGCLSPLLFNIVL EVLARAIRQEKEIKGIQLGKEEV KLSLFADDIMIVYLENPVSAQN LLKLIRNFSKVSGYKINVQKSK AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLLKEN YKPLLKEIKEDTNKWKNIPCS WVGRINIVKMAILPKNWKKTT LKFIWNQKRAHITKSILSQKNK AGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM LHTYNYLIFDKPEKNKQWGKD SLFNKWCWENWLAICRKLKLD PFLTPYTKINSKWKDLNVRPK TIKLEENLGITIGDIGMGKDFM SKTPKAMATKAKIDKWDLIK KSFCTAKEATIRVNRQPTKWEK IFATYSSDKGLISRIYNELKQIY KKKTNNPIKKWKDMNRHFA KEDIYA AKKHKMKCSPSLAIRE MQIKTTMRYHLTPVRMAIIKKS
10115	40483	A	10176	1	3492	
10116	40484	A	10177	1	3139	
10117	40485	A	10178	637	2760	
10118	40486	A	10179	2	3932	
10119	40487	A	10180	1	1865	
10120	40488	A	10181	1	5754	
10121	40489	A	10182	959	1615	
10122	40490	A	10183	701	6973	
10123	40491	A	10184	3	3319	
10124	40492	A	10185	1	3296	
10125	40493	A	10186	1	2296	

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10126	40494	A	10187	1614	2615	TLMQKSSIKYWQTESSSTSKSL STMIKWASSLGMQGWFNICKSI NVIQHINRTKGKGMHMSIDA AFDKIQQPFLUKTLNKLIGDGT YLKIIRAIYDKPIANIILNGQKLT FEKFPLKIGTRQGCPLSPLLFNI VLEVLRARIRQEKEIKIGIQLAKE EVKLSLFADDMIVYLENPVSV QNLLKLISNFSKVSGYKIYKIDV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQTRDVKDL FKVENHKPLLEIKEDTNKWKNI IPICSWVGGRINLVKMAILPKVI YRFNAIPIKLPMFTTFTELEKNYF KVMHEPKKEPVLPSQS
10127	40495	A	10188	141	401	
10128	40496	A	10189	1	156	MQFPKTKTKKKEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEGEE EKEEII
10129	40497	A	10190	1	1446	

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10130	40498	A	10191	272	2722	ETSCLPLVRVHYAEAITGRCTAP EDEGSLGQKPPARRSNNRTEGA WGKRQLMSSP/STEPVCLTIEG QEIDFLDGTGAASFVLSICPGRL SSTSVTIQGILQPPVTRYFSHLL SCNWETLLFSHAFLLMPERPTG LLGRDILAKAGAIYMNMGNKL PICCPLEEINPEVWALEGQFG RAKNAHPVQIRLKDPPTFFPYQR QY/PLRPEAHKGLQNIVKHLKA QGLVRKCSSPCNTPILEVQRPRL VQDLRLINEAVISLYPVVNPYPT LLSQIPEEAEWFTVLDLKDAFF CVPLHSDSQFLFAFEDPTNHTS QLTWMVLPQGFDRDSPHLFGQA LAKDLGHFSSPGTLVLQYVDDL LLATS*EALCQQA TLDDLNFLA NQGYKVSMSKAQLCLQQVKY LGLILAKGTRALSKE*IQPILAY PRPKTLKQLREFLGITSCRLWI PGYSETARPLYTLIKDTQRANT HLVEWESEAETAFKTLKQALV QAPGLSLPTQQNFSLYVTERAG IALGVLVTQTRGTPQVAHLSK ETDVVAKGWPHCLRVVAAVA VLVSEAIKIQGKDLIVWTTHEV NGILGAKGSLWSDNCLLRYQ ALLLEGPVLIQICTCMALNPATF LPEDGEPIKHDCQOIIVQTYAAR DDLLEVPLTNPDLNLYTDGSSF VENGI/RKVSVDVTILESKPLPPGT SAQLAELVALTWALELGKGR

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10131	40499	A	10192	1	2529	MTQEPSAIMREVPEMVNLIKGT GDIHNTEIQNDNGKVGMTKCM AKPKDELRLNLKILSESLESAQR QGVSKQEKVLQCRRAQDLQPT MPEPPIPSMGSCAARASPTSATP CSRAPSPIDHPTAAKCRMRMAR YWQAAPPAALVLDQLGEASW APESANLVGKWRTFVSSSGTA NAPISTLSKQTTGLYQSAGCGW GQNLGAKYRAPVGQLKATSTA ARLKTRVSGFLGKGLTTPDSS ELGPLDPTDHTSQLTWTVLPQG FRDSPHLFGQALAQDLGHFSSP GTLLIQYVDDLLLATSEALCQ KATLDLLNFLANQGYKVSRLK AQLCLQSEIARPLYTLIKETQR ANTHLVVSEPEAVI/AFETLKQA LVHAPALSLPIGQNFSLYITERA GIALGDLTQTCGTPQPVAYLS KEIDVVAKGWPHCLRVVAAVA ILVSEAIKIMQGKDLTVWTTHD VNGILGAKGSLWLSDNHLLRY QALLLEGLVLQICTCVALNTAT FLPEDGEPIDHCQIIIVQTYAT RDDLLEVLPTNPDNLNYTDGSS VVENGIRRAGYAIIVSDVTILESK PLVPGTSAQLAELVALTRALEL GKGKIIINVYTDISKYAYLILHAH AAIWKEWEFLTSGNPHGCHRE VMELLHVMVQETKEVGVLYHYS HQNGKERGEQQRKQLAEASAA FLWGRALDLQPTMPEPPIPSMG
10132	40500	A	10193	1	197	
10133	40501	A	10194	1	259	
10134	40502	A	10195	1	295	
10135	40503	A	10196	1	439	
10136	40504	A	10197	1268	1420	
10137	40505	A	10198	1	389	
10138	40506	C	10199	1	298	
10139	40507	A	10200	2	90	
10140	40508	A	10201	3	1252	
10141	40509	A	10202	2	82	WMKLETSKLT*EQTKHKCMFSLISGS
10142	40510	A	10203	149	244	
10143	40511	A	10204	485	668	
10144	40512	B	10205	1	598	
10145	40513	C	10206	422	784	

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10146	40514	A	10207	3	899	IYNHLIFDKPKDNKQWGWK\DSL FNKWCWENWLAICRKLKLDPF LTPYTKINSRWIKDLNVRPKTIK TLEENLGNTIQDIGMGKDFMTK TPEAMATKAKIDKWDLIQLKSF CTANETVIRVNRQPTEWEKIFAI IYPSDKGLISKIYKELYEKKTN LIKKWAKDMNRHFKEDFYEA KKHEKSSLLQGQVTKGGCCLP MNL LGTYRSEENPSEYQRRQLI KTLRVCKPSSSYFLTSDFLDTPS FSCEPTQTNELQGCSLRFRVAT AAGPVQVRGARLPFAAPERGL AQIPRQMDSKI
10147	40515	A	10208	3	352	APGRRRLCQPAAGPGAWPGS AVPGSVSPADARSPISGPSRAL RRHLRPSAAGPGLEIPHTDPH LPGVDYKEGRP/PSGKAGRGGP/ PGKGSASGARALGVAAAA TPRSTL
10148	40516	A	10209	1	510	
10149	40517	A	10210	73	327	
10150	40518	A	10211	1	957	MWSTCKLHGQAKYILCAEEL SWGAAASCLHGSTMSTTVVSMA CVGAWPLMGGQDKP/FLSARP STVVPRGGHVAE/RCHYRRGFN NFMLYK/EDRSHVPIFHGRIFQE S/FIMGPVTPAHAGTYRC/RGSR PHSLTGWSAPSNP/LVIMVTGN HRKP/SLLAHPGPLLKSGETV/L QC/WLSA/PSDPLDIVIT/GWENP CLSHVL*S*SHS*ELPADDGEKH GQMQRPEKGT*NPSSWSPSTE/ PSSKSGICR/HLHVLIGTSV VIFL FI/LLFFLLYRWCSNKK\DSDE QDPQEVITYAQL/NHCVFIQRKIS RPSQR/KTPLTDTSVYELPNA
10151	40519	A	10212	351	637	AWIGDMGLDWRYGLRVEISA WSGDMGLEWRYGL/REGMFN DTLRLIGEHHDGVSKANFSISR MKQDLAGTYRCYGSVTHSPYQ LSAPSDPLDIVII
10152	40520	A	10213	1	1314	
10153	40521	A	10214	1	1008	

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10154	40522	A	10215	3	1080	GQDKPLL SAWPSLVVPLGHVIL RCHSYLGFNNFSLYKEGVHRRKP SLLAHIPGRLVKSEETVILQCWS DVRFEHFLHREGFKDTHLI GEHHDGVSKANFSIGPMQDL AGTYRCYGSVTHSPYQLSAPSD PLDIVITGLYEKPSLSAQPGPTV LAGESVTLSCSSRSSYDMYHLS REGEAHERRFSAAGPKVNGTTFQ ADFLPGATHGGTYRCFGSFRD SPYEWSSNDPLLVSVTGNSRY LHALIGTSVVIIPFAILLFLLHR WCANKNAAVMDQEPAGNRT VNSEDSDEQDHQVSYA*L ¹ DH CVFTQREITRPSERPKTPPTDTS MYIELPNAEPRSKVVFPCRAPQ
10155	40523	A	10216	3	1379	
10156	40524	A	10217	352	1825	
10157	40525	A	10218	1	1497	MGLEWRYGPGGADM ¹ DLEWRY GPGVEMVWWSGDMGLEVEIR AWSGDMGLEWRYEPGDGDMG LEWRYGPGGGQDKPLLSTWPS LVVPPEHVTLRCHSNLGFNNFS LYKDDGVPVPELYNRIFWKSLF MGPVTPSHTGTYRCRGSHTHSP SGGSAPSNPLVIVVTGFRRKPSL LAHPGPKVKSEETVILQCWSDV MFEHFLHREGTFNHTLRLIGE HIDGVSKGNFSIGRMTQDL ¹ AGT YRCYGSVTHSPYQLSAPSDPLD IVITGLYEKPSLSAQPGPTVL ¹ AG ESVTLSCSSRSSYDMYHLSREG EAHERRLPAGPKVNRTFQADFP LDPATHGGTYRCFGSFRD ¹ SPYE WSKSSDPLLVSVTGNSSNSWPS PTEPSETGNPRHLHVLIGTSVV KLPFTILLFLLHRCWCSNKKNA SVMDQGPAGNRTVNREDSDEQ DHQVSYA*L ¹ DHCVFTQ ¹ RKITP PSQRPKTPPTDSSMYIELPNAES RSKAVFCPRAPQSGLEGIF
10158	40526	B	10219	114	1944	

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10159	40527	A	10220	20	1138	AGARPPVCTGSTMSLMVIMAC VGFFLLQGAWPQEGVHRKPSF LALPGHLVKSEETVILQCWSDV MFEHLLHREGKFNNLHLIGE HHDGVSKANFSIGPMMPVLAG TYRCYGSVPSPYQLSAPSDPL DMVHGLYEKPSLSAQPGPTVQ AGENVTLSCSSRSSYDMYHLR EGEAHERRLPAVRSINGTFQAD FPLGPATHGGTYRCFGSFRDAP YEWSNSSDPLLVSVTGNPSNSW PSPTEPSSKTGNPRHLHLVIGTS VVKIPFTILLFFLLHRWCSDKKN AAVMDQEPAGNRTNVSSEDSDE QDHQEVSYA*L DHCVFTQRKIT RPSERPKTPPTDSMYIELPNAE PRSKVVECPAPQSGLEGIF
10160	40528	A	10221	1	1334	MSLMVVSMAVCVGLFLVQRAGP HMGQDQKPFSLAWPSAVVPRG GHVTLRCHYRHRFNFMPLYKE DRIHIPHFHGRIFQESFNMSPVTT AHAGNYTCRGSHPHSPTGWSA PSNPVVMVTGNHRKPSLLAHP GPLVKSGERVILQCWSDIMFEH FFLHKEGISKDPSRLVQGIDHG VSKANFSIGPMMQDLAGTYRC YGSVTHSPYQLSAPSDPLDIVIT GLYEKPSLSAQPGPTVLAGEV TLSCSSRSSYDMYHLRGEAHE ERRFSAGPKVNGTFQADFPLGP ATHGGTYRCFGSFRDSPYEWSN SSDPLLVSVTGNPSNSWPSPTEP SSETGNPRHLHLVIGTSVVHILFI LLLFFLLHRWCSDKKNAAVM DQESAGNRTANSEDSDEQDPQ EVTYQLNHCVFTQRKITRPSQ RPKTPPTDIIIVYTELPNAESRSK
10161	40529	A	10222	50	492	RARHRVTRPSIRKHSGHIRRLC LTCSSGVFLQGLRAGSRGTGPG LRTGWRLSPRAPRRRLHTPSAS SP*CSQ*RGPSAGTAAGARRRW RCRGQLRHPAGTSPPGRRWTG TACGPPAAPPAWHSSWSCPHS GAGPPWSPACRTASL

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10162	40530	A	10223	3	3159	QAEFAAASTTPALGSDGVRVT MDSALTARDRVGVQDFVLLN FTSEAAFIENLRFRFENLIYTYI GPVLVSVNPNRYDLQIYSRQHME RYRGVSFYEVPPHLFAVADTV YRALRTERRDQAVMISGESGA GKTEATKLLQFYAETCPAPQR GGAVDRLLQSNPVLEAFGNA KTLRNDNSSRFKYMVDVQDFD KGAPVGGHILSYLLEKSRVVHQ NHGERNFHIFYQLLEGGEETL RRLGLERNPQSYLYLVK
10163	40531	A	10224	1	2810	MLNGCAHAHPIFPTRILSECPRG MLRAGFHLLNRREALPPSRSHIS AAVLAPGALLSWGPDHPLELY GLHSHQDPPTYEGVKGAPVG GHILSYLLEKSRVVHQNHGERN FHIFYQLLEGGEETLRLGLER NPQSYLYLVKGQCAKVSSINDK SDWKVVVKALTVIDFTEDEVE DLLSIVASVLHLGNIHFAANES NAQVTTENQVKYVLRLLSVE GSTLREALTHRKIIAKGEELLSP LNLEQAA YARDA
10164	40532	A	10225	1	416	FRGVARQLRTSAMTPVNGAH KDADLWSSHDKMLAQPLKDS VEVYNIKKESNRQRVGLELIAS ENFASRAVLEALGSLNNKYSE GYPGQGSPANFAVYTALVEPH GRIMGLDLPDGGHLTHGFMTD KKKISATSI
10165	40533	A	10226	135	840	GSPANF/AVYTALVETHGCMIG LDLPDGGHLTHGFMTDKKKIS ATSIFFESMPYKGGPHNHTIAG VAVALKQAMTLEFEVYQHVV VANCRALEALTELGYQTVTG CSDKHLILVDLHSIKGTDGRRRA EKVLEACSIACNKNTCPDDRNT LRPSGLRLGNPALTSGLLEKQ FQKVAFHFIHRGIELTLQIQSNAG IRATLKEFKERLAGHKYQGCV QALQEEVESFTLFLPLGPLPDF

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10166	40534	A	10227	2	1355	QLRTSAMTMPVNGAHKADADL WSSHDKMLAQPLKSDSDEVYNN IHKESNRQRVGLLEIASENFAS RAVLEALGSLNNKYSEGYPG QRYYYGGTEFIDELETLCQKRAL QAYKLDPPQCVGVNVPYSGSP ANFAVYTALVEPHGRIMGLDLP DGGHLTRGLMTDKKISATSIF F*SMPLYKANPETGYINYGGLEE NARLFHPKLIIAGTSCYSRNLEY ARLRKIADENGAYLMADMAHI SGLVAAGVVPSPFEHCHVVTIT THKTLRGCRAGMIFYRKGVAV ALKQAMTLEFKVYQHQQVAN CRALSEALTELGKIVTGGSDN HLILVDLRSGKTGGRAEKVL EACSIACNKNKTCPGDRSALRPS GLRLGTALTSGLLLEKDFQKV AHFIHRGIELTLQIQSDTGV RAT LKEFKERLAGDKYQAADVQALR EEVESFASLFLPLGPDF
10167	40535	A	10228	2	243	GTACNPAWPPGLAPHLTHYA DLLPGSPFHVALPPESELWETP DVSLITGPRLGQTPVTEAVSGR RGIAIAYEDEGSG
10168	40536	A	10229	1	1194	MESMFSSPAEALQRETGVPL LTPLPDLGVYELERVAGFVRD LGCERVALQFPDQLLGDVAV AARLEETGSKMFILGDTAYGS CCVDVLGAQAGAAQLIHFGP ACLSPPARPLPVAFV/LSSFTCG LGALCQGL*GPEPRPQSACGAA GEPACAHALDTGKTQDEGAR AGRLRARRRYLVERARDARV GLLAGTLGVAQHREALAHLRN LTQAAGKRSYVVALGRPTPAK LANFPEVDVVFLLACPLGALAP QLSGSFQPI LAPCELEAACNPA WPPGLAPHLTHYADLLPGSPF HVALPPESELWETPDVSLITGD LRPPPAWKSSNDHGSLALTRP QLELAESSPAASFSSRSWQGL EPRLGQTPVTEAVSGRRGIAIA
10169	40537	A	10230	35	429	KEKRYLVYLGCDCLEK*ESV* TNPVQPIELSAMMAYPVAALSP HVA/RLNT*MTNVTEKLSF*S*L T*I*V*PHVFSGYCTGQCRSS*A SSSSSSSSSSSSSSSSSSSSSS SSASDK*WAEASPRVR

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10170	40538	A	10231	73	393	RTQAPKLSQGGPRCIPPPKLCLE MESMFSSPAEAAALQRETGVPG LLTPLPDLGRSVALQFPDQLLG DAVAVAARLEETTGSKMFLG\
10171	40539	B	10232	191	367	DTAYGSCCVDLGAEQAGAQAQ
10172	40540	A	10233	131	1681	RTQAPKLSQGGPRCIPPPKLCLE MESMFSSPAEAAALQRETGVPG LLTPLPDLGVYELERVAGFVR DLGGERVALQFPDQLLGDAVA VAARLEETTGSKMFL/LGVDT AYGSCCVDLGAEQAGAQAALI HFGPACLSPPARPLPVAFVLSST FCGLGTLCDLWGPKPRPQSAC GAA\GEPACAHAEALATLLRP RYLDLLVSSPAFPQPVGSLSEP MPLERFGRRLPAPGRRIIEYG AFYVGGSKASDPDLPDLSRL LLGWAPGQPFSSCCPDITGKTQD EGARAGGLRARRRYLVERARD ARVVGLLAGTLGVAQHREAL AHLRNLVQAAGKCSYVLAAG RTPAKLANFPEVDVFLVLAAC LGALAPQLSGSFFQIPAPCELE AACNPWAPPFG/LVWPHLTH/Y IADLLPGSPFHVALPPPESELWE TPDVSLITGDLRPPPAWKSSND HGSLALTTPRQLEAESSPAASF LSSRSWQGLEPRLGQTPVTEAV SGRRGIAIAYEDEGSG
10173	40541	A	10234	3	605	AAAREAAAGRDMLAADLRCSLF ASALQSYKRDVSLRPPASAYAR GDCKDFEALLADASKLPNLKEL LQSSGDNQTPGDLVSLDFYP QKVLTNPQVQ/WECRSFEKDSK S*LGLLTRLFLHRTSCLKLS/SD PANAKFYETKGERDLIYAFHGS RLENFHSIIHNLHCHLNKTSLF GEGTYLTSDSLALIYSPHGHG WQH
10174	40542	A	10235	197	895	LGLLTRLFLHRTSCLKLS/SDP ANAKFYETKGERDLIYAFHGS LENFHSIIHNLHCHLNKTSLFG EGTYLTSDSLALIYSPHGHGW QHSLLGPILSCVAVCEVIDHPD VKCQTKKKDSKEIDRRRARIKH SEGGDIPPKYFVVTNNQLLRVK YLLVYSQKPPKRASSQLSWFSS HWFTVMISLYLLLLLIVFCGLL ALQDRGLPQVCPQIPCGWRPPS EGSQVFETQPG

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10175	40543	B	10236	1	1059	
10176	40544	B	10237	226	522	
10177	40545	A	10238	159	306	LGSGNLP*EINPLSSCSLFREEDP PTTSGPQTNPQKEHLTNFKSAA ED
10178	40546	B	10239	101	397	
10179	40547	A	10240	2	253	LQEFGRKDPPTTSGPQTDQAR EHLTNFKSSA/CQIPWNSGPRLS E*LLPRSSRLSS*RLT/RAQSPW KPTGQSQMLWVTLTVEGT
10180	40548	B	10241	1	409	
10181	40549	C	10242	1	462	
10182	40550	A	10243	1	861	
10183	40551	C	10244	1	140	
10184	40552	B	10245	1	1773	
10185	40553	B	10246	1	320	
10186	40554	C	10247	1	420	
10187	40555	A	10248	273	485	LGSGDLPWGINPLSSCSLLREK DPLTISGPQTHQPKHLTNFKSG PTENRTVQLTWQPLPEPELW PKAL
10188	40556	A	10249	508	558	
10189	40557	B	10250	76	358	
10190	40558	C	10251	83	414	
10191	40559	B	10252	1	1111	
10192	40560	C	10253	1	411	
10193	40561	B	10254	1	1054	
10194	40562	B	10255	57	229	
10195	40563	B	10256	1	222	
10196	40564	A	10257	230	1272	LLCSSACKCLMLGLHFVIVGNI CATLKEKYSSMLHLDVTMKKN GEKRTLQKRKKGMPPHPAYE DLNIAAITLPANVVLHQPSGFRT SGQLDPVWWSLDTDAHEIWCQ DPGLSGGDFPWEITPLSSYSLLH EKDPPTTSGPQTDQPKKHLTNF KSKTKETGFIHGPKTPAPVTDW EGSLPLVFNHCRDTSLLIHPCFK GVRPRRDACLGSPPLAASPAFL EKGQDLINLAFKVYNNRKKLQ FLASTVRQTAATSPAHKNFQMP EPQRPVGPPEPPPTGACYMCRK SGHIWTRNAGSPGFLLSRVPSV WDPTENRTVQLTWQPLPEPEL WPKALCLTDSFPDLLGLAA

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10197	40565	A	10258	1926	2448	DFIAVITTRKQLKTKYNAHHSK QAITKHFSKIDSLILCLKKKIM NRHFSKEDIYAACKHMKKCS SLAIREMQIKTTMRYHLTPVRM AIIKSGNNRRCRGCGEIGTLLH CWWDCKLVQPLCKSMWRFLR DLADPAIPLGLIYPKDYKSCCYK DTCTRMFIALFTIAKTWNQP
10198	40566	A	10259	1	1947	MNIDAKILNKILANRIQQHIKLL IHHDQVGFIPGRQGWFNCKSIN VIQHINRAKDKNHMISIDAEGA FDKIQQLFMLKTLNKLGDGT FKIIRAIYDKPTANILNGKKLEA FPLKTGTRQGCPLSPLLFNIVLE VLARAIQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQN LLKLIISNFSKVSQYKINVQKSK AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLEKEIKEDANKWKNPICSW VGRINIVKMAILPKVIYRFNAIPI KLPMFTFFTELEKTTLKFIWNQK RAHITKAILSQKNKARGITLPDF KLYYKATVTKTAWYWYQNRD IDQWNRTQPSITPHIYNYLIFD KPDKNKQWKGKSLFNKWCWE NWLAIKRLKLDPLTPYTKIN SRWIKDLNVRPKTTKLEENLG ITIQDIGMGMDFMSTPKAMAT KDKIDKWDLIKLSFCTAKETT IRVNRQPTKWEKIFTTYSDDKQ LISRIYNELKQIYKKKTNNPIKK WAKDMNRHFSKEDIYAACKH MKKCSPLAIREMQIKTTMRYH LTPVRMAIIKSGNNRCWRGC GEIGTLLHCWWINWMKKTWH IYTMYYASIKKNEFMSFAGA* MKLETH
10199	40567	A	10260	1	347	TNKIDRPLARLIKKEKKQID AIKNDKGDITDPTETQTITKEY YKHLIYANKLENLEEMDKFFDT YTLPRNLQEEVSLNRPIAGSEI EAIINSLPT/KKSPGPDGFTAKFY QRE

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10200	40568	A	10261	31	809	KPRLNYYVKNAAEASGADAINW KKGY/LVMEDEMNEMKREGKF REKRIKRNEQSLQEWDYVCRP TLHLIDVPETLNAHKRQERSK TDLTSLKLEKQEQTHSKAS RRQEITKIRAELEIETETLQKI NESRSWFFERINKIDRLARLIK KKREKNQIDAINDKGDITSDP TEIQTITREYYKHLAYANKLENL EEMDKFLDTYTLPRLNQEEVES LNRPTGSEIVAIINSLPTKKSPG PDGSTAEFYQRYKEEL
10201	40569	A	10262	209	3816	QGRPTFRFRKYREHHKDTFREE QLQDT*SSDSPKLG*KKC*GQ PERKVKLPTKGSPD*KRISRQ/ KTLQARRQSWFFKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITTDPTIEQITIREYYKHLAYANK LENLEEMDKFLDTYTLPRLNQEE VESVNRPTGSEIAITNSLPTK KSPGPDGFTAIFYQRYKEELVP FLLLKQPIEKEGILPNSFYEASII LIPKPGRDTTKGNFRISLMNI DAKIL
10202	40570	B	10263	1	2265	
10203	40571	A	10264	1	2832	
10204	40572	A	10265	1	2757	

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10205	40573	A	10266	1	2114	MKEKMLRAAREKGRVTHKGK PIRLTADLSAETPQARREWGPFI NILKEKNFQPRISYPDKLSFISEG EIKYFTDKQMLRDFVTTTRPVLK ELLKEALNMERNWYQPLQKH AKNMPNSIILPKGRDITTKEN FRPISLMNIDAKILNKILANRIQ QHKKLIHHDQVGFIPGMQGW NIHKSINVIQHINRTIDKNHMIIS IDAFAFKIQQLFMLKTLNKL GIDGTYLKIRIKYLGQLTREV DLFKENYKPLLNEIKEDTNK KNIPCSWGRINIMKMAILPKVI YRFNAISNKLPMFTFTELEKTTL NFIWNQKRARIKSIKSNKA GGITLPDFKQYKATVTKTAW YWYQNRDIDQWNRTEPSEITPH IYTYLIFDKPEKNKQWKGDSLF NKWCWENWLAVCRKLKLDPP LTPYTKINSRWIKDLNVRPKTIK TLEEILGITQDTGMGKDFMSKT PKAMATKAKIDKWDQIKLKS CTAKETTIRVNRQPTKWEKIFA TYSSDKGLIFRIYNELKQIYKKK TNNPIKKWAKDMNRPFSKEDIY AACKYMKKCSPLAIREMQIKT TMRVHLTPVRMAIKKSGNNR QTESQIMSELPITIAKRIKYLGI QLTKDVKDLFKENYKPLLNEIK EDTNKWKINIPCSWGRINIVK/T WPYCPSQMYMSPTWQPKTLQ LWRQPKYPWKGTHRRKK
10206	40574	A	10267	1	2952	MLLNQGRKLPVFAEETLKFK GTSNKPQTLEQISTIAAQKEAT VMVPGSNQEIPSGAYAIRALGF KHKTGRLEFQTLNLYLQEFLETP QWHLECOQERTVHSPGKAAEA REPSVIDRHLEQESSNWHLVGA ALGQSFQRKEQAIFAVLQPLL VIPRQTGSGVDLQKTPDLQQR GLIVRRKTNKQKGIHVNSTTRE QNWTENEFDKLTGEGFKRWVI TNSSELKEHVLTCQCKEDKNLEK SAIKLELRINKLIQN
10207	40575	A	10268	1	1797	

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10208	40576	A	10269	1	1751	MIISIDA EKAFDKIQQPFMLKTL NKLIGDGYFKIIRANYDKPTA NIILNGQKLEALPLKNGTRQGC PLSPLLFNTVLEVLARAIRQEKE IKGIQLGNVEVKLSLFADDMIV YLENPIVSAQNLLKLISKFSKVS GYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRIKYLGIQLTR DVKDLFKENYKPLLKEIKEDTN KWKNIPCSWVGRINIMKMAILP KVIYRFNAIPIKLPMPFFTELEK TTLKFIWNQKRARIKSILSQK NKAGGITPPDFKLYYKATVTKT AWCWYQNRDIDQWNRTEPSEI TPHIYNLIFDKPEKDKQWGKD SLFNKRCWENWLAICRKLKLD PFLTPYTKINSRWIKDLKVRPKT IKTLQENLGFTIQDIGMGKDFM SKTPTAMGTDKIDKWDLIK KSFCTAKETTIRVNRQPTKWEK IFTTYSSDNLISRIYNELKQIYK KKTNNPIKQWAKDMNRHFSIE DIYAAKHKMKCSSSLAIREM QIKTTMRYHLTPVRMAIHKSG NNRNHLDFKHILGICYL/D*KI YQP*LHLVSRNRKPEKLSPKQA
10209	40577	A	10270	1	4729	
10210	40578	A	10271	1	1428	

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10211	40579	A	10272	1	2718	MALFRVGMITRRLLGHANKFTR DLLVKKLLLYEFVVEIIPGLRTK TTLVGPLETGYTSSDVNSPHF MLDIALSHNVKSTQLLLRPWR NIDCSRNHKNAKKEEQMGDDE INRQQECSSPAMEQSWTENDF DELREEVFRRSNYSELQEEIRTN GKEVKSFEKKLDEWITRITNAE KSLKHLTELKTKARELQLEKQE LTHSKASRRQETKIRAEKKEIE TQKTLQKINESRSWFFKINKID RPLARLIKKKREKNQDTIKND KGDITDPTEIQTITREYYKHLV TNKLENLEEMDKFLDTYVLPRL NQEEVESLNRPTGSEIAIINSL PTKKSPGPDGFTAIFYQRYKEE LVPFLLKLSQSEIKERILPNSSYE ASIIIPKPGRDTTKKNFRPISL MNIDAKILNKILANRTQQHIKK LIHHEQVGCIPGMQGFNIRKS INVQHINRTKDKNHMIISIDAE KLISKFSKVSCHKIN/VKQSQAF LYTDNRQTESQIMSELPFTIASK RIKYLGIQLTRDVKDLFKENYK PLLNEIKEDTNKWKNIIPCSWVG RINIVKMALLP/RFSAIPIKLPMT FFTELEKTTLKFIWN/QKRARIA KSFLSQKNKAGGITLPDFKLYY KATVPKTAWYCYQNRDIDQW NRTEPSEIMLLIYNYLIFDKPDK KKEWGGKDSLFNKWCWENWLA ICRKLKLDPLFTPYTKMNSRWI
10212	40580	A	10273	396	1227	SLGRNSTSQKRVGANIQHS*RK EFSTQNFISSQTTLHK*RRNKIL YRQANAERFCHHQACPKTAPE RSTKVLERNRRLPARLIKKKREK NQIDATKNDKGDITDPTEIQTIT IREYYKHLVANKLENLEEMDK FPDVTYTLPRLNQEEVESLNRPT GSEIAIISKSLPTKKRPGPDRFTA EFYQRYKEELVPFLLKLFQSTE KEGILPNSFYEASIIIAKPGRDT TKKENFRPISL/NIDAKILNKILA NRIQQHIKKLIHHDQVGFIPGM QGWFINI
10213	40581	A	10274	1	2168	
10214	40582	A	10275	1	1845	

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10215	40583	A	10276	1	2877	MENDFDELREECFRQSNYSER EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMFLKTKAQELR EEWRLSRRCQLEERVSAE DEMNMKGEGKFKREKRIKNE QSLQEIWYVVKRPNLCLIGVPE RDGQNGTKLENTLQDVIQENFP NLARQANVQIQEIQRTPQRYSS RRATPRHIVRFTKVEMKEKML RAAREKEIQTTSIYKYKHLTYN KLENLEEMDKFLDTYTLPTLNQ EEVESLNRPTGAE
10216	40584	A	10277	1	1689	MIFSIDAEKAFDKIQPFMLKTL NKLIGIDGMYLKIIRAMYDKPA ANIILNGKLEAFPLKTGTROG CPLSPLLFNIVLEVLAIRAEK EIKGIQLGKEEVKLSLFADDMI VYLENPITSQNLKLSISYKSV SGYKINVQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLNKIKEDT NKWKNIPCSWVGRINIVKMAIL PKVIYTFSAIPLPMTFFTELEK TTSKFIWNQKRARIASILSQKN KAGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM PHIYNILFDKPKDNKQWGKDS LFNKWCWENWLDIWRKLKLD PFLTPYTKINSRSIKDLHVRPKTI KTLEENLGDITQDIGMGKDFMS KTSKAMATKAKIDKWDLIQLK SFCTAKETTIRVNRQPTWEKIF AIYSSDKGLIFRIYKELKQIYKK KTNSPIKKWVKDMNRHFSKEAI YAAKRHMKKCSSLAIREMQIK TTLSLPAQVSVV/RHGLSFCWD SRGICGKSGFLAYSINFPQSH WDQEQVM
10217	40585	A	10278	1	2142	

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10218	40586	A	10279	1	1722	MIISIDA EKAFDKIQQRFMLKTL NKLGDGLYLKIIRAIYDKPTAN IILNGQKLEALPLKGTGRQGCPL SPLQFNIVLEVLARAI RQEKEIK GIQLGKEEVKLSLLADD MIVYL ENPIVSAQNLLKVISNFSKVSGY KINVQKSQAFLYTNNRQTESQI MSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTKK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWYQKRARITKSILSQRNK AGDITLPDFKLYYKATV NKTA WYWHQNRHIDQWNRTKPSEIT LHIYNYLFFDNPDKNKKWGKD SLFNKWCWENWLAICRKLKLD PFLTPTYKINSRWIKDLNIRPKTI KTL EENLGITIQDIGMGKYFMT KTPKAMATKAKIDK WDLIKLK SFCTGKETIIRVNRPQTKWEKIF ATYSSDKGLISRIYNELKQIYKK KTNNPIKKWAKDMNRHFSKED IYA AKKHMKKCSPSLAIREMQI KTTMRYHLTPT/RLIVIGIEELR GKEKLETLYYWNSDTHQV*W LGWP*WKSDHKKEQPSF

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10219	40587	A	10280	1	2076	MDKFLNTYTIPLRNQEEVESLN RSITGSEIEAIHNNLPTRKSPGPD GFTPEFYQRYKEELVPFLKLF QSIKVEGFLPNSFYEGSILITKS GRDTTKKENLRPISLMNINAKIL NKILANQIQHHKLLHHEQVDF IPGMQGWFNIRKSINVIQHNR NDKNHMIISIDAEKAFDKIQQLF MLKTLNKLGDGTYLKIIRAIYD KHTANIILNGQKLEAFPLKTGT RQGCPLSPLLFNIVLEVLAARIS QEKEIKGIGLKEEVKLSLFAD DMIVYLENPIVSAQNLLKLIGNF SKVSGYKISVQKSQAFLYTNKR QTESQIMSELPFTIVSKRIKYLGI QLTRDVKDLFKENYKPLLNEIQ DETNRWKNCSWVGRINIVKM VILP/KELEKTTLKFIWNQKRAR IAKTILSQKNKAGGITLPDFELH YKATVTKTACYLYQNRDIDQR NRTEPSEIMPHIYNYLIFDKSOK NKKWGKDSLFNKWCWENWLA ICRKLKLDPLPPYTKINSRWIK DLNVRPKTIKLEENLGNTIQDI GMGKDFMSKTPKAMSTKAKID KWDLIKLSFCTAKETAIRVNR EPTWEKIFAIYSSDKGLISRIYN EFKQIYKKKTNNPIKKWAKDM NRHFSKEDIYAANRHMKKCSSS LAIREMQIKTTQVGGSEKSSAS ELGNKLIELDQSEEWROKED

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10220	40588	A	10281	1	2685	MGDFNTPLSTLDRSTRQKVNK DTQELNSAPHQADLIDYRTLH PKSTEYTFFSAPHHTYSKTDHIL GSKALLSECKRTEIITNYLSDDS AIKLELRINKLTQNRSTTWKLN NLLDDYVWHNEMKAEIKMFF ETNENKDTTYQNLWDAFKAVC RGKFVALNAHKRKQGRSKIDT LTSQLEKEKQEQTSHKASRRQ EITKIRAEKIEITQKTVQKINES RSWFFERINKIDRLARLIKKKR EKNLIDAIKNDKGDITDPTEIQ TTIREYYKHLANKLENLEEM DKFLDYTLPRLNQEEVESLNR PITGSEIVAIINSLTTKSPGPDG FTAEFYQRAIRQEKEIKGIGLK EEVKLSLFADDMIVYLENPIVS AQKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNI PCSW VGRINIVKMAILPKVIYRFNAIPI KLPMFTFTELKKTTLNFIWNQK RAHIAKS/VLSQKNKAGGITLP DFKLYYKATVTKTAWYWYQN RDTDQWNRTEPSEIMPRIYNYL IFDKPEKNKQWGKDSL FNKWC WKNWLAICRKLKLDPLTPYT KINSRWIKDLNIRPKTIKLEEN LGITIQDIGMGKDFMSKTPKAM ATKAKIDKWDLIKLSFCTAKE TTNRVNRQPTKWEKIFATYSSD
10221	40589	A	10282	1	1996	

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10222	40590	A	10283	1	1778	MIISIDAEKAFDKIQPFMLKTL NKLIGIDGTYLKIIRAIYDKPTAN IIPNGQKLEAFPLK TGT TQGCPF SPLLFNIVLEVLARVIRQEKEIK GTQLGKEEVTLSLFADDMIVYL QNPVSAQNLLKLIGNFSKVSQ YKINVQKSQAFLYTNNRQTESQ IMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFKWNQKRACIAKSILSQKNK AGGIMLPDFKLYYKATVIKTA WYWYQNRDIDQWNRTEPSEIM PHIYNYLIFDKPDQNKQWGKDS LFNKYYWENCLAI CRKLKLDLP FLTPYTKINSRWIKDLNVRKTI KALEENLGNTIQDIGMGKDFMS KTPKAMATKDIDKWDLIKPK SFCTAKETTIRVNRQPTKWEKIF ATYSSDKGLISRNYNELKQIYK KKTIGPIKKWAEDMNRHFSKE DTYAAKKJMKKCSSSLAIREM QIKTTMRYHLTPVRMVIKKSG NNRCWRGCGETGTLSHCWWD CKL/IQPLW/RFLRD*GPKTGGD S*MIQVKY*PQKKKGCPNA
10223	40591	A	10284	3	2875	

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10224	40592	A	10285	1	1838	MIIPIDAEEKAFDKIQPFMLKTL NKLGIHGMYLKIIIRAIYDKPTA NIILNGQKLEAFPLKGTGRQGC LPPLLFNVILEILARAIQEKEIK GIQLGKEEVKLSLFADDMIIYLE NPVSAQNLLKLISNFSKVSQYK INVQKSQAFLYTNNRQTESQILS ELPFTIASKRIKYLGIQLTRDVK DLFKENYKPLLNEIKEDTNKW KNIPCLSIGKINIMKMAILPKVIY RFNAIPIKLPMTFFTELEKTTLK FIWNQKRARIAKTILSQKNKDG GITLPDFKLYYKATVTKTAWY QYQNRDIDQWNRTEPSEIIPHV YNHLIFDKPDKNKKWGDLSLF NKWCWENWLAICGKLLDPFL TPYTKINSRWIKDLNVRPKTIKT LEENLGNTIQDIGMGKDFMSKI PKAMATKAKIDKWNLELKSFC TAKETTISVNRQPTWEKIFAIC LSDKGLISRIYKELKQRHKKKT NNPICKWAKDMNRHFSKEDIY AANRHMKKCSSSLAIREMPIKT TMRYLTPVRMAIIKSGNNRC WRGCGEIGTLSHCWWDCLNVQ PLWKA VWRFLKDLEIIPFDP ISLLG/TYPKDYKSCCYKDTCTQ STFTCRQHLPL
10225	40593	A	10286	1	2046	

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10226	40594	A	10287	1	1700	MEDEMNMKQEGKFREKRIKR NEQSLQEIWYVYKRPNLRLIGV PESDGENGTKLENTLQDIIQENF PNLARQTNIQEIQRMPORYSS RRATPRHIIVRFTKVEMKEKMS RAAREKEIQTIREYYKHLAYAN KLENLEEMDKFLDTCTLPRLNQ EEVESLNRTVTGSEIVAIINSLPT KKSPGPDGFTAIFYQRQESQI MSEFPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLNEIKEDTKK WKNIPCSWVGRINIVKMAILPK VIYTFNAIPIKLPMTFFTELEKTT FKFIWNQKRAHVAKSILSQKNK AGGITLPDFKLYKATVTKTA WYWYQNRDIDQWNRTEPSEIM LHIYSYLIFDKPEKNKQWGKDS LFNKWCWENWLAICRKLKLD PFLTPYTKINSRWIKDLNIRPKTI ETLEENLGITQDIGMGKDFMS KTSKAMSTKAKIDKWDLIKLS FCTAKETTIVNRQPTKWEKIF ATYSSDKGLISRIYNELKQIYKK K'TNNPIKKWVKDMNRHFSKE DIYAAKRHMKKCSSSLAIREMQ IKTTMRYHLTPV
10227	40595	A	10288	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDIYRTLHPKS TEYTFFSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRKKNLTQNRSTTWKLNLL LNDYVWHNEMKAEIKMFFETN ENKDTTYQNLWDTFKAVCRGK FIALNAHKRRQERSKIDTLTSQ KELEKQEQTHSKASRRQETKIR AELKEIETQ

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10228	40596	A	10289	1	2019	MDTIKNDKGDITDPTEIQTTIR EYYKHLKYANKLENLEEMDKFL DTYTLPRLNQEEVESLNRPVRG SEIEAIINSLPT/KKSPGPDEFTAE FYQRKAFFDKIQQAFTLKTNLK LVIDGTYRKIIRAI CDKPTANIIIL NGQKLEAFPLKTGTTRQGCPLSP LLFNIVLEVLDRAIRQEKEITCIG LGKEEVKLSLFAADDMIVYLENP IISAQNLKLSNFSKVSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASKKIKYLGQLTRDVKD LFKENYKPLLNEIKEDTNKWEN IPCSWVGJRNIMKMAILPKVIYR FNAIPKLPVAFFTELEKTTLKFI WDQKRAYIAKSILSQKNKAGVI MLPDFKLYYKATVTTKTA WYW YQNRDIDQWNRTEPSEIMLHIY NYLIFDKPDKDEQWGKDSL FN KWCWENWLDIWRKLKLDPFLT PYTKINSRWIKDLNVRPKTIKTL EENLGNITLIDGMGKDFMSKTP KAMATKAKIDNWDLIKLSKFC TAKETTIRVNRQPTKWEKIFTT YSSDKGLISRIYKELQIYKKKT NNPMNKWAKDMNRHFSKEDI YAAKRHMKKCSSLAIREMQIK TTMRYHLTPVRMVIKKSGNNR PPLSKEQPIFRLSILATTRDGN PAAVENVLHIKATLSFQQTHKA FYFQPS
10229	40597	A	10290	1	3144	MGDFTNPLSTLDRSSQKVNK DTQELNSTLHHADLIDYRTLHP KSTEYTFPSAPHHYTSKIDHVV GSKALLSKCKRTEHTNCLSDHS AIKPELRKIKLTQNRSTTWKLN NLLLNDYVWINKMKAIEIKMFF ETNENKDTTYQNLWDTFKA VS RGKFIALNAHKKQKRCCKIDTL ASQLKEVEKQEQTSHKASRRQ EITKIRAELEIETQKTLQKINES RSWFLERINKIDRPLARLIKKKR EKNQIDVIKNDK
10230	40598	A	10291	1	2274	
10231	40599	A	10292	1	2250	
10232	40600	A	10293	1	822	

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10233	40601	A	10294	1	2605	MKA EIKMFFETNENKDTTYQN LWDAFKAVCRGKFIALNAYKR KQERSKIDTLTSQLEKEKQEQ SHSKAGRRQEITKIRAELEKET QKTLQKINESRSWFFERINKIDR PLARLIKKEKNQIDTIKNDK GDITTNPTETIQTIREYYKHLA NKLENLEEMDTFLDYTLPRLN QEEVGS LNTPTGSEIVAIINSLP TKKSPGPDGFTA EYQRYKEEL PGRVPTKKENFRPISLMNIDAKI LNKILANRIQQHIKKLIHHDQV GFIPGMQGWFNIRKSINVIQHIN RAKDKNHMIISIDAEKAFDKIQ QPFMLKTLNKL GIDGTYFRIIRA IYDKPTANILNGQKLEAFPLKT GTRQGCP LPLFNIVLEV LAR AIRQEKEIKGQLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLIS NFSKVSGYNFYVQKSQAFLYT NNRQTESQIMSELPFTIASKRIK YLGQLTRDVKDLFKENYKPLL KEIKEDTNKWKNPICSVWGRIN IVKMAILPKVIYRFNAIPIKLP TFFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGITLPDFKLYY KATVTKTAWYWYQNRDIDQW NRTEPSEIMPHIYNLIFDKPEK NKQW GKDSL FNKWCWENWLA ICRKLKLD PFLTPYTKINSRWIK DLNVRPKTIKLEENLGITQDI GVGKDFMSKTPKAMATKAKID
10234	40602	B	10295	111	2440	

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10235	40603	A	10296	I	1795	MIISDAEKAFDKIQQPFMLKTL NKLSDGTYFKIIRAIYDKPTANI ILNGQKLEAFPLKTGTGRQCPL SPLLFNIVLEVLARAIHQEKEIK GIQLGKEEVKLSLFAHDMIVYL ENPIVSAQNLLKLI SNFSKVSQI KINVQKSQAFLYTNNRQTESQI MSELPTIASKRKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSGVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIVNQKGACITKILS/QKNK VGGITLPDFKLYYKATVTKTA WYWYQ\NRDIDQWNRKIPSEIM PIINYNLIFDKPEKNRQWGEDS LFNKWCWETWLAIWRLKLDLP FLTLYAKIN*RWIKDLNVRPKTI KTLLENLGITIQDUGMGKDFM SKTPKAMATKAKIDKWDLIQI KSYCTAKENTIRVNRQPTKWE KIFATYSSDKGLITRIYNELKQI YKKKTNNPIKKWAKDMNRHFS KEDIYAACKHMKKCSSSLAIRE MQIKTTMRYHLTPVRMAIIQKS GNNRTKRTIYRRNDDDDNDD NDDDSLMSLSTEIPFSSYSELN VVLHKPRPEPSASTILLHTA
10236	40604	A	10297	I	2851	
10237	40605	B	10298	I	3220	

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10238	40606	A	10299	1	2047	MENDFEELREEGFRSSNYSEL EDIQTKGKEVENFEKNLEECITR ITNTQKCKELMELKTKARELR EECRSLRSRCDQLEERVSA MED EMNEMKREGKFKRIQRNEQ SLQEIWDYVKRPNLRLIGVPET LHPRDEAHLKNLDAIKNDKGD ITTDPTIEQTTIREYYKHLYANK LENLEETDKFLDTYTLPRLNQE EVESLNRPTGSEIVAIINSLPTK KSPGPDGFTAIFYQRYKEEL/PD KQLQQLRIQNQCITKI'SILIHQ QQTNRPNHE*TPHNCFKENKI PRNPTYKGCEGLQGELOTTAQ GNKRGYKQMEHSMMLGRKN QYHENGHTAQGNLQIQCHPH* ATNAFLHRIGKNYFKVHMEPK KSPHRQVNPKEQSWRHHTT *LQTHLQGYSNQNSMVLVPKQR YRSMEQNRALRNNAAYLQLSD L*QT*EKQEMGKGPI**MVLG KLASHM*KAETGSLPYTLKYN QFKMD*RLKR*T*NHKNPRRKP RHYHSGHRHGGQLHV*NTKSN GNKSQN*QMGSN*TKELLHSK KKKNY*QTEQATCKMGENFHN LLI*QRANIQLQ*TQTNLQEK KN KQPHQKVVGKGHEQTLLKRRHL CSQKNHEKMTITGHQRNAN QNHNEIPSHAS*NGNH*KVRKQ VLERMCRNRNTFTLLVGL*TSS

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10239	40607	A	10300	1	2704	MYSHVITVCRHVKNKDILLNR QPTLHRPSIQAHRAIRILPEEKVL RLHYANCKAYNADFDGDEM AHFPQSELGRAEAYVLACTDQ QYLVPKDGGQPLAGLIQDHMVS GASMTIRGCFFTREHYMELVY RGLTDKVGVRVKLLSPSILKPFPL WTGKQHINRTKDKNHMISIDA EKAFDKIQPFMLKTLNKLGD GTYLKIIIRAIYDKPTASII.LNGQK LEAFPLKTGTRQGCLSPLLFNI VLEVLARAIRQEKEIKSIQLGKE EVKLSLFADDMIVYLENPTVSA QNLLKLSMNSFSKVSQYKINVQ KSQAFLYTNNRQTESQIMSGLP FTITSKRITVYLGILTRDVKDLF KENYKPLLEIKEDTNKWKNNIP CSWVGRINIVKMAILPKVIYRF NTIPIKLPMTFLTELEKTTLKF WNQKRAHIAKSILSQKNKAGGI MLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEIMPHI/Y YNYLIFDKPEKNKQWGKDTLF NKWCWENWLAICRKLKLDPFL TPYTKINSRWIKDLNVRPKTIKT LEENLGNTIQDIGMGKDFMSKT PKATATKAKIDKWDLIQLKSFC TAKETTRVNRQPTWEIEIFAIY SSDKGLISRIYNELKQIYKKKTN NPIKKWAKDMNRHFSEEDIYA AKKHMKKCSSSLAIREMQIKTT MRYHLTPVRMVIHKSGNNRRC
10240	40608	B	10301	1	3345	

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10241	40609	A	10302	248	2623	RQWAGVVGRCSHLASWVSSNT SETGAIRSSTEVDAPDDSMMLST CDIDLTAARRAWLGCLPTKKSP GPDGFTAIFYQRCKEELVPFLL KLFQSI/EKEGILPNLFDEASII PKRGRDITTKENFRPISLMNID AKILNKILANRNQQHIKKLIHH DQVGFIQMGQWFNICKSINVI QHINRTKDKNHMISIDAFAKAF DKIQQPFMLKTLNKLGDGTYL KIIRAIYDKPTANIILNGQKLEAF PLKTGTGRQCPLSPLFNIVLEV LARAIRQEKEIKGIQLGKEEVKL SLFADDIMIVYLENPIVSAQNLL KLISNFSKVSAKYINVQKSQAF LYTNNRQTESQIMSVFPFTIASK RIKYLGIQLARNAKDLFKENYK PLLNEIKEDTKWKNI PCSWVG RINIVKMAILPKVIYRFNAIPIKL PMTFFTELEKTTLKFIWNQKRA RIAKSILSQKNKAGGITLPDFK LYLQGLQ*PKTAWYWY\QNRD IDQWNRTEPSEITPHIYNLYLFD KPEKNQWGDLSFNKWCWE NWLATCRKLLKDPFLTPYTKIN SRWIKDLNVRPKTIKTLLENLGI TIQDIGVGKDFMSKTPKAMAT KAKIDKWDLIKLSFCTAKETA IRVNRQPTTWKIFATYSSDKG LISRIYNELKQIYKKK\TNPIKK WAKDMNRHFSKEDIYAANKH MKKCSPLAIREMQIKTMRHY

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10242	40610	A	10303	1	2467	MGDFNIPLSTSDRSTRQKVND TQELNSALHQADLIDYRTLHP KSTHEYTFPSAPHHTYSKIDHIVG SKALLSKCRRTEIITNCLSDHSA IKLEIRIKKLTQNCSTTWKLNLL LLNDYWVNNEMKAEIKMFFEI NEDKDTTYQNRWDTFKAVCR GKFIALNAHKRQKERSKIDTLT SQLKELEKQEQTHSKASRRQEI TEIRAELEKIEITQKTLQKMNES RSWFFEKINNIDRLLARLIKKKR EKNQIDAINKHKGDIITNPTEIQ TTIREYDKHLYANKLENLEETD KFLDTYILPRLNQEVEESLNRPI TGAEIEAIIISLRTKKSPGPGGF TAEFYQRYKEKLIVLEVLARAI RQEKEIKGIQLGKEELKLSLFAD DMIVYLENPVISAQNLLKLISNF SKVSGYKINVQKSQAFLYSNNR QTESQIMSELPFTIASKRIKYLGI QLTRDVKDLFKENYKPLLENV KEDTNKWKINPCSWIGRINIVK MAILPKVIYRFSAIPIKLPMTFFT ELEKTTLKFIWNQKRSRIAKSIL SQKNRAGGITLSDFKLYYKATV TKTAWYWYQNRDIDQWKNTE PSEIMPHIYNYLIFDKPDKNKK WGKDSL FNKWCWENWLAICR KLKLDPFLLPYTKINSRWIKDL NVRPKTIKLEENLGITQDTGM GKDFMSETPKAMATKDKIDKW DLIKLKSFACTAKETTIRVNRQPT
10243	40611	A	10304	2	2480	
10244	40612	A	10305	1	4793	MGDFNTPLSTLDRSTRQKVND DTQELNSALHQADLIDYRTLH PKSTEYTFPSAPHHTYSKIDHIL GSKALLSKCKRAEITNYLSDHS AIKLELRINKLTQSRSTTWKLN NLLNDYWVNNEMKAEIKMFFEI ETKENKDTTYQNLWDAFKAVC RGKFIALNAHKRQKERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELEKIEITQKTLQKINESR SWFFERINKIDRPLARLIKKKRE KNQIDTIKNDK
10245	40613	A	10306	1	4320	

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10246	40614	A	10307	1	3229	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIIDYRTLQ PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRINKLTQSRSTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDDTTYQNLWDAFKAV CRGKFIALNAHKRQERSKIDTL LTSQKLEKQEQTHSKASRRQ EITKIRAEKKEIETK\TLQKINE SRSWFFERIKKTDRPLARLIKKE REKNQIDTI
10247	40615	A	10308	1	3392	MGDFNTPLSTLDRSRQKVNK NTQELNSALHQVQLIDYRTLH PKSTEYTLFSAPHHTYSEIDHVV GSKALLSKCKRTEIITNCLSDHS AIKLELRINKLTQNCSTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDDTYPNLWDTFKAVC RGKFIALNAHKRQERSEIDTL TSQKLEKQEQTHSKASRRQE ITKIRAEKKEIETQKTLQKINESR SWFFEKINKIDRPLARLIKKE KNQIDSIKNDK
10248	40616	A	10309	1	4137	MGKKQNRKTGNSKKQRASPPP KEHSSSPATEQSWMENDFDEL EEGFRSNSYSELREDIQTGKE VENFEKNLEECITRITDIEKCLK ELMELKTKARELHEECRSLRSR CDQLEERVSADEDEMNMKQ EGKFREKRIKRNESQLEIWDY VKRPNLPPIDVPESDRENGTKL ENTLQDVIQENFPNLARQANQI QEIQRMPPQRYSSRRATPRHIIVR FTKVEMKMLRAAREKAFKQ ASRREDIAKVTSQ
10249	40617	A	10310	1	5195	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIHIYRTLH PKSTEYTFFSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRINKLTQSRSTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDDTTYQNLWDAFKAVC RGKFIALNAHKRQERSKIDTL TSQKLEKQEQTHSKASRRQE IMKIRAEKKEIETQKTLQKINE\ SRSWFFERINKIDRPLARLIKKE REENQIDAI

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10250	40618	A	10311	1	2958	MKQEGKFKREKRIKNEQSLQEI WDYVKRPNLHLIGVPESDREN GTKLENTLQDIIQEDFPNLARK ANIQIEIQRTPTORYSSRAATPR HTIVRFTKVEMKEKMLRAARE KGRVTHKGKPIRLTADLSAETL QARRELNQEEVESLNKPVGTGSE VVAIINSLPTKKSPPGDFTAEF YQKYKEEPVPFLLKLFQSIEKE GILPNSFYEASIIIPKPRDRTTK KENFRPISLMNIDAKILNKILAN RIQQHINKK
10251	40619	A	10312	5211	7687	TDTSQKKTFFYAAKRHMKKCSS SLAIREMQIKTTYHAGPDGFTA EFYQRYKEELVPFLLKLFQSIEK EGILPNSFYEASIIIPKPRDRTT KKENFRPISLMNIDAKILNKILA KRIQQHIKLIHHDQVGFIPGM QGWFNIRKSNVQIHNRKADK NHMIISIDAFAFDKIQQPFMLK TLNKLGDGTFFKIIRAIYDNPT ANIILNGQKLEAFPLKTGTRQG CPLSPLLFNIVLEVLAIRQEK EIKGIQLGKEEVKLSLFADNMI VYLENPIVSAQNLLKLISNFSKV SGYKINVQKSQAFLYTNNRQTE SQMSQLPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDT NKWKNIPCSGIEGRINIVKMAIL PKNWKKTTLFIWNQKRAIA KSILSQKNKAGGITVPDFQLYY KATVTKTAWYWYQNRDIDQW NRKEPSEIMPHIYDSLIFGKPKD NKQWKGDSL FNKWCWEDWLA ICRKLKLDPLTPCTKINSRWV KDLNIRPKTIKTEENLGNITQD IGMAKDFMSKTPKAMATKAKI DKWDLIKLSFCTRIAKEPTIRV NRQPTKWEKIFATYSSDKGLIS RIYNELKQIYKKKTNNPIKKWA KDMNRHFSKEDIYAAKHKHM KCSSSLAIREMQIKTTMRYHLT PVRMAIIKSGNNRCWRGCGE TGTLHCWWDCKLAQPLWKS

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10252	40620	A	10313	1	4525	MGDFNTPLSTLDRSTROKVNK DTQELNSALHQADLIDYRTLH HKSTEHTFFAAPHHITYSKIDHIL GSKALLSKCKRTEIITNYLSDHS AIKLELRIKNLTQNRSTTWKLN LLLNYYVWHNEMKAEIKMFFE TNKNKDTTYQNLDWTFKAVCR GKFIALNAHKRKQERSKIDTLT SQLKQLEKQEQTHSKASRRQEI TKIRGELKEIETQKTLHKINESR SWFFERINKIDRLARLIKKKRE KNQIDAIINDKG
10253	40621	A	10314	1	1185	MEDIKRTQNKLESEMKAELAEM KNTLDGINDHGRDSRRKIRKLQ DNGGDDPTGNTQRKKNLINGP SLSVHIGEKRGRRSWAETLTP LQTKALRLGPTTPSARRKCGIV PNLQTRKTEAYRYPDTHPGETP VGTAVLSIQPKLESVIDVRVN MSSFHPEPELQPTQTSVLPDQD ATVAGSTTKFP EEQEARQGRVR ERPATRERPVP GGVSVPGLHHI HFLRGPSPLASLTRITVLEAVV CFFSVWSIVGLSGFHTYLISNSQ TTNEDIKGSWSNKRKGKENYNP YSYGNIFTNCCVALCGPISPRT/ LSHTGQRPTPIECEPHNLVTSA ETLLASKPD/PTEEGTSSPTRRS QQHPPMASPTGPRSHRVCTCL EKREEEGVGQRLSPLCKPRL
10254	40622	A	10315	44	302	GLLGPGPTAC*CGPHCGIHPES SPQSWCLCHSHRSSRAPPLARL SGDRHPGWRTWGGRDARSVA RGQWWCLVEPVLFPFSTRSAFW

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10255	40623	A	10316	3	2182	IRDPGKKPVMFLFHGGSYMEG TGNMFDGSLAAAYGNVIVATL NYRLGVLGLSTGDQAAKGNV GLLDQIQALRWLSENIAHFGGD PERJITIFGRYSQPGLSYHIAFGPV VDGDVVDPDPEILMQQGEFLN YDMLIGVNQQGEGLKFVEDSAE SED/GAFDFTVSNFVDNLVGYG EGKDVLRETIKFMYTDWADRD NGEMRRKTLLALFTDHWVAP AVATAKLHADYQSPVYFYTFY HHCAEGRPEWADAAHGDPEL YVFGVPMVGATDLFPCNFSKN DVMLSAVVMYWTNFAKTGD PNQPVPYDTKFIHTKPNRFEV VWSKFNSKEKQYLHIGLKPR WSRFRGVLVQVFHDICEKEAP KSSLLRKQTQPKKQSSPAVHL RCTMDPVMMTVSPPAHRHRR RGSPTCAHCPVAVAPDTDDE KPHQYPAICSYHWDVPEDWEG FQHTQGTWVPWSQDAPESPQ TIRFQPTVEERPLKTGIWSELGL RAYVYPVNPSPSPAPSHKNG RIVYDARDMRRRLRELTREVE ALSGCYPLASGSSAEETSKNW VYRSLTGSQKMSQLHRVPFFD QEDPDSYLEEDNLPFPYKYP RRGWGFGYQRAGLPSNVGLW GHQGGILASLPPSLYLSPELRC MPKRVEARKCQDLGDSILLLLG SFILLNVWINVVTLLWKHLKSS
10256	40624	B	10317	37	241	
10257	40625	A	10318	2	815	
10258	40626	A	10319	1	943	RAGGQGVG*GWGPPSVPCSVH GGKGL/PPEEGPQVTHLEFGR GDGLLTPWPLTGDGRGPSA/S LASQRTCSQ*GMWLPAAQPSPS HPGPAGTVGQSHLHL*GLLGP PPHCLLMRPTLRDSSRVFTSKL VSPVQPQVQGGPTTRKTVWRS ASWMENLGRKGCQVCSTWPM VVPGGACTSIWEWEADRVTPG GHRGSSCSHAAGGANAAAPHG PRGRPGGHAAAGGRHSTDGRS SCSPRPDPGAARPQSAVHTDY RSPSLGTFLAQPFGESKSDQSA PGIRGQKAPLAVARRGQQTFRP RGQARGRGRTFR

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10259	40627	A	10320	39	621	SCPEEESSLLSPGTSWPLHAW ACSAAQVTGRERVVADWPGY HPGGPTAPHWRAGPLSDKTRPS RDVGTWDTGRAGCPPPPGRNP GPPDQRKALGVVTSFGSQLG NGTPNSCLSPRCQWIQLRGSS RTGPPPPGSVPEAAVSCPGIHT LFLRSGAGKIQG*LLGPGWEL GQAGTEPPLPLAPPPHRSCG
10260	40628	A	10321	1	496	AAATYVQNQSEDCLYNLNLYVP TEDGPLTKKRDEATLNPPDTDI RDPGKKPVMFLHGGSYMEGT GNMFDGSVLAAYGNVIVATLN YRLGVLGFLSTGDQAAKGNYG L/LDQIQALRWLSENIHFGGDP ERITIFGSGAGASCVNLLLSHH SEGLFQKAIQSGT
10261	40629	A	10322	1	4304	MLPVWFTDNLGAAATYVQNQ SEDCLYNLNLYVPTEDEGLTKKR DEATLNPPDTDIRDPGKKPVMFL FLHGGSYMEGTGNMFDGSVLA AYGNVIVATLNLYRLGVLGRYS QPGLSYHIAFGPVVDGDDVVPDD PEILMQQGEFLNYDMLIGVNG EGLKFVEDSAESDEGVSASAFD FTVSNFVDNLYGYPEGKD/DW ADRDNGEMRRKTVLLALFTDH QWVAPAVATAKLHADYQSPV YFYTFYIIHCQAEGRPEWADAA
10262	40630	A	10323	1	2765	MDVGFSRTTVQTLRSRSHCKNIK QKISQWEGRANGISNPEKWCPK DFGVRYNCHQEIIRLKKNPJAER KSKNLDVTSRENVGLDINENTK SHDQSENENKKHEYDDTHFFK NESESNWVCSRVEIESCKEDV LDPETSLPPGNFYTSQILWKKIE ALPPDKLLNLALEHCDSSSEKEL NFRVLDSSYGITKSLENIYSEPE GQECGSPINPLPKPRRTFRYLSE SGVTPYKERNCDKKYCENNSC AQSSLASQPE
10263	40631	A	10324	2	597	RWLIPKVMRIYDTQKKMDREA SQAALQKMLTLLMLPPTFGDLL REEYIGDNGDPQTLQAQFQEM MADSMFVIPALQVAHFQCSRA PVYFYEFGHQPSWLKNIRPPHM KADHVKFTEEEEQLSRKMMKY WANFARNGNPNGEGLPHWPLF DQEEQYQLNLQPAVGRALKA HRLQLWKKALPKIQIELEEPE ERHTEL

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10264	40632	A	10325	2	1766	PGQPLGEQQRVRRQRRTETSEPT MRLHRLRLASAVACGLLLLL VRGQGQDSASPIRTTHTGQVLG SLVHVKGANAGVQTFLGIPFAK PPLGPLRFAPPEPPESWSGVRDG TTHPAMCLQDLTAVESEFLSQF NMTFSDMSMEDCLYLSIYTPA HSHEGSNLPVMVWIHGALVF GMASLYDGSMALAAENVVVI IQYRLGVLGFFSTGDKHATGN WGYLDQVAALRWVQQNIAHF GGNPRVVTIFGESAGGTSVSSL VVSPISQGLFHGAIMESGVALLP GLIASSADVISTVVANLSACDQ VDSEALVGCLRGKSKEILAIN KPFKMIPGVVDGVFLPRHPQEL LASADFPQPVIVGVNNNEFGW LIPKVMRIYDTQKEMDREASQA ALQKMLTLLMLPTTFGDLREE YIGDNGDPQ/TLPKRKF/QKMM ADS/MFVIPALQVAHFQ/CS/RAP VYLPTSSQH/QPSWLKNIRPPH MKADHGDLEFPVRSFFGGNY IKFTEEEELSRKMMKYWANF AR/NGNPNGEGLP/HWP/LFDQE EQYLQLNLQLA VGRALKAHRF /QFWKKALPQKIQ/LEEPPEERH
10265	40633	A	10326	2	435	ILAEFGSLHLEFLHUTELSGNQV FAEKVRNIRKVL RKIEKPFGLYP NFLSPVSGNWVQHHVSVGGGLG DSFYEYLIKSWLMSGKTDMEA KNMYEYEALET/HKLGPEAFWF NSGREAVATQLSESYILRPEV VESYMYLWRQTHNTK
10266	40634	A	10327	3	583	

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10267	40635	A	10328	1	1299	MHLNQLPPILSRLGAVGFFGSM KAHLVSVSRQVRNIRKVLKIE KPFGLYPNFLSPVSGNWVQLPI PGSVAAGEMPASYPYRRAPE VRRVCEALPHHVSVGGLGDSF YEYLKSWLMSGKTDMEAKN MYEALAEIETVLLNVSPGGLT YIAEWRGGILDHMKMGLACFS GGMIALGAEDAKEEKRAHYRE LAVQITKTCYESYAR\SDTKLGP EAFWFNSGREAVATQLSEE/YT YILRPEVVESYMYLWRQTHNP SYREWGWVVLALAEKYCRTE AGFSGDSKTCYSRHPQPTTSR QSFFLAETLNRCLVSACNGPDT GLEARDTAESETVISPAVKGSR GEKAMVRETDKPAKICIGKSK NGKSDLKAASKMDAQFRSLCF EEVTPLWFEKVLNMGASPSPV SPGGLSLEVWSLVMWHKDARP
10268	40636	C	10329	186	401	
10269	40637	A	10330	194	482	
10270	40638	A	10331	224	495	
10271	40639	B	10332	138	1810	
10272	40640	A	10333	1	1351	MGGVGEGPGREGPAQPGAPLPT FCWEQIRAHDPQGDKWLVIER RVYDISRWAQRHPGGSRLIGHH GAEDATDAFRAFHQDLNFVRK FLQPLLIGELAPEEPSQDGPLNA QLVEDFRALHQAEDMKLFDA SPTFFAFLGHILAMEVLAWLLI YL/LGPVWVPSALAAFILAIQ AQSWCLQHDLGHASIFKKSWW NHVAQKFPVMGQLKGFSAHWW NFRHFQHHAKPNIFHKDPDVT VAPVFLGESSVEYGGKKRRYL PYNQQLHYFFLIGPPLLTLVNFE VENLAYMLVCMQWADLLWA ASFYARFLSLSYLPFYGVPGVL LFFVAVRVL\ESHWVFWITQM NHIPKEIGHEKHRDWVSSQLAA TCNVEPSLFTNWFSGHLNFQIE HHLFPRMPRHNYSPVAPLV\KS LCAKHGLSYE\VKPFL\TALVDI VRSLLK\SGDIVLDA\YLHQ
10273	40641	A	10334	43	399	

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10274	40642	A	10335	1	2229	FLKVC PQNNAETFGCLGTGEEK GDRGNQQTQKPLHYKSWSLFHR SCPRDFYGSKVGFQGGKENG G\GESVYGGFFEDGVS\VKDH\ KEFLLSMANRGKDTNGSQFFIT TKPTPHLDGHHVVFGQVTSQG EVVREIENQKTDAAASKPFAEVR ILSC\GELIPKSKVKKEKKRHK SSSSSSSSSDSDSRYS\QSSSDS SDSESATEEKSKKRKKKHKRKN RKHKKEKKKKKSKKSASSES EAEN\LEAQPVLLFRPEIPLP IPENRFLMRK\SPPKADEKERKN RERERERECNPPNSQPASYQRR LLVTRSGRK\KGRGPRRYRTPS RSRSDLFRRS\ETP\PHWRQEM QRA\QRMVSSGER\WIKGDKS ELNEIKENQSRSPVRVKERKITD HRNVSESPNRKNEKEKKVKDH KSNSEKDIRNSEKEDKYKNK VKKRAKSKSRKSKKEKSKSKER DSK\HNRNEEKRMRFKELKGR DHENVKEKEKQSDSKGKDQER SRSEKSKQLESKSNEHDHKS KEKDRRAQSRSECDITKGKHS YNSRTRE\RSRRRDSSSRVRSRP HDRDRSMK\IEYHRYRDQVYS RRVRSRERRTPPGRSRSRDR RRRRRDRSSSEREDSQSRNKDK YRNQESKSSHRKENSESEKRM YSKSRDHNSNNSREKKADRD QSPFSKIKQSSQDDELKSSMLK
10275	40643	A	10336	3	3366	

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10276	40644	A	10337	3	2431	GCLQELSVLFARGEPRGPHNL LHYMLALIGVPEVFWAFLFHCS LGLLEEKLAFLKGEKIVWLRS SFYFQHCLVDKSTLLPSSSVSLG IFHEEKNSGEFPFAKAVRLALV PLRYVKLEDRDNWISVDSVTSE IKLAKLPDFESRYVQNGTYTVK IVAISEDYPRKTITGTVLINVEDI NDNCPTLIEPVQTICHDAEYVN VTAEDLDGHPNSGPFSSVIDKP PGMAEKWKIARQUESTSVLLQQ SEKKLGRSEIQLISDNQGFSCP EKQVLTLTVCECLHGS/GCREA QHDSYVGLGPAALMILAFLL LLLVPLLLLMCHCGKAKGFTF IPGTIELHPWNNEGAPPEDKV VPSFLPVDQGGSLVGRNGVGG MAKEATMKRKVSSAIVKGQH EMSEMDGRWEEHRSLLSGRAT QFTGATGAI/MTTETITARATG ASRDVAGAQAVALNEEFLK NYFTDKAASYTEEDENHTAKD CLLVYSQEETESLNASIGCCSFI EGELDDRFLDDLGLKFKTLAEV CLGQKIDINKEIEQRQKPATETS MNTASHSLCEQTMVNSENTYS SGSSFPVPKSLQEANAELVTEI VTERSVSSRQAQKVA TPLPDP ASRNVIATETSYVTGSTMPTT VILGPSQPQLIVTERVYAPAST LVDQPYANEQTVVTVTERVIQPH GGGNSPLEGTQHLQDVPYVME
10277	40645	A	10338	5	354	RPRLTSQDIKKPDC/DGEDAIGR GFECDLHLEKIVHFALHLEKN VNQSLLEHLKATDKNDPHLC DFIETHYLNEQVKAKELGHDV TNMHEMGAPDSGVAEYLFDKH TLGSDNES

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10278	40646	A	10339	I	2024	GEALMYHTHFSELLDEFSQNVL GQLNDPFLSEKSVSMEVEPSP TSPAPLIQAEHSYSLCEEPRAS PFTHITTSDFSNDDEVESEK WY LSTDFPSTSIKTEPITDEPPGLV PSVTLTITAISTPLEKEEPPLEIEQ WGLIPRARPLFPKIKLEPHEVDQ FLNFSPKEAKHLHIIFPSWAACT CGSSGNSAIRIILAYSALRVPT ETKKPRDLFGKTGREKGKEETS REKLYVAERERKAPVDHLHLP TPPSSHGSDSEGLSPNRLHPF SLPQTHSPSRAAPRAPSA LSSSP LLTAPIHLQSGPLVL TEEER TLIAEGYPIPTKLPLSKSEKAL KKIRRKIKNKISAQESRRKKKE YMDLSLEKKVESCSTENLELRKK VEVLENTNRASHGELVIGVLGK GRRWDPLLTSPHAGDQCLGSV QGWAGECTPRQLDGSRTTLISE EDPGSPMGGEALGAIVSYA WRGREALHASRVGAVIQAPIA AGSDICLSDIRESATSSQTNISVT RTLQLQLKQLQTLVMGKVSRT CKLAGTQTGTCLMVVVL CFAV AFGSFFQGYGPYP SATKMALPS QHSLQEPY TASVVRNLLIYE EHSPP EESSSPGAGELGGWDR GSSLLRVSGLESRPDVLPHFIIS NETSLEKSVLLELQQHLVSAKL
10279	40647	A	10340	I	489	

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10280	40648	A	10341	1	2665	MESTLTLATEQPVKKNTLKKY KIACIVLLALLVIMSLGLGLGLG LRKLEKQGSCKKCFDASFRGL ENCRCDVACKDRGDCCWDFED TCVESTRIWMCNKFRCGETRL ASLCSDDCLQKKDCCADYK SVCQGETSWLENCDTAQSSQ CPEGFDLPPVILFSMDGFRAEYL YTWDTLMPNINKLKTGHIHSKY MRAMYPTKTFPNHYTIVTGLYP ESHGIIDNNMYDVNLNKNFSL SKEQNPAAWHGQPMWLTA MYQGLKAATYFWPGSEVAING SFPSIYMPYNGSVFEEIRISTLL KWLDPKAERPRFYTMFYEEP DSSGHAGGPVSARVIKALQVV DHAFGMLMEGLKQRNLHNCV NIILLADHGMQDQTYCNKMEYM TDYFPRINFFYMYEGPAPRIRA HNPHDFFSFNSEIIVRNLSCKRK PDQHFKPYLTPDLPKRLHYAKN VRIDKVHLFVDQQLAVRSKS NTNCGGNGHGYNEFRSMEAI FLAHGPSFKETEVEPFENIEVY NLMCDLLRIQAPNNGTHGSLN HLLKVPFYEP SHAEEVSKFSVC GFANPLPTESLDCFCPHLQNST QLEQVNQMLNTQEEITATVK VNLPPFGRPRVLQKNVDHCLLY HREYVSGFGKAMRMPMWSSY TVPQLGDTSPLPPTVPDCLRAD VRVPSESQKSCFYLAADKNITH
10281	40649	A	10342	590	900	PLYSATVPSAFCSGQ/LVPHIKS FCRLNIFNR*LIELRHLVFFVLLL FRDLQHIMACNMRDAVRFFVC FLVIFFREGLSRSSCQKCSRKSQ NCGLFYNFFDVHVVH
10282	40650	A	10343	1	804	
10283	40651	A	10344	207	299	
10284	40652	A	10345	738	1007	EDASCDegSTARAVHSMEPAG ARNRQKPHFPQVRGAEPHPW* RCSHPA VAVDPGIALSGKPLC SWRLGSDLPTVWPLPTDPPVS VS
10285	40653	A	10346	150	509	QLPAGSGEGPYHLEGQLSYCHR GGEKALAAALLSSPTSKTRSPSEP DPEQDEQLRFCKRHLGYQQP RSPVEIRLQHVAIAYQTHHAYD *FVQLYNQHVAQPVLEFPYPGA VVALLSRHL

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10286	40654	A	10347	120	620	SYVKYFPHQPAQKYFQQIHSAL GLHNADHVHKKHLLGDNRYPIW IMQPSAHHPARQPEHDNHFR*V QQLYDGDSDHRQFL*HQILFDRT PVSVDQSVEKKG*DHPVRPQ*A APGHVHYLTIPERSSQHYHPGA LQE*TSHPDHIQARGSILASVLS GSDRWRRTYRCL
10287	40655	A	10348	599	1185	MCQNLMTHSKSTEWKITKRFL TETEKHIRTSSLSMKAIHHPA/H NHTLRDPHYVEDKGHKYLVFE ANTGTENGYQGEESLFNKAYY GGGTNFFRKESQKLQQSACKR DAELANGALGIIELNNDYTSEK SNEAADHFHVPQAKGNVVI TSYMTNRGFFEDKKATFAPSFL MNIKGNKTSVVKNSILEQQGLT
10288	40656	B	10349	1	975	
10289	40657	A	10350	1	1080	
10290	40658	B	10351	58	1128	
10291	40659	B	10352	1	1029	
10292	40660	A	10353	10	108	
10293	40661	B	10354	208	2237	
10294	40662	A	10355	1	1153	
10295	40663	A	10356	1026	1274	LHIEKSNEAADHFHVACHR*R *ACTCHCNPWFPRPLPQDPDCP TSATVEPLYPIRSRGRTRKPAE GSRAPGCCCCQRPQK
10296	40664	A	10357	434	1128	MCQNLMTHSKSTEWKITKRFL TETEKHIRTSSLSMKAIHHPA/H NHTLRDPHYVEDKGHKYLVFE ANTGTENGYQGEESLFNKAYY GGGTNFFRKESQKLQQSACKR DAELANGALGIIELNNDYTLKK VMKPLITSNTVTDEIERANVFK MNGKWYLFDTDSRSGKMTIDGI NSNDIYMLGYVSNLTPGYPKPL NKTGLVLQMGDPNDVTFITYS HFAVPQAKSNVNVNYGA
10297	40665	A	10358	300	491	SYVKYFPHQPAQKYFQQIHSAL GLHNADHVHKKHLLGDNRYPIW IMQPSAHHPARQPEHDNHFR*V QQLYDGDSDHHRQFL*HQPAQKY FQQIHSALGLHNADHVHKKHLLG DNRYPIWIMQPSAHHPARQPEH DNHFR
10298	40666	B	10359	1	1226	
10299	40667	A	10360	1369	1548	
10300	40668	A	10361	1	1365	

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10301	40669	A	10362	1560	2384	MCQILMTHSKSTEWITKRFLTE TEKHIRTSSLSMKAIHPA/HNH TLRDPHYVEDKGHKYLVFEAN TGTENGYQGEESLFNKAYVGG GTNFRKESQKLQSAKKRDA ELANGALGIELNNDYTLKKVM KPLITSNTVTDEIERANVFKMN GKWYLFDTDSRGSKMTIDGINSN DIYMLGYVSNSTLTPYKPLNKT GLVLQMGDPNDVTFYSHFA VPQAKGNNVVITSYMTTRGFFE DKKATKAPSLMNIKGKNSKV VKNSILEQQGLAVN
10302	40670	B	10363	783	881	
10303	40671	A	10364	1	1359	
10304	40672	A	10365	1512	2010	ENFPHPAQKYFQQIHSAGLH NADHVHKHLLGDNRYPIWIMQ PSAHPARQPEHDNHFR*VQQL YDGDShRQFL*HQILFDRTPVS VDQSVEKKG*DHPVRPQ*AAP GHVHYLTIPERSQHYHFGALQ E*TSHPDHIQAK*WHYR/GHYS YARN*RIHHRGWSWR
10305	40673	A	10366	62	368	TGARRVPWPRGARLRGRARA RSDSEGSAGDPPSPFPWWGW RWVTTAASPANLWPSVARSTM VDRAINL/FFLKMKGDALTED KREQAQNEQSAWKFTPGR
10306	40674	A	10367	2	305	CTINNPFS/HGVGFKQHPQA LTEIQKFAMKEMGTPDVRIDTR LIKAVWAKGIRNVPIRVRRLS RKRNEDEDSPNKLYTLVTYVP VTFKNLQTVNVDEEN
10307	40675	A	10368	129	283	HLILFLKHKYCFAREEEEEK*R GVGGEHEEEEEEEEEEEEEIEI FKSIVY
10308	40676	A	10369	777	1755	DIWDQTEHQSSGPWSYGTSTDP EPTSDLAIVIFEKRGGEHEEEE KEEEEGRRR/EEEEKEEEE/GRRR EEEEKEEEEEEE/GRRAQEEEE KKEEEEEEEEEWCLGEEESQPG HAEVPSPHKMGALTLRVEGV KEQEAKLLRSSDLMKGDFFSTS QHPPQCSKRTNSNADAKSKK KERPIMTFRQKTFRIRILPLPQ GRIAGSNKLSAKLCTDGRGAG DVGVLTVNMLKRLHFTIDHFLF KHQMSPSASWNLWSLLDQDSL KCQICLEGYAQGGKPDVQLLPP RLTADWKGHRWGQMMGLDE KLTPSSVMVTSVALFWEVSAQ

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10309 10310	40677 40678	A A	10370 10371	1 1	444 3799	MNRQLSKEDIQMANKEHEKML NITNDQGNANQNHNAIQPYSC KNGHNRRKIDVSMNMVNRHEFY TAVHKASDLSFKPTSEKDLDTK LQANFPNLVKAPDKARICFCGK PYQPYVQGSPPSPEIVEENESQ LLHFLCVGSSKEEIDLGNPKGS QHTGLGHSMSGKCNFYFLLPILLV HGWSHLHPCVASMKVAGTQ RTQDQDEAQEKEKRDKRKA LVAALQTYKTQNPQGAPANCY KCGKLGHFKKDCCHSSKRKPL
10311	40679	A	10372	1	990	MTQKKNQTEQKEQKNEQKKQ HNERKEHKKKQTEYKTHETNR PRKTERAEHQKRENEGKRR RHKKRT/RERKKTNEETETRK REKPEQARQARKEKQKRQGE RQKEEKKRKNRNQENEEEN EQDRREQKEETRKRGPRKRRE HKEEEGRREKRRKRTKEKG RRAQQKERREEEQQRRRRRR GKRKKNESEDEEDKASNHRQ QERERQKRKGAEARRPAETG RRRRKRRQRKA/AKQRQERQ GDGVLPAPWTAHPQPSQCW SARAPGGSahrPRRYLLTGQA NGSLAMWDLTTAIGRPRPGPCR WPDGARADGTAGTL
10312	40680	A	10373	99	1365	KEAEGRALARLLGPSEERFAAH EGMRPMRAVFTRQGHIITGFT RMSQRELGLWDPNNFEPPVAL QEMDTSNGVLLPFYDPDSSIVY LCGKVLTAGQGEQGTGWRG GPCPGAPLNRLLQGDSSIRYFEI TDEPPFVHYLNTFSSKEPQGM GFMPKRGLDVSKCEIARFYKLH ERKCEPIIMTVAPRKVRAWDRD LGRRSDAVPRIRQGPEPALEAD EWLSGQGRRNPCFSLRIDGYC CPPTHRDLRVTKRNLIDVRPPS GPRRKPSRPATPPCRSSTPLETL LEEIKPLRERVQAQEQRITALEN MLCELVDGPHYPRAPGRASGL PTDPFGGAVRRACVPVPPPLVPL ARAVRTLPLRYASSIAALVERM KAHMWAKGHLTRDATAKRCS PMAQTITTQHLHVPCDREDESR WNYICSS

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10313	40681	A	10374	1	361	MINPNPERSDDL VFWGLFRAG GMWSAIIAPVMILLVGILLPLGL FPGDALSYERVLAFQSFGRV FLFLMIVLPLWGLHRMHAM HDLKIHVPAGKWV\FYGLAAIL TVVTLLIGVVTI
10314	40682	B	10375	70	256	
10315	40683	A	10376	224	414	LRWRSLPAFQSGNLSVPAALM NRANARGEAVCVLGRSSRFLA H*LALGRSAAASGSSLKGG
10316	40684	A	10377	439	595	RAISCCPSHLVKRKTTLAPNTQ TASPRALADSLMQLARQVSRLE SGQ*AQRN
10317	40685	A	10378	1	391	FSSGTVPGDRPDEFIGDTLME RRNRRTGRTEKARIWETANTL AITMLMSTAMPAAAAADGVTF VPVTPHTFRHSYAMHMLYAGI PLKGLQSLMGHKCIRSTGRLPQ RFLGLEWGLPGHPGGRLLAMAE
10318	40686	A	10379	278	694	GHRSPALAIAGCPTIQNGAGPQC AAITRVRAARWCGYPGSGIPTI PEDSFMLYPRALTTHQTGFSPA WGKPSVDRLLATLSGPGGEGQ YSCCPSHLVKKKTTLAPNTQTA SPRALADSLMQLARQVSRLESG Q*AQRN
10319	40687	A	10380	2	371	SVQVFIRDKLMERRNRRTGRTE KARIWEVTDRTVRTCDCGGGL PAAAADGVTFECSAPPNIRFR/H SYAMHMLYAR*YPLKGLLSPI G/HKCIRSTGRLPQRFLEWGL LPGHPGGRLLAMAEV
10320	40688	A	10381	276	508	
10321	40689	A	10382	464	763	
10322	40690	A	10383	1	715	MQHLSHGSRRLISENFRGCQ DQAVSQTLTRPPLVSKEASFF LLPFDLHVLGLPPAFNLSDQT LQFKSLTLVTSVRVPLEVARG LSMLGLLRFMSSLLAVGDMGQ GDQVEFQDTKGNSEGRASSQP MTPLTPTRVRRCPGPTWGAK AEGVGRAEAAADPGSEGDDVV LSRTGLLLAGLLHYFRGRHHE EIMYNENTRRSQLMLFDKFRS VLVVTTHEDPVIAVFQALLP
10323	40691	B	10384	72	195	
10324	40692	A	10385	1	2331	

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10325	40693	A	10386	1	706	MTTSRSDTRSQDDPSAHLASPK LPQRLPKDLSEAQVERLLQAPLI DQPLELRDKAMLEVLVYATGRLR VSELVGLTMSDLSLRQGVVRLV GKGNKERLVLGEEAVHWLET YLEHGRPWLLNGVPINVLFFPSQ RAQQITRQALWRRINHYDELA GIDSEKLSPHVVRHAFATYFAG SGGCIADFCGGSCAGSAAESC LWFGATGLYLHHAWSGVWS RECSGAAWRDRDVGEGGE
10326	40694	A	10387	39	209	EPGTYYVNETDKSHSPCRPCVL LS**GIYLGVSVR*NGITYGALL AHIPNKFQVDY
10327	40695	A	10388	2	930	AWTHAGILLKHKYSFLVGCASI SDVIAQVVFVAILLHSHLECRE PLLIPNLSLYMGALVRCITLCL GYYNKIHDIIPDRSGPELWGDA TIRKMLSFWWPLALILATQRI RPVNLVFSRHLGGSSAATEAV AHLTATYPVVMHPYGLTEIR AVYPAFDKNNPSNKLVSNTV TAAHIKKFTFVCMALSLTLCLFV MFWDTRV*GKSLIDHSGSLW PLQELCVVPLWIFSFPPVPTV RAHLTGWMLTLKKTFLAPSS VLRIVLIASLVVLPYLVGHG ATLGVGFLLVAGFCGENSTMG
10328	40696	A	10389	1	1389	GDATIRKMLSFWWPLALILATQ RISRPVNLVFSRDLGGSSAATE AVAILTATYPVGHMPYGLWTEI RAVYPAFDKNNPSNKLVSNTV VTAHHIKKFTFVCMALSLTLKD SVQKPDISLTGRLVQTLPTMR HQRGESKDAPLASWLEPSTS SEASQTSSKLTINSQGEKAKQ KLECGTSLIVLRSECKNQERIK AEKRNRSWTTLCGLGAWRPLL FELPVIVQTPDQTNRFQFRYP KTQSGLCSEFFHFDLLTLEAFV KVWFPGLLILIEYASSKNRKS KMLQNLKLLSADMTLKLFCFVM FWTPNVSEKILIDII.GVDFAE LCVPLRIFSFPPVPTVRAHLT GIFLMTLNYTFVLPASSVLRIV PHRPASWVLPYLVGHGATLGV GSLLAGFVGESTMVA/LATCY VYRKQKKMENESATEGEIDS AMTDMPPTTEVTDIVEMREEN

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10329	40697	A	10390	57	556	TGRCTCHDRHYWSPVERIAY NVEAARVVEQRTDLDKLVIE TNGTIDPEEAIRRAATILAEQLE AFVDLRDVRQPEVKKEKPEFDP ILLRPVDDLELTVRSANCLKAE AIHYIGDLVQRIEVELLKTPNL GKKSLTEKDVLASRGLSLGMR LENWPPASIADE
10330	40698	A	10391	536	787	GRD*PDYAENAHVMPVVED ASDMLLAITQAGRMLMFPVSD LPQLSKGKGNKIINIPSAEARG EDGLAQLYVLPQSTLTIH
10331	40699	B	10392	868	900	
10332	40700	A	10393	1	278	MNPQEANYAYLRG/EVELVRLP DAEGRIAAE/GALPYPPGVLALE EGI/NLLPGFAPELQGVYIEE/HD GSGIIMLPTKLAEVGTI
10333	40701	A	10394	1	811	
10334	40702	A	10395	1	682	
10335	40703	A	10396	442	546	
10336	40704	C	10397	1	1776	
10337	40705	A	10398	2	1354	YFSPAAMKALDLLIKWTRSDQ NLGGCNTGLIRPISPIVLIYKLVI GEQMIDVLGPEKRRRTTQEKI AIVQQSFEPGMTVSLVARQH VAASQLFLWRKQYQEGSLTAV AAGEQVVPASELAAAMKQIKE LQRLLGKKTMENELKEAVEY GRAKKWIAHAPLLPGDGDCTS FSDEPMTGWMAAAVVTLMIR MCFSVYTMLESCQRMVIVGY GRRIPDRQNLMIGGSKP/SIFRQF C/PDFEHLQEPYE/LLWE/MYGN RGYQLVLSFMQKFIDQSIFANT QYDPSRFPSGKVPIQQLKDLL TAYKFGVKTLYYQNTRDGAED AQDDLVPISIQDDGCEGACILIR RASVASGSGCRMQRERLILATA RICRPDKTRQRRIRHRMRKMP YPALNSQQDTLMAYTTFSQTK NDQLKEPMFFGQPVNVARYDQ QKYDIFEKLEKQLFFLLASGRS
10338	40706	C	10399	1	1269	

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10339	40707	A	10400	1	1909	MGFHHVQAQAGFELLISSDLPAL ASQTARITAREARAPVEENKKA QLERDKQLSEQQQAALAKE KAQVKQLIEMNRITIANGDIGF NFTDGNLIKKIFVDKLTQAQLIN GRLAIARLLVDNNSEGEYAIIPA SVADKIAQRDASSIVLHLSA EEQDEDDPYADFKVPDDLMMWP TVYGRSVDRIIRSRRIQRSCAM PDATLCASYQAYGLRAKHPSFS SQGVPHCVDPVTLKIASEAPSI VGGTLPVPMTSQPSVTSMQLL LDLDTIPNEPLHYDWEALRESI KTHGLRNSTLSALMPSETSSQIS NATNGIEPPRGYVSIKASKDGIL RQVVDPYEHHLDAYELLWEMP GNDGYLQLVGIMQKFIDQISISA NTNYDPSRFPSGKVPMMQQLLK DLTLAYKFGVKTLYYQNTDRG AEDAQDDLVPISIQDDG/CESGA CLIRRASVASGSGCRMQRERLI RPTARICRPDKTRQRRIRHRMR RVLPRGATRDRDPSLEAGYQW LPGRGLVIEPQAQVMYQGVQQ DDCTAASRARVVSQSGDDIQTR LGLHSEWRTAVHVIPTLDLNDY HDPHSTEIEEDGSTISDDAVKQR GEIKVGVGTGNISQVSLRGSVA WQKGSDDFAQTAGFLSMTVK
10340	40708	B	10401	1	1329	
10341	40709	A	10402	1419	1788	ALTSVLPRPSVHW*SPKPRNVD WHIGRGVAIIMQKSGIPDIDQA NCMIKLESDDGTFFIVHSGGADIG TGLDVTVTKLAAEVLHCPPQD VHVISGDDTHALFDKGAYASS GTCSFGNAARLAAEN
10342	40710	A	10403	73	477	SMFPRIPFGY/WHI/GSRVAIIQ K/SGIPDIDQSNLHDQLESHGTFI VHSG/GFDYGTGLDTV/VLTKL AAEV/LHCPPQDVHVISGDDTH/ ALFDKGAYASSGTCSFG/NAAR LAAVNPRALAYSYGGGGARV CIWGGWGRR

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10343	40711	A	10404	I	756	MSIAYQEIPQNERLRLSDSSITS VVEYLLAVVARSVYTSDDMAIF REHHSYMSLSMAACRKIRPCQ ELPRSHIPMISAMWSQSPDHV VQHEREQQSGFGDGTESHSTSD SNTEVRQNCSPPIGGVRNHRAL RGHQPAELEPENILKLLLMVAE RKAHKGWYYSGDLCRMDEAG YIKITGRKKDIIVRGGENISSREV EDILLQHPKIPNA\CMGAMSD RLGERSCAV\VLKAPHHSLSL EEVLCWRGC
10344	40712	A	10405	252	1245	GSRLPGASITRSLEFIAGQAVK FNPLLPVSLVKRNTTLAPTHTT ASPRALADSLMQLARQVSRLD SGQRSVVFVRWSRRSIIVDSHA GLITTTQRALGQSDMYRGSLPISE LRHIGPRHLRGVLRVVRCLPFSE PMLVECNPLLPSSLIIEPSLEPT LRFASRIALPDSTVLQIFSGVLP LSSGQAYIQFTYSETPRSTPREA NSAHILSVHQWKCQHIVMAAR VKVGYPQWTPISLSAGLSAVLY KPVERGGRCSHSCSTALSPQGF LSSLLRFISEGVFKSFTDKQMLR DFVTTTRPALIVLLWQPLNVEGT SSTSHCIIMPTCNDHRD
10345	40713	A	10406	269	432	
10346	40714	A	10407	332	933	RVSRGRKVVFYRPEEDAGDEK GYESFPWFIKRAHSPSRGLYSV HINPYLIPFFIGLQNRFTQFRLSE TKEITNPYAMRLYESLCQYRKRP DGSIVLSLKIDWIIERYQLPQSY QRMPDFRRRLQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLA\PNTQTA\SPRAL ADSLMQLARQVSRLESQQAQ
10347	40715	A	10408	I	531	MRWKIDLARISKEIIDFYITQGV NRIGFIAGEDEPGKADIREVAFA EYGRLKQVVREEDIWRGGFSSS SGYELAKQILARKDYPKPLFV ASDSIAIGVLR\AIHERGLNIPQDI SLISVNDIPTARFSFPLSTVRIH SEMMGSGQVNLVYEKAPDGR ALPLLVFVPSKCLKRGTTTR
10348	40716	A	10409	I	1059	
10349	40717	A	10410	2187	2429	

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10350	40718	A	10411	1	835	MRPFGDYPDGGIDDLKISFSVP AAGVGPHFDQYDVFIHQGTERR RWRVGEKLQMKQHCPHDDL QVDPFEAIIDELEPGDILYPPG FPHEGYALENAMNYSVGFRAP NTRELISGLPDYVLQRELGGNY YSDPDVPPRAHPADVLPQEMD KLREMMMLAELSTHPDPFKQWLG EFISQSRHDLDIAPPDPYPQDE FSDALNQGKVLGALGGLRVL MGDAVYPNGEKMDSPRPALD ALASTIALTAKNFGDALEDPSF LAMLAAALVNSGYWFFEG
10351	40719	A	10412	249	474	VYLLIVLAVLYTNNRQTESQIM SELPFTIASKRIKYLGIQIATRDV KDLFKDNYIPLKEI*EDTSKW KSIPCSWI
10352	40720	A	10413	157	413	ALVCS/SSLAIREMQIKTTMRYH LTPVRMAIIKSGNNRCWRGC GEIGTLLHCWLDCKLVQPLWK SVW*FLRNLELIPFDPAIPLL
10353	40721	A	10414	342	528	
10354	40722	B	10415	32	587	
10355	40723	A	10416	1	2141	
10356	40724	A	10417	1	748	
10357	40725	A	10418	321	411	RNRDRYKQWKQDFFHDSYNR QRGCGRWLYRRHHR*CRRYRR QQPHLCRLYES*KKSCFCHLYR SRF/RLRVKYPRDMYSLGTFL RSPVAIRIPLSRNQVQR
10358	40726	A	10419	1	2235	

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10359	40727	A	10420	1	1884	MGKDFMTKTPKAMATKAKID KWDVILKLSFCTAKETTRVNR INKIDKPLARLIKREKNQIDT IKNDKGDITDPTIEQTIREYY KHLTYTNKLENLQEMDKFLDTY TLPRLNQEEVETLNRPTGSEIV AIMNSLPTKKSPGPDGFTAEIF QRYKEELMILIPK/PGQDITKKE NFRPISLMNIDAKILNKILAKRI QQHIKKLIHHDQGVFPGMQG WFNIRKSINVIQHINRAKDKNH MTISIDAEKAFDKIQPFMLKTL NKLGDGTYFKIIRAIYDKPTAN IILNGQKLEAFPLKTGTQGCPL SPLLFINIVLEVLAIRQEKI GIQLGKEEVKLSLFAADMIVYL ENPTVSAQNLLKLISNFSKVSQ YKINVQKSQAFLYTNKRQTESQ IMSELPFTIASKRIKYLGIQLPRD VKDLFKENYKPLLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VTYRFNAIPIKLPMTFFTELEKT TLKFIWNQKRARIASII.SQKN KAGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIT PHIYNILIFDKPEKNQWGWKDS LFNKWCWENWLAICRKLKLDLP FLPTYTKINSRWIKDLNVRPKTI
10360	40728	A	10421	1	822	
10361	40729	A	10422	2738	2949	
10362	40730	A	10423	1	1134	
10363	40731	A	10424	1	2118	
10364	40732	A	10425	938	1147	SLETRKSAPCTIMFRICIAGCCW LPCGTPTSVLTKRWH**P*VIFL WSRRIHTASCLPSQRSITGHVH HQ
10365	40733	A	10426	2	1624	
10366	40734	B	10427	1	3690	
10367	40735	A	10428	1	1056	
10368	40736	B	10429	1	2265	
10369	40737	A	10430	1	2037	
10370	40738	A	10431	1	2406	
10371	40739	B	10432	670	2568	
10372	40740	A	10433	3	4072	
10373	40741	A	10434	1	3171	
10374	40742	A	10435	1	1542	
10375	40743	A	10436	1	1008	
10376	40744	A	10437	1	2241	
10377	40745	B	10438	1	2682	

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10378	40746	A	10439	644	949	MRKPTLGRTYSPRPSPAAARG ASRAALGPGHGLETRKSAPCTI MFRICAGCCWLP CGTPTS VLT KRWH*P*VIFLWSRRIHTASCLP SQRSITGHVHHQ
10379	40747	A	10440	1	1088	MARKDIQVLIIGTYEYLVKGE KVLTLAIKLVKWSGYPGLC LPEYHLGEVEGEDDM EVTAMD GRCLLEVKG SERLQVADQECV GDGSGRLCPDRCECEQRLQLV RPGLCNPRAIALTTKPQSPSPNI KRLVIGE QMIDVLGP EKR RRT TQEKIAIVQSFEPGMTVSLVA RQHGVAAASQEGSLTAVDAGEQ VVPASELAAMKQIKELQRL GKKTMENELLKEAVEYGRAKK WIAHAPLLPGDGERTDDWMDG RRSRHTDDTDVL*SASWRQQV QRQEQPVLRRRQ*DFLLGWL LHHVAGQGRSPSPVQSSAEQL RSFPVWYAVCVSPALRHQSSVL
10380	40748	A	10441	1	2781	MGGKONRKTGNSKKQSASPPP KERSSSPATEQSWMENDFDEM REEGFRRSNYSELREDIQTGK EVENFEKNLEECITRINTKCL KELMELKTKARELREECRLRS RCDQLEERVSVMEDEMNMN DGENGTKLENTLQDIIQENFPN LARQANVQIEIQRTPQRYSSR RATPRHIIVRFTKVEMKEKMLR AAREKDFKPTKIKREKEGHYIM VKGSIQQEELTKIYAPNTGAP RFTKQVLSDLQRDL
10381	40749	A	10442	1	2445	
10382	40750	A	10443	1	1428	
10383	40751	A	10444	1	2478	

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10384	40752	A	10445	1	1746	METQKTLQKINESRSWFEKIN KIDRPLARLIKKKREKNQIDTIK NDKGDITTDPTIEIQTIREYYKH LYANKLENLEEMDKFLDITYTL PRLNQEEAESLNKPTGPEIEAII NSLPTKKIPGPDGFTAIFYQRY KEELQHIKKLIHHDQVGFIPGM QGWFNIHKLINVIQYINRTKDK NHMIIISDAEKASDKIQPFMLK TLNKLGDGTYLKIIIRAIYDKPT ANIILNGQKLEAFPLKTGTRQG CLLSPLLFNIVLEVLAIRQEK EKKCIRLGKEEVKLSLFADDMI VYLENPIVSAQNLLKLSNFSKV SGYKINVQKSQAFLYTNNRQIE SQIMSELPFTIASKRIQYLGQILT RDVKDLFKENYKPLLEIKEEDT NKWKNIPCS WIGRINIMK MAM LPKVIYRFDAIPKLPMTFFTELE KTTLKFIWNQKRARIKASILSQ KNKAGGITLPDFKLYYKAIVTK TAWYWYQKRDVDQWNRIEPS ETIPHICNHLIFDKPKDNKQWG KDSL FNKWCWEIWLAIGRKRK LDPFLTPYTKINSRWIKDFNIRP KTIKTEESLGIIQDISMGKKFTS
10385	40753	A	10446	2	541	
10386	40754	B	10447	1	1533	
10387	40755	A	10448	753	1468	LVTYSYLLPRHPDRGRGYHFD MGVWIKN*IKPMS*REQL*PWL PLKRS LICFLSAHFWLVVRRPK R/WCKPVQVSATFTVIADNNLY RQNSFVYSFTECTNDG*LAITSF CRDQAVRLVNEVFTGCCREICT /CATGYARRYGIDRSVLQSRPIH SQKK*NRSSLYSSGK*L*PALQC WWF/CTTSLPVIRVVKEILLPLL VSITVSLRVKYPRDMYSCLGTF LRSPVAIRIPLSRNQVKR
10388	40756	A	10449	753	1468	LVTYSYLLPRHPDRGRGYHFD MGVWIKN*IKPMS*REQL*PWL PLKRS LICFLSAHFWLVVRRPK R/WCKPVQVSATFTVIADNNLY RQNSFVYSFTECTNDG*LAITSF CRDQAVRLVNEVFTGCCREICT /CATGYARRYGIDRSVLQSRPIH SQKK*NRSSLYSSGK*L*PALQC WWF/CTTSLPVIRVVKEILLPLL VSITVSLRVKYPRDMYSCLGTF LRSPVAIRIPLSRNQVKR

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10389	40757	A	10450	753	1468	LVTSYSLPRHPDRGRGYHFD MGVWIKN*IKPMS*REQL*PWL PLKRSLICFLSAHFWLVRVRPK RWCKPVQVSATFTVIADNNLY RQNSFVVSFTECTNDG*LAITSF CRDQAVRLVNEVFTGCCREICT /CATGYARRYGIDRSVLQSRPIH SQKK*NRSSLYSSGK*L*PALQC WWF/CTTSLPVRVVKIILLPLL VSITVSLRVKYPMDMYSLGTF LRSPVAIRIPLSRNQVKR
10390	40758	A	10451	753	1468	LVTSYSLPRHPDRGRGYHFD MGVWIKN*IKPMS*REQL*PWL PLKRSLICFLSAHFWLVRVRPK RWCKPVQVSATFTVIADNNLY RQNSFVVSFTECTNDG*LAITSF CRDQAVRLVNEVFTGCCREICT /CATGYARRYGIDRSVLQSRPIH SQKK*NRSSLYSSGK*L*PALQC WWF/CTTSLPVRVVKIILLPLL VSITVSLRVKYPMDMYSLGTF LRSPVAIRIPLSRNQVKR
10391	40759	B	10452	1	2259	
10392	40760	B	10453	1	684	
10393	40761	A	10454	1	1419	
10394	40762	B	10455	1	462	
10395	40763	B	10456	1	915	
10396	40764	B	10457	1	1659	
10397	40765	A	10458	1	1659	
10398	40766	A	10459	1	1224	MIVYLENPIVSAQNLLKLISNFS KVSGYKINVQKSQAFLYTNNR QTESQIMSELPFTIASRKIKYPGI QLTRDVKDLFKENYKPLLKEIK EDTNKWKNI PCSWVERINIVKM AHLPKTAKNGPVLPLHSEEKIP FNFH*LFR*TITATKA*QKRR* MCQNLMTHQNRQSRGRSQIYF* RRKNISDRSAVYR*QQLYIRR QPYAERPSHVEDKGHKYLVFE ANTGTENGYQGEESLFNKAYY GGGTNFFCKESQKLQSSAKKR DAELANGALGIIELNNDYTLKK VMKPLITSNTVTDEIERANVFK MNGKWYLF TDSRGSKMTIDGI LPISDPTIKQDFRLLGGQTSVDRL LQLSQGQAVKGNQLLPVSLVK RKTTLPNTQTASPRALADSLM QLARQVSRLESGQ

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10399	40767	A	10460	1	2241	MEDEMNMKQEEKFREKRIKR NEQTLQEIWDYVKRPNLHLIGV PESDGENGTKLENTLQDIIQENF PNLARQANVQIQEIQRMPQRY SRRATPRHIIVRFTK VEMKEKM LRAAREKDRSMRQKV NKTQEQ LNSALHQADLDIYRTLHPKST YTFFSAPHHTYTKIDHILGSKAL LRKCKRTEIITNYLSDHSAIKLE LRKLNLTQNRSTTWKLNLLN DYVWHNKMKAIEKMFETNEN KDTTYQNLWDAFKA/EIQITIK EYYKHLYANKLENLEEMDKFL DTYTLPRLNQEEVESLNRPIGT AEIVAIINSLPTKSPGPDGFTA EFYQRYKEELVPFLKLFQSIK QGILPNSFYEASTLIPKGRD EKENFRPISLMNIDAKILNKILA KRIOQHKKLIHHDQVGFIPGM QGWFNHKSINVIQHINRAKDK NHMIISIDA EKA FDKIQQRFML KTLNKLGDIGTYFKIIRAIYDKP TANIILNGQKLEAIPLKAGTRQG CPLSPLLFNIVLEVLARVIRQEK EIKGIQLGKEEVKLSLFADDMI VYLENPIVTAQNLLKLSNFSKV SGYKINVQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDT NKWKNIPCSWVGRINIMKMAIL PKVIYRFNAIPKLPMTFFTELE KTKFIWNQKSAHITKGLSQKN
10400	40768	B	10461	1	1254	
10401	40769	A	10462	551	868	SIQHWSRISSLRVYRSKAVAAA LLPMNCSLWSTQAGFLPRFG*R *TRHLSTIEPEDYNLLFRVSLK LSVWLPTWQSKSNGWSQKCL WMHLKFDLSNALLPPTGF
10402	40770	A	10463	1	2985	MEDEMNMKREGKFREKRIKR NEQSLQEIWDYVKRPNLHLIGV PESDVENGTKLENTLQDIIQENF PNLARQANVQIQEIQRTPQRY SRRATPRHIIVRFTK VEMKEKM LRAAREKGHCNSGKSHRSLWE QNKGIFFTICDDAEDLQSPSTA GPWFGVLYTKGGPYQEDIFSE EVHTGPKLRKKIQEYQLTSKWS KSDVQVSVERRMAGGNPNQCH IGEVLLDGFTA EYFRRYKEELV PFLKLFQSIKEG
10403	40771	B	10464	1	2277	

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10404	40772	A	10465	1	1064	
10405	40773	B	10466	1	1827	
10406	40774	A	10467	1186	1208	ATKMVRLSVAALVQRMKEFCA AKFPAVITCWWSVWAQSA*WR *CWRKTKI
10407	40775	B	10468	1	1992	
10408	40776	A	10469	1488	1920	RVRVTAVITERDCVSRSRWTAV IVRHCTGRSLPAASTVKQYRTS CWERWN/CRFGNDLPSPVVEWL TDN/EFMLPG**NTPVRPDVGLE PT*TRACQESRCN/RLTPGIVL EIIGVWMQQRWSLECRLAIPCIG WLPRVVGEESGA
10409	40777	A	10470	1	1659	
10410	40778	A	10471	1	987	
10411	40779	A	10472	1	1278	
10412	40780	B	10473	1	1556	
10413	40781	A	10474	1	1905	
10414	40782	A	10475	644	949	MRKPTLGRTPSRPPSPAAARG ASRAALGPGHGLETRKSAPCTI MFRICIAGCCWLPCGTPTSVLT KRWH*P*VIFLWSRRIHTASCLP SQRSITGHVVHQ
10415	40783	A	10476	1	1217	
10416	40784	A	10477	83	1134	
10417	40785	A	10478	2450	2607	

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10418	40786	A	10479	1	2604	MPLRAFNVPVSSFRWARGMTIV AALMTVFFIMQLVGQVPAALW VIFGEDRFRWSATMIGLSLAVF GILHALAQAFVTGPATKRFGEK QAIHAGMAADALGYVLLAFAT RGWMAFPIMILLASGGIGMPAL QAMLSRQVDDDHQGLQGSL AALTSLSIIGPLIVTAIYAASAS TWNNGRACSSSVTRIVSILSRFI GIITPMNRNPPYTEASVTKQEK TALNMAFRIRSQTLTLEKLNE LDADEQADICESLHDHADELRYR SCLARFGDDGNSYDHDYAKLA CLQVEGRGGGTFAHELLAVEY AGWISPAFRLKVNQTFIDYRTG RLQPAIPQSLPEALRLAADLAE QKQRLEQKMLMDAPKVEFAER VATASGVLIGNYAKVGLGLGQN YLFTWLRDNGILI/CNR* TQERP QTRIHISWVFH/LLKKP*SIQAM EAG/LSFTTRITGKGQQWLMKR LLDARNRDRYKQWKQDFFIDS YNRQSAGHILSQCANLAATTSE YFIHKPHRLIAAETGYSQSTVV RAFREA VNKGILSVEIVGDHRE RRANLYRFTPSFLAFAAQAKNA LIESKLKISSAATKVAVLAKTL ALFNFLSTPPCQNDTPSPCQDD VAJKNKKSQVKKTKRSVSGGA GTTSKKLTSWIAKAKAKADN LRLSKKRTQKHEFKQKVEAAA RKYAYLKNKRSPDIGISNFDN
10419	40787	A	10480	1	2559	

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10420	40788	A	10481	1	1676	MLNGEKLAVKQEALLAAISEK DANIALLELSSSKKKTQEEVAA LKREKDLRVQQLKQVVEGRGG GTFABELLAVEYAGWISPAFRL KVNQTFIDYRTRGLQPAIPQSLP EALRLAADLAEQKQRLEQKML MDAPKVEFAERVATASGVLI NYAKVLGLGQNYLFTWLRDN GILIATGERRNVPKQEYISRGYF TLKETVIDTSNGSRISFTTRITGK GQQWLMKRLLDADVVRTTSIV MLAKVTFSLCITMSDFTFSGYE LACFVTHSGLSRSSAGHILSQCA NLAATTSEYFIHKPHRLIAAETG YSQSTVVRAFREAVNKGILSVE IVIGDHRERRANLYRFTPSFLAF AQQAKNALIESKLLKISSAATKV KAVLAKTLALFNFLSTPPCQND TPSPCQDDVAIKNKKSQVKKTK RSVSGGAGTSLKLLTSWIAKA KAKADNLRSLKKRTQKHEFKQ KVEAAARKYAYLKNKRSPDIG GISNFDNLPHCMTVNEALNAVL AKNKDNEQWGAAGAYIADIT DGEDRARHFGLMSACFGVGM VAGPVAGLLGAISLHAPFLAA AVLNLNLNLLGCFMLQESHKG ERRGELLKIVVLPGDHVVGQEIT AEAIVLKAISDVRSNVKDFE NHLIGGAAIDLQGGGGKPRCVS KSLMLH/CWHSCLRPWR*QR VQRJRL*VHP*AFFAPAVAFALP
10421	40789	A	10482	1	3213	
10422	40790	A	10483	1089	1373	
10423	40791	A	10484	2720	2968	TTTLVRLPCRSPPKRIKALRSQ RRKSILKPLS*SR*STTK*RNTP CSQVSSLRLSTRYRRRMKHSV NLVWTWVPYSSAP
10424	40792	A	10485	2	2264	
10425	40793	A	10486	1693	1980	
10426	40794	A	10487	1776	2026	SLETRKSAPCTIMFRICIAGCCW LPCGTPTSVLTKRWH*P*VIFL WSRRIHTASCLPSQRRSSNRACSS SVTRIVSILSRFIGI
10427	40795	A	10488	1323	2064	
10428	40796	A	10489	53	243	WTVPLGAVPPVRMHEGLGCW CKLNGEVCMSGMCLLCWWD D*RHDLKANLDRMLNVCQDGR KR
10429	40797	A	10490	1	3117	
10430	40798	A	10491	1	1227	

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10431	40799	B	10492	1	2119	
10432	40800	A	10493	938	1147	SLETRKSAPCTIMFRICIAGCCW LPCGTPTSVLTKRWH*P*VIFL WSRRHTASCLPSQRSITGVHH HQ
10433	40801	A	10494	1	2822	MVKGSIQEEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MEDFNTPLSTLDRSTRQKVNK NTQELNSALHQADLIDIRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRINKLTQSRSTTWKLN NLLNDYVWHNEMKAEIKMFF ETNENKDDTTYQNLWDAFKAVC RGKFIALNAYKRKQERSKIDTL TSQLKELEKQEQTHSKASRRQE ITKIRAELEIETQ
10434	40802	A	10495	2	163	
10435	40803	A	10496	4051	4355	MRKPTLGRTPSRPPSPAAARG ASKAALGPGHGLETRKSAPCTI MFRICIAGCCWLPCGTPTSVL TKRWH*P*VIFLWSRRHTASCLP SQRSITGVHHHQ
10436	40804	B	10497	1692	1781	
10437	40805	B	10498	1	3477	
10438	40806	A	10499	179	439	KKELVNLTTD*SLENR/WIDVL GPEKRRRTTQEKIAIVQSF/G TGDDGLPRCPATWCSSQPVISL A*AIPGRKSYCCRRRTTGCSCS
10439	40807	A	10500	1	7456	MYQANGKQKKAGVAILVSDKT DFKPTKIKRDKEGHIYIMVKGI QEEELTILNIYAPNTGAPTFIQ VLSDLQRDLDSHTLIIGDFNTPL STSDRSTRQKVNKDTQELNSAL HQADLIDIRTLHPKSTEYTFSS APHHTYSKIDHILGSKALLSKC KRTEIITNYLSDHSAIKLELMIK NLTQNHSTIWKLNLLNDYV VHKEMKAEIKMFFETNENKDT TYQNLWDTFKAVCRGKFIALN AHKRKQERSKIDT
10440	40808	A	10501	2476	2718	WPLRGRGGHRAAPGRHLHLQ RLLLRLHLTACLLQDALDG/GP PRCWRGSCRWCSAGPPRSWA RRPSATRSPSPWPALECS

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10441	40809	A	10502	2	4517	HRLANWIKSQDPSVCYIPETHL TCRDTHRLKIGWRKIYQANG KQKQAGVAIHISDKTDFKPTKI KRDKEGHYIMVKGSIQQEKLTI LNVYAPNTGAPRFIMQVLSDLQ RDLDSHTLIMGDFNTPLSTLDR LTRQKVNKDTQELNSALHQVD LIDIYRTLQPKSTEYTLFSAPHH TYSKIDHILGSKALI.SKCKRTEII TNYLSDHSAIKLELRIKKTQIR STAWKLNLLNDYWVHNEM KAEIKMFFKNNEN
10442	40810	B	10503	88	501	
10443	40811	A	10504	1	971	MWALFMIRNVKKQRPVNLDLQ TIRFPITAISILHRVSGVITFVA VGILLWLEYRLSYLKGSSKLR DYGQLLTLEIPAALLPIHTGIVN QNINCTETLTASSDNLLRRAFC GDTHLHEVHLNTLFFNHFLCFA VIFDETRNKDICATSGQHAHFV DKKRKRELLSHMIGKGNWQQV LVFTRTKGHANHLAEQLNKDG IRSAAIHGNKSQGARTALADF KSGDIRVLVATDIAA/RGLDIEE LPHVVNYELPNVPEDYVHRIGR TGRAAATGEALSLVRSFFDWC DDCAAAGGMGNRNAQLADGI YHLRCIELYLGDMADFL

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10444	40812	A	10505	1	2201	MSFDSLGLSPDILRAVAEQGYR EPTPIQQQAIPAVLEGRDLMA AQGTGKTAGFTLLQHLITR QPHAKGRRPVRALILTPRELA AQIGENVRDYSKYLNIRSLVVF GGVSINPQMMKLARGVDVLV ATPGRLLDLEHQNAVKLDQVEI LVLDEADRM LDMGIHDIRRVL TKLPAKRQNLFSATFSDDIKA LAELLLHNPLEIEVARNTASD QVTQHVHFVDKKRRELLSHM IGKGNWQQVLVVFTRTKHGAN HLAEQLNKDGIRRAAKHGKNC KCAYSKFQKPSPHIFTMLIGVC GVNQSAITNVSNVSNMAKISGS GSHRLTKRVIKRDMPINHPV AYSRRRLQTELLFWHARWLN HTRRQFRIKEGDNNGQCFLW TGRFNFNLPSFGRIQHQQRNNA VGFSLGAFVITFIAGRACMPSLF VISTVCLTMVYVFPAYDGV GRFYRASGSSLPVALQYTPNGA SRRYINQWRPSRMLSSKKQKW RKGMSESLHLTRNGSILEITLDR PKANAIADAKTSFEMGEVFLNFR DDPQLRVAITGAGEKFSGAGW DLKAAAEGEAPDADFPGGGFA GLTEIFNLDKPVIAAVNGYAFG GGFELALAADFIVCADNASFAL PEAKLGIVPDSGGVLRPLPKILPP AIVNEMVMTGRRMGAEALR WGIVNRVVSQAELMDNARELA
10445	40813	A	10506	1	168	MCEKNLAYAHKVKAALEKGA SPGDFPREDYETNWEGRFTLA DLNIHGKRALGMDV
10446	40814	C	10507	1	3861	
10447	40815	A	10508	1	7407	
10448	40816	A	10509	290	661	QPLPEGRW/THLWHNDEL DGS RWHK/QQHGLSLPVYVRDNT LRALGNNDQRPDYVWHE/GTA FHLFNLKAARTGNTITAI DASE ANNWTLCLRNQVKNGLQDG SQAESQGLVVKPQGNALTITL
10449	40817	A	10510	3	510	KFHFMSPFPAHSMVQALE*LYA LGGLDKDCRLTEPLGMRIAEFP LNPMPFAKMLLESGNFCSQEIL SIAAMMQIQNIFVVPNHKSHAI RVHRKFAVEEGDHLTMLNIYE AFIKHNKDSKWCQEHFLNYKG LVRAATVREQLKKLLVKFQVP RKSEGD PDLVLRICVS

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10450	40818	A	10511	1	1920	MIWGRAWWLTPVIPALWAAK VAGRVAEERGAVLGHEVG YCI RFDDCCTDQLATRIKRLTESFSLI LSVIMLDEAHERTLYTDIAIGLL KKIQKKRGDLRLIVASATLDAD EEVETVVSMLIEQARALARIG MKRHLRLVPMYAGLPSFEQMK VFERVSRSVRKVIVATNVAETSI TISGIVYVIDCGFVKLRAYNPRT AIECLVVVPVSQASANQRAGR GGRSRSGKCYRLYTEEAFDKLP QSTVPEMQRSNAPVILQLKAL GIDNVLRHFHMSPPPAQSMVQA LELLYALGSLDKDCRLTEPLG MRIAEFPLNPMFAKMLLESGNF GCSQEILSIAAMMQIQNIFVVP NQKSHAIRVHRKFVVEEGDHL TMLNIYEAFIKVSTTTARSAAST HHPLEHNKDSKWCQEHLNYK GLVRAATVREQLKLLVKFQV PRKSSEGDPDLVLR CIVSGF FA NAARFHTSGAYRTIRDDHELHI HPASVLYAEKPPRWVIYNE LL QTSKY YMRDVT AIESAWAVGS WLHTFYSTRERTCSLESQKGPR SRDPLRREPTVYSCRD CWRPLL HAAAPGPRWGELAPAPVECLV ALKWAAACSLVLSRCPQHLH PCWDPGGLCAWAGILLCCSGQ SGSWLTQHAH
10451	40819	A	10512	3	414	
10452	40820	B	10513	62	1408	

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10453	40821	A	10514	1	1388	MGTSSIFLCVLFLCGALGLTMS PARGRRLRCYICGF TKPCHPVPT E CRDDEACGISIGTSGCRGIFQVP DQQRDSRSHFPADVTKITWAC GQSPPGFKPLFPSCSSPKTGQM DVLIDLDFGFELRNRGIWGE GA IRDTEEKSADNLEPCSSPPPLEE VICCEGNAGFYEVGCVSTPLEA GYSVLGWNHPGFAGSTGVPPF QNEANAMDVVVQFAIHRLEFFH PQDIIYA/LAIGGFTATWAAMS YPDVSAMILDASDDL VPLALK VMPDSWRGLVTRTVRQHLN LN NAEQLCRYQGPVLLIRKTDQD NLTPVPMKDICSNRANCLLVKA LQHRYPGVM AE EGLLVARQW LEASSQLE EASIYSRWEVFED WCLSVLR/SY/QAEHGADFPW SVGEDMSA/DGR/RQLA/FLAR KHLHNFEATHCTPLPAQNFFRC PWHPGLTQLGLIMEEWGERRH
10454	40822	A	10515	1	1519	MGLFKPLLLASFFPAQASW G VSSPDQVQGVKGSCLLPICFIS PADVEVPDGITAIWYYDYSGQR RVFMGNPEHRVCNLLKDLQP EDSGSYNFRFEISEVNRWSDVK GTLVTVTARSLSPGRHLETLH MAMSWQDHGRILRCQLSVAN HRAQSEIHLQVKYAPRGVKILL SPSGRNILPGEVLVTLTCQVNSSY PAVSSIKWLKDGVRLQTKTG V LHLPQAA WSDAGVYTCQAENG VGSLVSPPISLHIFMAEVQVSPA GPILENQVTLCNTPNEAPSD LRYSWYKNHVLL EDAHSHTLR LHLATRADTGFYFCEVQNVHG SERSGPVSVVNVHPPKTP TMM VFVEPEGGLRGILDCRV DSEPL ASLTLHLGSRLVASSQPQGAPA EPHIHVLASPNALRVDIEALRPS DQGEYICASNVLGSA STSTYF GVRALHRL/LSVPA AALPGGTA/ VWASCSCCWA WGPATPGGTG YYLTGTYKSGGQTQMLSASLF
10455	40823	A	10516	3	615	
10456	40824	A	10517	373	631	SGGPDTDVVSIPYSCSRMHLCS *LCELLSFSWETLCRAVKENEL PKKE*RAPANQGPTGESSLGL SDSPLQPGGDGVEERRALLF

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10457	40825	A	10518	1	5521	MANRFRSGEDSGGAIWQDCVE EGASELGFLESLLYTQGNDRKQ CSLTNQGRQVFALLMLRKGHLL HVFVILFGPAGAPPQPLPSVEQ VPLSLVPGPKGVAVSRTPPFFH QVHDCPFQDPKWEEQGSWDKI AALAIAELTLTSPVARDTSDPQ CAQQAFLHGQASWGVSSPQD VQGVKGSCLLIPCIFSFPADVEV PDGITAIWYYDYSGQRQVVSHS ADPKLVEARFRGRTEFMGNPE HRVCNLLLKDLQPEDS
10458	40826	A	10519	1	1149	
10459	40827	A	10520	111	370	SHRRSLGEAARHPSFRPAGTAF E*VSQKVVHPRDLEDRSACVPV GCSLTRESFFRLNNQPHGTRFLP IPSNPESSRRVPSAHLTV
10460	40828	A	10521	1	220	
10461	40829	A	10522	654	967	
10462	40830	A	10523	2	1415	
10463	40831	A	10524	2	293	CGKAFTQHSRLIQH/QRMHGTGE KPYEYWEFGEKPRIYLQRKTFM KLDTTTGEQSYQRNQMEPCP YGEKPCCKECKGKSFR/SSLE RHQRAHTGEKP
10464	40832	A	10525	51	378	GDFSPOKPPMAPHGCLTYLAFQ KVKEGKKEKKEKKRKKRKK KERKKERKKERKKRKKRKEK EVEGKEGRKEGRKEGRKEGRKE KKEISKKEIVAPTSNLNPKCSVL
10465	40833	A	10526	1	235	
10466	40834	A	10527	545	793	NKEMHWPCITGLCSHPWGFK DCSLLE*RLPGQQEQNSIERKK RKKEKKEKKEKRRKKRKKGKKE ERKKERKYHFILLGMPTS
10467	40835	A	10528	127	376	
10468	40836	A	10529	3	710	EPG/NPERLK/GFSYPEFEDLDA LFSTLGLNEESVDSFDDYLP GVDSFGDKYQD/RNSDQYH GCQDRFRDGSQDMGQCGGR D*DDD*GSRDYDRGYDSATGS CRRAFSGYLRDDY/WESSET EQQPPTGSEGVPPVQPSERP AKKDENKVDGMN/APKVQSGN SGRGPDGNGKDCWRESRDKD GKKDQVCRSAPESKKPEENPAS KFSSASKCAAHSVVDGEDEKEG

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10469	40837	A	10530	1	548	MQRSENDILGMDLRPLICIKDE KEEVGEKEEGEKEEEEECEEQEE EGGKEWEEPGNYHLGQSLSHD WQSSETEQPPPTGSEGKVPVPQ PSEERPAKDKENKVDGMN/APK VQSGNSGRGPGDGGNKDCWRE SDRKDGKKDQVCRSAPESSKKP EENPASKFSSASKCAA VSDGE DEKEGADYTK
10470	40838	C	10531	37	289	
10471	40839	A	10532	1	1062	
10472	40840	A	10533	1	1977	
10473	40841	A	10534	1	2050	LPLLHAGFNRRFMENSSIIACYN ELIQIEHGEVRSQFKLRACNSVF TALDHCHAEIETSDDHVIQYV NPAFERMMGYHKGELLGKELA DLPKSDKNRADLLDTINTCIKK GKEWQGVYYARRKSGDSIQQH VKITPVIGQGGKIRHFVSLKKLC CTTDNNKQIHKIHRDSDGNSQT EPHSFRYKNRRKESIDVKSISR GSDAPSLQNRYPSPMARIHSM IEAPITKVINIINAAQENSPVTVA EALDRVLEILRTTELYSPQLGTK DEDPHTSDLVGGLMTDGLRRL SGNEYVFTKNVHQSHSLAMP INHSMDEVPPCISQLLDNEESWD FNIFELEATHKRPLVYLGLKVF SRFGVCEFLNCSETTLRAWFQV IEANYHSSNAYHNSTHAADVL HATAFPLGKERVKGSLDQI.DE VAALIAATVHDVDHPGRTNSF UCNAGSELAVLYNDTAVLES HHTALAFQULTVKDTKCNIFKN ID/RGNHYRTLQAIIDMVLA MTKHFHVNKFNINSINKPMAA EIEGSDCECNPAKGNFENQILI KRMMIKCADVANPCRPLDLICIE WAGRISEYFAQTDEEKRQGLP VVMPVFDNRNCSIPKQISFIDY FITDMFDAWDAFAHLPALMQH LADNYKHWKTLDDLCKCKSLRL PSDRLPKPSHRGGLLTDKGHCES
10474	40842	A	10535	2	445	ERTFNCCYPGCHFTVHGMKD LDRHLRIHTGDKPHKCEFCDKC FSRKDNLTMHMRCHTSVKPHK CHLCDYAAVDSSSLKKHLRIHS DERPYKCQLCPYASRNSSQLTV HLRSHTGPGPADLLEHSRLHQ ADHPEKCCEPSYSCSSAA
10475	40843	A	10536	1	957	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
10476	40844	A	10537	1	1438	MSRRKQAKPQHLNSEEPRPARR ECAEVAPQVAGEPASELDDDDV PKANCLSTESTDTPKAPVITLPS EAREQMATLGERTFNCCYPGC HFKTVHGMDLDRHLRIHTVP FCFSKVYWNGFQLGMISPPKGT MSGDIFDCYNWRRKGSTGCIW TGGGGTPICPGYHLGQIFVAILT KKPLTLTPYVFEGDKPHKCEFC DKCFSRKDNLTMHMRCHTSV KPHKCHLCDYAAVDSSSLKKH LRIHSDEPHYKQ\VCPIASRNS SQLTVHLRSHTA\GDTPPQCWL CSAKFKISSDLKRHMIVHSGEK PFKCEFCDVRCMTKANLKSIIIR IKHTFKCLHCAFQGRDRADLLE HSRA/LHQADHT\EKCEPCSYSC SSAAALRVHSRVHCKDRPFKC DFCSFDTKRPSLAKHVDKVHR DEAKTENRAPLQKEGLREGSSQ HVAKIVTQRAFRCECTCGASFVR DDSLRCCHKQHSDOSEKQNL
10477	40845	A	10538	1	1427	MIAFDSMSHIQVMLMQEESTAP ATLEHILGHSQLCGSDGLAHAA VWVLAHLHYWFTGLSPGPM VLPLHPAIISSFFHLWRVAFISKA GKPRAAGHLLKRFLRCQFQRA ASSLLFTTVEAMLGTESGTEKV MRGAGTWYHIIENWPSAECV WTEEYQQGRQEDSAEDRKLF VGMNLNQSEDDVRRLEAFG NIEECTILRGPDGNSKGAFAVK YSSHAEEQAALNALHGSQTM GASSSLVVKFADTDKERTMRR MQQMAGQMGMFNPMIPFGA YGAYAQALMQQQAALMASVA QGGYLNPMMAFAAAQMQMA ALNMNGLAAAPMTPTSGGSTP PGITAPAVPSIPSGVNGFTGLP PQANGQPAEEI\FANGIHPYPA QSPTAADPLQQA YAGVQQYAG PAAYPAA YGQISQA FPQPPMIP QQQREGFVSFDNPASQA TAIQA MNGFQIGMKRLK VQLKRPKDA NRPY

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10478	40846	A	10539	1	547	AAAPMTPTSGGSTPPGITAPAV PSIPSPGVNGFTGLPPQANGQP AAEAVFANGIHYPYPAQSPTAAD PLQQAYAGVQQYAGPAAVPA AYGQISQAFPPPPMIPQQQRE GPEGICNLFIYHLPQEFGDSIEL MQMFLPFGFRE/RFDNPASAQT AIQAMNGFQIGMKRLKVQLKR PKDANRPY
10479	40847	A	10540	96	1080	WFKCYGCNSS/RDWQRSTYLLS WEVRG/RPVDPDSGCKAVVALC SQPAHPSNICKVGGCLTK\HLL LMGAMGIRVACLEVWRDGEER GGEEATFTSLAERQVGTAAHRH LHQPALYIQRKVPAALHMCVV QKPSLFQADSRAPLEQGLRQQA SLATARPIVSGANAGPAGLKVP QAAQLQLSPYLHRGVGDEACR YGRSQPTRKAFALCICAAPALP CPALDGSWMVCGLGQETRTSL ANVQSFTQRPQQPLTVWMLN RGRKPAQGTLTVICPIGPHLLT STITESVCVPRRNKYHSRTLPA AQHCQWLVTAVPTALGLVIRA GSKKLC
10480	40848	A	10541	1	392	
10481	40849	A	10542	1	110	FFWSHS*VYYTCFLLNQ*KHLK PGPSGSLSPSISGN
10482	40850	A	10543	1	978	MAAATRGCRPWGSLGLGLV SAAAAWDLASLRCTLGAFCE CDFRPDLPGLECDLAQHLAQ HLAKALVVKALKAFVRDPAPT KPLVLSLHGWTGTGKSYVSSLL AHYLFQGGRLSPRVHHFSPVLH FPHPSHIERYKN/DLKS WVQGN LTACGRSLFL/DEMCK/MPPGL MEVLRPFLGSSWVYGTNYR KAIFISINTGGEQINQVALEAW RSRRDREEILLQLEPVISRAVL DKPAPLPSPNSGHHWKERLLD AVVPFLPLQRHHVRHCVLNEL AQLGPQAKGMRVVQAVLDSTT FFPEDEQLFSSNGCKTVASRIAF

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10483	40851	A	10544	1	560	ATSPHQSQQSTVDVQQLHDPQP YPQHAIQVQHIVSEPTASAPSS AQGSSSTQGGQLQQQQQQQQ NSSVQHTYLPASAWNSFRGYSE IQMMTLPPGQFVITDSGVA TPV TTGQVKAVTSGHYVLSESQSEL EEKQTSALSGGVQVEPPAHSDS LDPQTNKQQQTQYIITTTTNG NGSSEVHITKP
10484	40852	A	10545	3	205	
10485	40853	A	10546	2	348	ADQARGKPTWEAVSATQFOLD FPIT*CYGLL*QRVSRRHIGALQ GKPVPLLVHLLYPITPREGLG DRARLCLKQQQQQQQQQQQQ QLLLLLLLLLLLLLLQQCEGT EGRPPFD
10486	40854	A	10547	1	1146	MVTYKLVLRGCESTWNLENH FSSWQKRA/IRLWTVLDAIDQ MRLPVVRTWCLKEWHYGSLA GLNKAETSAKHGEAQSNISKGC RYADLTEDQLSSGESLKEIVPQI KEGKWVLTAAHGNSLRGIVKH LEGLSEEAIMELNLTGPIPIVYE LDKNLKPIKPMQFLGDEVTLCK AMEAVAAQSKAKRRPAGML LSPGTPSLAIPSSAPAPCTCHTD HIWNSPVYSDLAIRANPFCVHI SKANYLVNELHTAVNVAGLYI GWRCPHYLWDCFRIGDESRCF CGHLLREHRIISDJSVPCKVSQC RCFMFCFIPSRPEEVGCCCGCFE SNFLCAACDRRWEHETFFDTQ KTRQRGGRPRGADYVFAEMA VLREAILSNSDF
10487	40855	A	10548	2	516	GRLNERYHGGTLGLNIAETA KHGEAQVKIWRRSYDVPPPPKE PDHPFYRNIRMDRRYADLTED QLPSCESLKD TIARALPFWNEEI GPQIKGKRVLIATHGNSLRGIV KPWEGLSEEAIMELNLTGPIV YELDKNLKPIKPMQFLGIDEET VRKAMEAVAAQGKAKK
10488	40856	B	10549	123	237	

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10489	40857	A	10550	1	952	PAA PQVAGRLGLGCPLHLHVF AVVSAMLLRLRCVPRVLGSSV AGLRAAAPSPFRQLLQAPRL CTRPFGLLSVRAGSERRPGLLRP RGPCACGCGCGSLHTDGDCAF VDFLSDEIKEERKIQKHKTLPK MSGGWLELNGTEAKLVLRKVA GEKIPVPFNNNSIPPFTYGEKD PSQSQKVVEDREPELTSLPKFVV EVKNDGGRKALVLDCHYPED EVGQDEDAESDIFSTRREVVSFQS TGESEWKDTNYLTNLTSLDWA LYDHLMDFLADRGVDNTFADE LVELSTALEHQEYITFLEDLQEV LSRAHRADRC
10490	40858	A	10551	1	879	AAGCRKENSLDLRSQFPRGRDS EDFNVKEEANA AAEIRYTHIL NRVLPPDIRILA WAPVEPSFSAR FSCLERTYRYFFPRADLDIVTM DYAAQKYVGTDFRNLCKMD VANGVINFORTILSAQVQLVGQ SPGEGRWQEPQLCQFEVGTGQ AFLYHQVRCMMAILFLIGQGM EKPEIIDEVLLNIEKNPQKPQYSM ACFEPLVL\YACKFENVKWIYD QELRSSNITHLQQLWANHAVK THMLYSMLQGLDTPVPCGMG PKMDGMTWGNVVKPSVIKQTQ CLCRREDAHI
10491	40859	A	10552	231	358	
10492	40860	A	10553	2	319	
10493	40861	A	10554	573	1660	MAAPTARPVLTLLVALFGM GSWA AVNGI WVLPVVVKELP EGWSLPSYVSVLVALGNLGLL VVTLWRRLAPGKDEQVPIRVV QVLGMVGTALLASLWHHVAP VAGQLHSVAFLALAFVLALAC CASNVTFPLFSLHPPRFLRSFF LGQGLSALLPCVLALVQGVG RLECPAPINGTPGPPLDFLERF PASTFFWALTALLVASAAAFQG LLLLLPPPPSVPTGELGSLQVG APGAEEEEVEESSPLQEPQSAA GTTGPDPKAYQLLSARSACLL GLLAATNALTNGLVLPVQSFSC LPYGRALALPPGLWCWAVLPI WACFLGHGCCAGPWQGWGG LLSAGRVLWGLPDGRWQS

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10494	40862	A	10555	154	850	QFFRVITCLPFKGPDYRLYKSEP ELTTVAEVDENGEKSEPVSEI ETSVVKGSHFPVGVVPPRAKSP TPESSTIASYVTLRKTKKMMDL RTERPRSAVEQLCLAESTRPRM TVEEQMERIRRH/QQACLREKK KGLKCFSVLSDQSPLOQSPNLR DNPFRITQTTRRDDKELDTAIR ENDVKPDHETPATEIVQLKETE PQNVDFS/IRGLLDPCPSVILPGR SIKRAKNQNS
10495	40863	C	10556	39	436	
10496	40864	A	10557	2	959	
10497	40865	A	10558	34	1044	QGCAGAGPLHPARLPCCVHGC PVRMHALSCHVRCHFVTFR LMYLDWLPTVIEPCGVGSNKV PVVQHPHHVHPLTLITYSNEH FTPGNPPPHLPADVDPKT/GMC SCGTGRCAVARTCRIRSCVPCE ALSPCDARGAHSAGIPRPPHPPD ISPYYPPLSPGT/QGQPVYPITGG FRHPYPTALT/NASMSRKHQD SKKEEEKKKPHIKKPLNAFMLY MKEMRAKVVAECTLKESAAIN QILGRRLGYNARAFGLKRGWR LDKYRGFVWMEMAVVWSLPPA FSFQGGKKKKRKRDKQPGETND KPESSLGASSLMVVGNWYTRN QEKHIPTLELDHTVSV
10498	40866	A	10559	2	398	
10499	40867	A	10560	174	362	
10500	40868	A	10561	14	266	
10501	40869	B	10562	67	474	

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10502	40870	A	10563	1938	3291	ERRKRFGMLDATDGGPTEDAA LRMEVDRSPGLPMSDLKTHNV HVEIEQRWHQVETTPLRREEKQV PIAPVHLSSDGGDRLSTHELTS LLEKELEQSQKEASDLLEQNRL LQDQLRVALGREQSAREGYVL QATCERGFAAMEETHQKKIED LQRQHORELEKLREEKDRLLAE ETAATISAJEAMKNAHREMER ELEKSQRSQISSVNSDVEALRG QYLEELQSVHRELEVLSQYQS AKCLENLAHAQALEAERQALR QCQRENQELNAHNQELNNRLA AEITRLRLTLTGDDGGGEATGSP LAQGGDAH*LKGLMVRVKESEI QYLKQEISSLKDELQTALRDK KYASDKYKDIYELSIKAKA\A DCDISRLKEQLKAAATEALGEKS PDSATVSGYDIAKSKSNPDLFL KKDRSCVTRQLRNIRSKSLKEG LTVQERLKLFESEDLKKD
10503	40871	B	10564	58	4405	
10504	40872	A	10565	3	156	NSSHHCHHHHHHHHHHHQH QHNCVHQHHHHYHHYDYHH DDNYHHHHHHHH
10505	40873	A	10566	10	445	HRSTITRQCPSGLETRIALLP VFPSPGSRTPPSTPGSSSPQPR/P PLTRGPGPPRTHALASGTRGPA RGEEKVADTPHHGEGGCPNSE KEPFLHPTAPPRLPTSPESGP VPHTLQAPPLRRHLGGTPAGA PASPQSSEWGG
10506	40874	A	10567	1	288	
10507	40875	A	10568	50	542	TLSPERLSPELRLPYMITLGDA VHNFADGLAVGAFAISWKT GLATSLAVFCHPELPHGLRPL LAAPGAVPCAKELLLNLASALT AFAGLYVALAVGVSESEAWI LAVATALLFLYVAICDMLPAML KVRDPRPWLLFLHNVLGLLG WTVPADAVPVRG
10508	40876	A	10569	1	690	
10509	40877	B	10570	34	465	
10510	40878	A	10571	1	624	
10511	40879	A	10572	3	933	

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10512	40880	A	10573	1	1481	RRFPAGAVAVIERGVRGGSQR CRTMADQLYLENIDEFVTDQN KIVTYKWLSTLGVHVNQAKQ MLYDYVERKRKENSQAQLHVT YLVSGSLIQNGHSCHKVAVLRE DKLEAVKSKLAVTASIHVYSIQ KAMLKDSGPLFNTDYDILKSNL QNCSKFSAIQCAAAVPRAPAES SSSSKKFEQSHLHMSSETQANN ELTTNGHGPPASKQVSQPKGI MGMFASKAAAKTQETNKETKT EAKEVTNASAAGNKAPGKGN MMSNFFGKAAMNKKFVNLDS EQAVKEEKIVEQPTVSVTEPKL ATPAGLKKSSKKAEPVKVLQK EKKIRGKRVALSDDDETKETENM RKKRRTIKLPESDNSEYEVFPD SSGAYEAESPSPPPSPPLEPVP KTEPEPPSVKSSSGENKRKRKR VLKSKTYLDGEGCIVTEKVYES ESCTDSEELNMKTSSVHRPPA MTVKKEPREERKGPKKGTAAAL GKANRQVSITGFFQRK
10513	40881	A	10574	1	100	

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10514	40882	A	10575	2	2271	PELLTEGVKEPIMDSQERDSGD PLVDESLKRQGFQENYDARLSR IDIANLTRREQVQDLFNKKYGEA LGKYPVQVQPYKRIKSNPGSVII EGLPPGIPFRKPCTFGSQNLRIJL AVADKIKFTATNPFQGLIPKPD EDDANRLGEKVILREQIKELF NEKLR*GPWGLNRPVLVPYKL IRDSPDAVEVPGLPDDIPRNP TYDIHRLKILKAREHVRMAIIS QLQLLQQQQHHISEGRPFAEIC NDAKVPGESEARKPPFCVGT LFLKKREPEVSMNKDRYPQE APRNLQSLRTLLDILDDPRGGC VHLRQSQSRWRGADTRELPRG MLEGLRQLLSAIGCPRDPTCAP AQPGDQPLQRLAFTLANEPQTV LEKPPPRFRRRGAARSPEQLYTP RRGGVLPAPERTQSASADAGS LACRALVDSGCPPTGPPCKGS RRLTITSGVDCGLLKQMKLEQ EKVVLQGLEMMAGSRLQRLQ PVQDRQCRLLGQSRASADFPA GSPHPLGRLLPKVQEVARCVGE LLAAAGASRALPTSSSGPLCPA LTFTSFGWQQQTILMLKEQNR RLTQEVTEKSGRVMQLEKQSA LIMKQLFEAQALSQQDGEASGL HLHLARLGWAEPQGSSTVQPF GGRPVSPNVSGWRPAAQAVP EWAPSCPTCHPGFPGPPAPGR TEPLTRFWLLVLTWAGALLSLH
10515	40883	A	10576	346	3136	ALRTRRLWPGGHCRAEAPQWP P/ASPLAPATAAAHSRHLSLCL SDKGSMSDEDCPGTSGELGLR PKIEPEVLIIQVTPDALPTSE EMTDSMPGHLPSEDSGYGMET LTDKKWTDGAKAIGISEPIKV LYSKFLMHPEELFVVGLEPISL RRPNCFGIAKLWKILEASNSIQF VIKSGEEIRWDRELFRCRACSM GGSLQIAKSYTTGLESKSCDP AVESKASAGQDEMOPHARPKL LTEGVKEPIVD
10516	40884	A	10577	60	352	
10517	40885	B	10578	1	720	
10518	40886	B	10579	1	1478	
10519	40887	B	10580	1	1895	
10520	40888	A	10581	2	413	

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10521	40889	A	10582	2	969	WGSWAPQSRGCPYPQPGAAQGR ALAPQHRGSCSPPTWGGGKE/Y LMRAHFGLPSVEAEDKEGKPP SVKFEIPYFTTSGIQVRLAPGSL YGRKRSSLGKSHPSLLQVDGQ YSQQQAGAGHPRTGKRGSQTPG ARQRVEPGKCWPVVCVPHVPC PPTSTALRKHLRPQRAIYTSRLA PGALGGHSCVCLLPGLAGLAC GAFPGPAWVTRCCHSARSVL HQGAPPGPDITVPARLPEPEVE VSCRGRPALNAQQSPPLPPP PPSAAAEASCSSHHVQRRLRAG PEGQGFYLFHNRNKHSLKLA PREPFCVVTDSRIQFGPHI
10522	40890	A	10583	50	1083	NPRAIFKSVRTCPVPTQPCRNV KARSCGVGATGTSFTLSVWPH RYITQEGHKLETGAPRAPGTVT NAVWCVRSEGKIRKNEVFLDVI ESVNLLVSAINGNVLRSEIVGSI KMRVFLSGMPELRLGLNDKVL FDNTGRGKSKSVLEEDVKFHQ CVRLSRFENDRTISFIPPDG/EFE LMSYRLNTHVKPLIWIESVIEK HSHSRIEYMIKAKSQFKRSTA NNVGDPHFPLPNDCLRLNPSFK/T TVGERLSWVPENSEIVWSIKSFP GGKEYLMRAHFGLPSVEAEDK EGKPPDSVFKFEIPYFLTSGIQ VRYLKIIIEKSGYQALPWVRYIT QNGDYQLRTQ
10523	40891	C	10584	175	454	
10524	40892	A	10585	1	193	LLPRPGSGDLFLSPVLPS/HSAS WACPLPRSPMPSSCC*R*RKE MASGFSKGPTLGCCPTCP
10525	40893	A	10586	2780	2965	SPSQGESIPT*WRPTGPSPTSSP GPA*SSLSRPSRSSASASPMCMC VRPSMWAASLLKSL
10526	40894	A	10587	1	1502	
10527	40895	A	10588	1256	1990	RCAPMTTCAWASCCSPWPTPF GTGPSTSVSTSWPWPQFWGWG WL*VGAAPAGGRQHPSPALPR RSSGRSKLSRPSLCQLVPGIL*T RLLSPQKESLPWRGWSWREFPL PQLNLTATEADPGVSSLSAQ RHLHSYKIKVLSRQESLAPAPA SGYPESTALPQNGRGPWAVGF GQIPFLCIHNVGRSLGAGPGSG KPLPCVFRSTFSSSHQYCRLLGR KHNFHTFKGKRLCCGCGPDGR

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10528	40896	A	10589	375	678	RCCCTTRPARKCRTTMGIRHS TWPAPTATRTTHSGSRSPGSTA ASPRGLCRPALTDPCPGHLSG LPVASV*AGSCPHVPGDQTTRK SGTVFPTQCTRP
10529	40897	B	10590	1	2452	
10530	40898	B	10591	1	1140	
10531	40899	A	10592	1	1617	
10532	40900	A	10593	1	1448	RERSCLHLVCIRCSDVVEGMS VLGLCSMASWIPCLCGSAPCLL CRCCPSGNNSTVTRLIYALFL VGVCVACVMLIPGMEEQLNKIP GFCENEKGVPCNILVGYKAV YRLCFLGLAMFYLLLSLLMIKVK SSSDPRAAVHNGFWFFKFAAAI AIIIGAFFIPEGTFTTVWFYVGM AGAFCFILIQVLVIDFAHSWNE SWVEKMEEGNSRCWYAALLS ATALNYLLSLVAIVLFFVYYTH PASCSENKAFISVNMLLCVGAS VMSILPKIQESQPRSGLLQSSVIT VYTMYLTRS/CMTNEPETNCNP SLLSIIGYNTTSTVPKEGQS/VQ WWHAQGNIGLILFLLCVFYSSIR TSNNGQVNKLTLT/SGESTLIGR WVGARSDGITGRDGGTDVSPE AVRINGK/RDGCSLYSYSFFHF MLCLASLYIM/MTLSWYRYE PSAWMESQWTAVL/WVKISSS WIGIVLYVWTLVAPLVLTNRDF
10533	40901	A	10594	3	343	GVLLCRL*QGQNYW/NFLQTK VTGNMRDKRTTPMPEFLHASW PNTELRYWKENCPEQKGP*PM MALMS*GCPLPWPAPNVTSSSKG WSPGQLWMYRFGRPLRISSETG WSLWLT

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10534	40902	A	10595	1	2500	MEDAWGIRKETGRVKEEAKEV TGWGNWNRNVEKSSMRKVK AARPGFKLPMSTDIIPKCTIKD LLPKEKSSTEAVFHTVVLERHE SPDIEDFSFKEPQKNVHDFECQ WRDDTGNYKGVLMQAQKEGKR DQRDRRDIENKLMNNQLGVSF HSHLPELQLFQEGEKMYECNQ VEKSTNNGSSVSLQQIPSSVQT HRSKKYHELNHFSLLTQRKA NSCGKPYKCNECGKAFTQNSN LTSHRRIHSGEKPYKCCECGKT FTVRSNLTIHQVIHTGEKPYKC HECGKVFRHNSYLATHRRHHTG EKPYKCNECGKAFRGHSNLT HQLIHTGEKPFKNECGKLFTQ NSHLISHWRIHTGEKPYKCNEC GKAFSVRSSLAIHQTIHTGEKPY KCNECGKVFRYNSYLGRRHRV HTGEKPYKCNECGKAFSMHSN LATHQVIHTGTSPKFCNECSQ VFTQNSQLANHRRHHTGEKPYK CNECGKAFSVRSSLTTHQAIHS GEKPYKCECGKSFTQKSHLRS HRGIHSGEKPYKCNECGKVFA QTSQALRHWRVHTGEKPYKCN DCGRAFSRSSLTFHQAIHTGE KPYKCECGKVFRHNSYLA TH RRIHTGEKPYKCNECGKAFSM HSNLTTHKVIHTGEKPYKCNQC GKVFIQNSHLANHQRTHTGEK PYRCNECGKAFSVRSSLTTHQA
10535	40903	A	10596	330	432	
10536	40904	A	10597	1	147	
10537	40905	A	10598	1	380	RTRGRGQRGMELVQVLKRGL QQITGHGGLRGVYLRVFFRTNDA KVGTLVGEDKYGNKYEDNK QFFWHRWLHSMDDPPTTKPL TARKFIWTNHKFNVTGTPQY VPYSTTRKKIQEWIPSTPYK
10538	40906	A	10599	9	536	VLKRGLQQITGHGGLFRGYLR VFFRTNDAKVGTLVGEDKYGN KYEDNKQFFGDERLQASGLA LTLCEQTEEGSCLWSQRSLGK SQSMNFKNKSTRSFQRTVSAGK TKYYHPVAVGRQQQARA TCD HVDPRTEHGPAA WPHYWPLR GLKHALLTFTVALQYRAQPLFR LPNLPL
10539	40907	A	10600	239	263	
10540	40908	A	10601	1	600	

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10541	40909	A	10602	1	1178	
10542	40910	A	10603	1	1038	MHLEVNSSPEPLDENLDNTVTS ALSGHEQRIQTSPLVLLTTKTEI LARFSQLQFPEEQSSFAYPANC VKSKGMNTKLLPLRLKVCREL TIDS DRDILYRTLFMGDSGMGK VQFEFGEEVHIVIKSTGFGPFSS YATLEPFVAVQLWGGGQHYQ GQQPPMGMMGQVNGNHMM GQRQIPPPYRPQQGPPQQYSGQ EDYYGDQYSHGGQGPPEGMN QQYYPDGHNDYGYQQPSDEQ GYDRPYEDSSQHYYEGGNSQY GQQHDA YQGPPPPQQYPPQQQ QYPGQQGYPKQQQGYGPGSQ GPGPQYPNYPQQGQGYGGYI PTQPGPPQPPQRPYQYDQGQY
10543	40911	A	10604	130	213	LKVST*AMPLPR*TPSRRCQP*R TGTS
10544	40912	A	10605	124	208	LKVST*AMPLPR*TPSRRCQP*R TGTS
10545	40913	B	10606	140	589	
10546	40914	A	10607	1	302	
10547	40915	A	10608	2	98	
10548	40916	A	10609	2	190	
10549	40917	B	10610	1	856	
10550	40918	A	10611	123	1287	AFSLGK\MSEKLLFGPNGERMP FSKVKALCAGLQATVAAPKNA EENKAIQDVAKDTAFLGITDEA TEGQFMYLTGGRLTYSNWKKD EPNDHSGEDCVILLNGLWN GISCTSSFIAIFQWAHYQYRQAE NYPKGELHTLRVKLCGPSWPT NAIHFRRLLMPLGPTVLLMTM AVFQLSQAVAMCSWCCGLVLP PAGCLQDKASKPRETQAQPL CVRGNFRIPSRQDFAAALARAL SGLDLWASLVVPFADFLGSSLS VPWFYSLEND EEDLTRLSRLN GERTFLESPGKKRIGAGTPPMS QEAVMLAVMERDPGQCRGEE GPTECRAMWPGWGRHSLPGH PAMLCFLGSDLEIRGSNGWE PPFIPGLQPELARGIQSGRGAE
10551	40919	A	10612	292	445	LSICLQSAVCTPGMD/PAAPCSL GILDWGTLPSTAEPGREGPADA WVDPGVR
10552	40920	A	10613	363	575	HLLPTQGAALCPAEGWPAPWQG YTPTCDCAEDTTQLERAGQLPP VF*SCHRRGGVSSQ*GSPGPVQL LHQPE

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10553	40921	A	10614	3	638	SSKLSGLTINNVVDIILAHHFGQE ELQANLDI.IQTYRMHIAQDINQ DNLQLFLNSYNRRDLIERPIL GQNDNKSCTLKGSTLLVVGDN SPA VEAVVECNRLNPINTTLAL KMA DCGGLPPG*FSPGKLT EAF KYFLQGMGYIPLVLCYSTSGS MTSVARSRI THSTSSSLGSGESP FSRSVTSNQSDGTQESICESPDV LDRQQTMEVSC
10554	40922	A	10615	3	1152	KSCFNAFFNFEDMQEITQHFAV CHVDAPGQEQEAP/SPFPTGYQ YPTMDELAEMLPVLTLSLKS IIGIGVGAGAYILSRFALNHPEL VERPLCSLMVDPC/ALKGWIDW AASKLSGLTTNVV\EIILAHHFG QEELQANLDLIQTYRMHIAQDI NQDNLQLFLNSYNRRDLIER PILGQNDNKSCTLKCSTLLVVG DN SPAVEAVMADCGGLPQVVQ PGKLT EAFKYFLQGMGYIPVCA AQSP EHRVSTASMTLRLARSRT HSTSSSLGSGESPFSRSVTSNQS DGTQESCESPDVLD RHQTMEIS LDDVLLSALLRNGKSAQKKKI SAKPKLEFLCPRPGTCDHGSRE KQGH SRGP GQFPGRWP GRAVA ETRGAIDHRL
10555	40923	A	10616	169	270	GICPFLQLSFYHLLD* DTRYLQI LRLQLKPHSFH

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10556	40924	A	10617	1	1551	MRKDSCASSMHQQVSRSKKRA GQKTPPEDQEGGQRALRSSHIR LGQFLLIEDCKTPSPSLGADAI AKQRKTSVSAAASVSATIPIRR VQGPTVVGSWARGVSAASGP RGITGPKGKARSEKGC SL SHGPQ TNKPLVVQKGQKMEQANHVP GLVISVVYKDILKKIVQRETSH LIHVRYAEAITGRRRTAPEDKGS LGRDMLAKAGAIHYMNMGNKL PIWCHLLEEGIVLEWALEGQF GRAKNACPQIRLKDPTTFPYQ RQYPLRPEAHKGLQDIVKHVK AQGLVKKCSSPCNTPILGVQKP NGQWSLVQDLRLISEAVIPLY VVPNPYTLTSLQIPEEA EWFPVL DLKDAFFCIPLHYDSHDSQFLF AFEDPTDHTSQLIWTVLPGQFR DSPHLFGQALAQDLGHFSSPGT LVLQYVDDLLATSSAASCQQA TLDLLNFLANQGYKASRSKAQ LCLQQVKYLGILARGTRTLGK ERIQPILAYPHKTLKQLWGFL QIT/GFCQLWIPR*SKI
10557	40925	A	10618	1	1022	MKPSVWALIQNLSPYEKGILG LTKRHQGRCLTDGROGIQPLPP SQAHTGIPLHPYSIQVDCAIDR GKLCFCCIGECNYSDDQGPQT VAGSWARGISAAVSVSATILISR VQGPLHVLGQEVFLLRRQTNL AGSERTENGAGQSPGGACYQC GLQGHTKDCPMRNKLP RP CP LYQGNHWKDGEPHEDCQIIIV QTSAAREDLLEVPLANPDNL Y TDGSSFVENGEVAKA VIAQFPT TVGVSCLDGRLRVLEVLARIR /LGEGNKGY S I R K R G S Q I V P C R *HDCISRKPHHLSPKSP*ADKQL QQSLRIQNQCAKITSILIHQ*QT
10558	40926	A	10619	1	2091	
10559	40927	B	10620	1	2269	
10560	40928	A	10621	1	1776	

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10561	40929	A	10622	112	1465	LLKGARCLIQRPFA/LQETHR AHTLLEWEPQAEATFTTLKQA LLQAAALTLPTQNFSLVYVTD AEIALGVLIQTGTTQPVAVLT IEKGKERGEQHKQLAEAAER KERKRQEVREKEKEKTERQSK KEREEETKMESEKRETEKEVS TLAALEEFSPQPSGLAEAGA GSLFSWGGVEGEVGGGAAH SAHRLVQVPGQVRVQVFENP LLKAIKSDLPRSSLWSGRKTSV SAAALKEIRKEISKGTQPLGYR LCPLQAVGGGEFGPTKIHVPFS LSDLKQIKADLKGKFSDDPDYR DVLQGLGKTFDLTWRDVMALL DQTLAFNEKNAALAAASEFGGI WYLSQVNDRMTEERDQFPFG QQAIPMDPHWDLDSHDGWS HKHLLTCVLEGLRGIRKKPMN YSMMSTIIQKKEENPSAFLQL WKSRLRYTPPSSKSL
10562	40930	C	10623	52	690	
10563	40931	C	10624	199	285	
10564	40932	A	10625	59	411	SWPSDKQTLVVQRGQKMEQA NHPDPTDHMSQLMWT/VLPQG FRDSPHLFGQALAQDLGHFSSP GTLVLQYVDDLLATSSAEASCQ QATLALLNFLANQGYK/LSRSK AQLCLQQVKYLCL
10565	40933	A	10626	280	571	DIYVPIRII*KLPAAYAD/PAVPP CTSGRIWL*IHAGAWSSFWLVS Y*LLPQFQILLVYSEIQLPGLV LGECMCQGICPFLLDFLVYLR GVCSIL
10566	40934	A	10627	60	148	WGRGEPLCLAQGL*THQSAPC QNRPLGSL
10567	40935	B	10628	1	397	
10568	40936	A	10629	55	219	LGKHLGSLIDPRGSWVTGEYI FLRPPIAA*GRQ*DFLPPELWW TSLNNSWAFS
10569	40937	A	10630	3	494	
10570	40938	A	10631	2	689	
10571	40939	A	10632	157	277	DV*SNNSMTSLQVRCRTSMYLS GSSENFPRSTWICDAVAETPLA QEPATVPGP
10572	40940	A	10633	230	543	PSDRQTLVVQRGQKIEQANHL VGLVTSVVWKTDLKKIVHGM FMSLISC/PRQLSSRSITIQGILGR AVTRYFSLHSCNWTLLQIDQ GHQATDGLTNGTPNELN
10573	40941	B	10634	1	669	

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10574	40942	A	10635	119	409	GDICHHGLTPVGSHSLSCSR* QVA*VGAVTAATIGTGILLQQL AFLVCNWLLSGSSENFPRSAI CFKSEREKGTICIQVGNPSPPTA CKGHN
10575	40943	A	10636	3	482	LSSYSGGDLEKLYV*LRDCKYT NQHSVSSSRFVNIPISTLCLTQG L*MHPMDTLYLATLGGDLENL CVHTLYLANLVGMWRTFVSSS GIVNAPISTLSKQTT*LSVKWTN QQDVGGARQENKSRLPEPAVT TPLGSPPTPWKLCFALCNKSC YCPK KKK
10576	40944	A	10637	1	2331	
10577	40945	A	10638	879	1353	SNNRTEGARGKRLMSSP/STE PRVRLTIEGQETDFLLDTGAAFS VLISCLGRLSSRSVTIR*ILGQPV TRYFS/QPLSCNWETLLFSHAFL IMPESSTPLLGRDILAKAGAIHYI NMGKNLPICCPLLVEGINPEV WALEGQFGRAKNARPLQIRLK
10578	40946	A	10639	345	1996	
10579	40947	B	10640	97	1110	
10580	40948	A	10641	728	5171	
10581	40949	C	10642	1	2049	

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10582	40950	A	10643	1	2019	MNAHPEFRMAMKDGELVIWD SVHPCYTVFHEQTETFFSLWSE YHDDFRQFLHIYSQDVACYGE NLAYFPKGFENMFVVSANPWV SFTSFDLNVANMDNFFAPVFTM GKYVTQGDKVLMLAIQVHHA VCDGFHVGRMLNELQQYCDE WQGGAQYPLRPEAHKGIQDIV KYLKAQGLGRKCSSPCNTPILG VQKLNGQWRLVQDLRLIN/EGF F*SSKLQAMQAMFAENSMSSV YSPTQEA EYWLPHGILQPADCF FEAASTRSMWPRE/DWLSTT/S LTTWNMDFADFGTTIKQDFRLL GQTSVDRLLQLSQQAVKGNQ LLPVSLVKRKTTLAPNTQTASP RALADSLMQLARQVSRLESGH LDHGSHSYRRSDNSLDPRSHSC CRSDIGLGRSHLYCRSDYQRE TTIPSMVPKGNQAPCMKSNNNA LIVLGTVTLDVIGLVMVPVLP GLLRDIVHSDIASHYGVLLAL YALMQFLCAPVLGALSDRFRGR RPVLLASLLGATIDYEIMATTPS WEDEEPIEHSQQIIVQTYATR DDLLEVPANPDNLNLYADGSSF VENGIRRAGYAI VSDVTVLENS LAAVTLQNRQGLDLLTAEKGG LCTFSGKECCFYTNQSGISSPLE DITTAGPFLHPIQQEVARAIIGQ FPTAFGVSCLEGRLRGEASWTS
10583	40951	A	10644	803	1171	
10584	40952	A	10645	1	2148	
10585	40953	A	10646	1094	3886	SNDRTEDDCGKHPFMSSSP ^A TEP WVCLIEGQEIDFLDITGTTFSV LIPCLGRSSRSVTIQILGQPVT RYFSHLLSCNWETLLFSHAFLV MPESPTPLLRDILAKAGAIISM KTGNKLPICCPLEGINPEVWA LEGQFGRAKNAHPLQIRLKDPI SFPYQRQYPLRPEAHKGLQDIV KHLKAQDSVRKCSSPCNTPILG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYLLSQVPEEAEW FTVLDLKD
10586	40954	A	10647	762	1298	

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10587	40955	A	10648	893	2165	GPRGTGPKGKARSEKGRSLSHG PQTNKPLVVQKGQKMEQANHP VGLVISVYVYKDKLKVQRETS HPLIHVRYAEAITGRRRTAPEDK GSLGRDMLAKAGAIHMMNMG KLPIWCHLLEEGIYLEVWALEG QFGRAKNACPVQIRLKDPTTFP YQROYPLRPEAHKGLQDIVKH VKAQGLVKKCSSPCNTPI LGVQ KPNGQWSLVQDLRLISEAVIPL YPVVPNPYTLLSQIPEEAEWFP VLDLDAFFCIPLHYDSDHSQF LFAFEDPTDHTSQLIWTVLPGQ FRDSPHLFGQALAQDLGHFSSP GTLVLQYVDDLLATSSSEASQ QATDLLNLANQGYKASRSK AQLCLQQVKYLGILARGTRTL GKERIQPILAYPHPKTLKQLWG FLEITGFC*LWIPGYSKIARPLYT
10588	40956	A	10649	2	403	
10589	40957	B	10650	51	1038	
10590	40958	A	10651	581	1128	SPCRAQRHSCMWGLWQQSPCS PGSWQDSSPAQSGPPR*PFSVP SSPWCLPSTWPLSPSPLPASWR RKTSAPSLLSLATAGPP*AGVC E/AKTPKKKYSDDDEEESEEN SRDSESDFSDDFSDFFVETRRL RSRRNQKRQINYKEDSESDGSQ KSLRRGKEIRRVHKRLSSSESE GYFFIKS
10591	40959	B	10652	1	4296	
10592	40960	A	10653	2	447	KEKKRNKKKKTIGSPKRIQSL NNKLLNSPAKTLPG/AC/GSPQK LIDGFLKHEGPPAEKPLEELAS TSGVPGLSLQSDPAGCVRPPV VKYCTDLIEEKDLEKDLVIKY MKRLMQQSVEVWNMAFDLIL DNNQVVLQQTYGSTLKVIT
10593	40961	C	10654	286	336	
10594	40962	A	10655	421	638	

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10595	40963	A	10657	1	888	MMNEKNLEKGLGVDSVDKDA MNAAIQQAIIKAQPSMSPKKAPP APAKEARNVVAVGTGGRGTHD RDPSEKPPRLQWFEQQA KLA KQQEEDSEEEEDLDGDVLEIG KSKIKVLAESVSDWEDIDSDEE LECEDTEAMDDVVEQDAEEEE AEEGPPLGAIPITDCLFCSHHSS LMKNVAHMTKDHSSFFPDIEYL SDIKGLIKYLGTHSSSNVCKGL WDLEKRP SIDLK/CRT*YSTKRH /CTRTLSASSHFILCQWFSVLS/P VHASTDQEIQEMHDDQSNPQN AVVREHCVGWGWGV
10596	40964	A	10658	1	1545	MATYTCITCRVAFRADMQRA HYKTDWHRYNLRKQVSMAP VTAEGFQERVRA/HGPSRRRRA RARP/LYCTVCSKKFASFNA YE NHLKSRRHVELEKKAVQAVNR KVEMMNEKNLEKGLGVDSVD KDA MNAAIQQAIIKAQPSMSPK KAPPAPAKEARNVVAVGTGGGR GTHDRDPSEKPPRLQWFEQQA KKLAKQQEEDSEEEEDLDGD VLEIGKSKIKVLAESVSDWEDI DSDEELECEDTEAMDDVVEQD AEEEEAEEGPPLGAIPITDCLFC SHHSSSLMKNVAHMTKDHSSFF PDIEYLS DIKGLIKYLGKVGVG KICLWCNEKGKSFYSTEAVQA HMNDKSHCKLFTDGDAALEFA DFYDFSWRLAVGGHDWVERLT ASHYFYGYYPGARVGHRS LMR YYQRFGLSRAVAVAKNRKAV GRVLQQYRALGTGSGAAL MRERDMQYVQRMKSKWMLK TGMKN NATKQMHFRVQGSQK EIQIFHSSEIDGIATAVEDDFASP TPTKDAKN
10597	40965	A	10659	3	943	

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10598	40966	A	10660	1	2427	MATYTCITCRVAFRDADMQRA HYKTDWHRYNLRKKVASM VTAEGFQERVRA\HGFSRRRA RARP/LYCTVCSKKFASFNAYE NHLKSRRHVELEKKAVQAVNR KVEMMNEKNLEKGLGVDSVD KDAMNAAIQQAIIKAQPSMSPK KAPPAPAKEARNVVAVGTGGR GTHDRDPSEKPPRLQWFEQQA KKLAKQKEEDSEEEEEEDLDGD DWEDIDSDEELECEDTEAMDD VVEQDAEEEEAEGLPLGAIPIT DCLFCSHHSSLMKNVAHMTK DHSFFIPDIEYLSDIKGLIKYLGE KVGVGKICLWCNEKGKSFYST EAVQAHMNDKSHCKLFTDGD AALEFADFYDFSRLAVGGHD WVEVEGRIRGCGSREDNECLL VCNFSVIGVAIQTRKGRTPIRA EELPSEKNLEYDDETMELILPSG ARVGHRSMLMRYYKQRFGLSRA VAVAKNRKAVGRVLQYQYAL GWTGSTGAALMRERDMQYVQ RMKSKWMLKTGMKNNAATKQ MHFRVQMDRCGIAVLVFKAPS FYLIMAPKKHSGDAGDSNMPK GSRKVLPLSEKVKVLKEKKLY AEVAKIHGVKLQTFGVSVTAH KGSVDPKSEQQQDILLQRVKEQ SFHSVEADPAEAGAGSGLSQLR KGLPQCSSRLNGSSSATKVGAG AEEAPRASEGCEGCQHA VTSQ
10599	40967	A	10661	3	658	GTKGWAFPIITDCLFCSHHSSLMKNVAHMTKDHSFFIPDIEYLS DIKGLIKYLGKVGVGKICLWCNEKGKSFYST EAVQAHMNDKSHCKLLQDGDAALEFADFYDFR SSYPDHKEGEDPNKAEELPSEKNLEYDDETMELILPSGARVGH RSLMRYYKQAIWLKVLNLWQLPKIRKAVGRVLQYQYRSPGIGLS TGAALMRERDMQYVQRMKSKMGC
10600	40968	A	10662	1	221	MNPLANSTLTDVHPHFIFKQMA ELDRDMDEAGNHHSQQINTRT ENQTPHVLTHKWELNNENTRT QGREHHTSEEFIAIQPEYYQKE KNSNDINLEGTSYWTEHNCSGI YKVINCLESEIHSEEN*CN*IFLSDNIQVELR*IFLMCDVPCPVSV CSHCSTPTYE

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10601	40969	A	10663	1	1815	MHEAGNHHCQQSNTKRKENQTP DVLTHK WEGFDQLRLEGLLCD VTLMPGD TDDAFVPHRVMMMA SASDYFKAMFTGGMKEQDLM CIKLHGVS KVLGRKIIDFIYTAK LSLNM DN LQDITLEAASF LQILP VLD FCKVFLISGVTL DNCVEVG RIANTYNL TEVDKYVNSFVLKN FPALLSTGEFLKLPFERLAFVLS SNSLKHCTELELFKATCRWLRL EEPRMDFAAKLMKNIRFPLMTP QELINYVQTVDFMRDNTCVN LLEASNYQMMPYMQVMQS DRTAIRSDTHLVT LGGVLRQQ LVVSKELRMYDEKAHEWKS LA PMDAPRYQHGI AVIGNFLYVV GGQSNYDTKGKTA VDTVFRFD PRYNKWMQVASLNEKRTFFHL SALKGYLYAVGGRNAAGELPT VECYNPRNTNEWTVVAKMSEPH YGHAGTVYGGVMIYSGGITHD TFQKELMCFDPTDKWQKAP MTTVRGLHMCCTVGERLYVIG GNHFRGTSYDDVLSCEYYSPH LDQWTPIAAMLRRQSDVGVA V FENKIYVVGYSWNNRCMVEI VQKYDPDKDEWHKVFDPESL GGIRACTLTVPPEETTPSPRES
10602	40970	A	10664	1	1226	MNEIEFRLERTPVDESDDIEQH DEIPTGKCIAPFDKRLKHFRVT EGSPVTFCTKIVGIPVKVYWF KDGKQISKRNEHCKMRREGDG TCSLHIESTSDDDGNYTIMAA NPQGRISCSGHLMVQSLPIRSRL TSAGQSHRGRSRVQERDKPLQ ERFFRPHFLQAPGDMVAHEGR LCRLDCKVSLPPPDMTWLLN GQPVL PDASHKMLVRETGVHS LLIDPLTQRDAGTYKCIATNKT GQNSFSLELSVVAKEVKKAPVI LEKLQNCGVPEGHPVRL ECRVI GMPPPVFYWKDNETIPTCTRER ISMHQD TTGYACLLIQPAKKS D AGWYTL SAKNEAGIVSCTARL DIYAQWHHQIPPPMSVRPSGSR YGSLSKGLDIFSAFSSMESTM VYSCSSRSVVESEDEL
10603	40971	C	10665	166	229	
10604	40972	B	10666	251	371	

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10605	40973	A	10667	79	1391	PWEGSAPATSPLEGDSAWGSA DGSESWSCRELLQPGDVLGESC GLTPPALPAHCIQEGCLPPLTQE LRCCQPPRMGRWALDVAFWL KAELTLGLELLYYCFFIGINFY NKWLTKSF/HIFPLFMTMLHLA VIFLFSALSRAVQCSSHRAV VLSWADYLRRVAPTAALREVA SLFRKPSAEMLCPPARQGEA RELSQNPRIIRAGEGRLQGHRQV ATVICAPAPFSVMGLSPELQQCI VGNFASRYTMTKSSAVLFIIFS LIFKLEELRAALVLVVLLIAGGL FMFTYKSTQFNVEGFA/WCWG PRSSVAFAGPSPRCSRRLNSAS RIPSTPCSTCSHSCS/WGLFPLFA VFEGTGLLLRVLGSFLGGILA FGLGFSEFL/VSSRTSSLTSLIA GIFKEVCTLLAAHLLGDQISLL NWLGFASASREYPTSLPS
10606	40974	A	10668	1	1129	MGRWALDVAFWLKAVLTLGL VLLYYCFSIGITFYNKWLTKSF HFFLFMTMLHLAVIFLFSALS ALVQCSSHRAVVLVSWADYLR RVAPTALATALDVGLSNWSFL YVTVSLYTMTKSSAVLFIIFS FKLEELRAALVLVVLLIAGGLF MFTYKSTQFNVEGFA/WCWGP RSSVAFAGPSPRCSRRLNSAS IPSTPCSTCSHSCS/WGLFPLFAV FEGHLSTSEKIFRFQDTGLLR RVLG/SLFLGGILAFGLGFSEFL VSRRTSSLTSLIAGIFKEVCTLL AAHLLGDQISLLNWLGFASAS REYPTSLPSKPCIPEVTQSPFQK PLVSVLLPVTLSDSDAGSVPGG SAAVPTPLGRCCGHLQSGWVGP
10607	40975	A	10669	566	1026	PVMPKLIYVIRTGKQLKISLGH VDFQTVPSFLQQLNV/WQTICA SEHPDRNDCAVLRQKRLSGS VENTSGKRKCWGGQSGFTTSE LEETEEDSLSDYGDVDRK DALAEPFCMLIGEIFELRGKPY QLEIHWQVPTGPDHLEEEANEK

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10608	40976	A	10670	1717	2340	GIDVQGGKNSFSLSSFLERLPRD FFSHQEETEEDSDLSYGGDDV DGRKDALAEPFCFMLEIFEFLR GMFKWVRRTLIALVQVTFGRIT NKQIRDTVSWIFSEQMLVYYINI FRDAFWPNGKLAPPTIRSKQE SQETKQRAQQKLEENIPDMLQS LVGQQNARHGII/NKYSNALQE TRANKHLLYALMELLLEI.CPE LRVHLDQL
10609	40977	A	10671	181	399	NRVIVPSQIMKRKRKVSIVLN VTGY*/RGM/RKPGLLNLASGFL LSTSPTSSENSRCRLGWQIDPW EEGETYV
10610	40978	A	10672	66	535	CWWQDPLQRTQKSVTATSTK IDISNVKIPKHPADAYFKKQQL WKPRNRKLAGKLSIPAARDAP RARPPHEAPPPPPPELRYRVPP RPAPSSWRHPSGKGRRGPPGIG GRIVGERQLRTEYGNDRPREG DPAPGCCGGARTLSLYGEIKLR VKF
10611	40979	A	10673	67	585	SAAKSEMAGEKVEKPDTEKKK PEAKKVDAGGKVKGNLAKK KPKKGKPHCSRNPVLVRGIGRY SRAMYSRKAMYKIRKYSAAK SKVEKKKKEKVLATVTKPVGG DKVGGTRGVKLRK/MPRIYPT EDVPRKLLSHGKPFQHVRLK RASITPGTILILTGRHRGKRVVF
10612	40980	A	10674	2	282	CIALYCHLLNICSVKVKAEMQNL GREFIVPGMDSATSLIWATK/DL MNAVIEAPEKKPLLKREKQDES QSEIKWASQKKHLNPVQALSEF KAMDSI
10613	40981	A	10675	2	2798	
10614	40982	A	10676	14	2858	PDWRETKRPSASGLWNLALA QLAAEMTAVHAGNINFKWDPK SLEIRTLAVERLLEPLVTQVTTL VNTNSKGPSNKKRGRSKAHV LAASVEQATENFLEKGDKIAKE SQFL*E*LLAAVEYVRKQGD MKTAAGEFADDPCCSSVEQGNM VQAA*TLASVATCLLILA/DMG NVYITLLIQLKVVEDDILKLRNA GNEQDLGI*YKALKPEVNK/VNI MAVKRQQLKDVGHRRDQMAA ARGILQKNVLIIFYTASRA
10615	40983	A	10677	1	4545	

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10616	40984	A	10678	1	1921	MAGLGMGEEGIPGGERWEHKK RAHIVSNHRITRTGTHPYTHSPY PHKDNVHTARREHKTQDLGTI RSVGHSSSEHTQHTTPTDTPVPLV VIVCRVCYRPPHGETRAEYTRH RGQNNRRTKFWVGIKEENLAQ QERTEEQLANIARGGYVLKDC AGQPELIFIATGSEVELAVALAAYE KLTAEGVKARVVSMPSTDAFD KQDAAYRESVLPKAVTARVAV EAGIADYWKYVGLNGAIVGM TTFGESAPAELEEFEGFTVDNP LASRAVRLRLPFNNDQVEAAV GWKLAVRHNGPTALILSRQN LAQVERTPDQVKEIARGGYVL KDSGGKPDII.IATGSEMEITLQ AAEKLAGEGRNVRVSLPSTDI FDAQDEEYRESVLPNSVAARV AVEAGIADYWKYVGLKGAIV GMTGYGESAPADKLPFFGFSTA ENIVAKAHKVLGVKAGSHIPRK KYDVPGKKSFPVKYSTIGSPSP ERPVSITTPNSFVIITANRVLHC NADTPEEMHHWITLLQRSKGD TRVEGQEFIVVEKLIRGLAMED SRNMFAL/S*IQPRRQSH*KSN RRS*CLSQV*KRASW*AFTNI* WPDRLHGLRKYSF/WSPGNIHHL RHCRML*VVRLRLRLNAVYE
10617	40985	A	10679	1	2940	
10618	40986	A	10680	2	404	
10619	40987	A	10681	2	546	WCPHRWRPHTLTPTAAPAVTK SPEATLHYGQVSWNSQNLHLE GQLQASASLQGSFMLK**GDPLD F/VMSPPRPLFERLKARISQSTK TFTPCERLEKRRSTFLEGLTLLRS FRTGSVVQRQVEEEQMLDMWI KEEVSSARASIIDKWRKFQGMN QEAMAKYMALIKEWPGYGST LFDVEGTDIT
10620	40988	A	10682	1	555	
10621	40989	A	10683	1	627	

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10622	40990	A	10684	1	7232	MPEPPTHSMGSCAAGASLTSTA PCSTAPSPIDHLRAKECERTAQ DWQAAPPAALVRDPLAALVRT WRTFMSSSRIVNTPIGTLCLAQ GFQWFSVLSQVHASTDQEIQE MHDEQANPQNAVGTLDVGLID SVCASDSPDRPNSFVIITANRVL HCNADTPEEMHHWITLLQRSK GDTRVEGQEFIVRGWLHKEVK NSPKMSSLKLLKKRWFVLTHTPG LLQEFREDALNWGPDEKIFKET ELVNDMDKINGRIERAE
10623	40991	A	10685	1	2146	IDSVCASDSPDRPNSFVIITANR VLHCNADTPEEMHHWITLLQR SKGDTRVEGQEFIVRGWLHKE VKNSPKMSSLKLLKKRWFVLTHT NSLDYYKSSEKNALKGLTVL NSLCSVVPDEKIFKETGYWNV TVYGRKHCRYLYTKLLNEATR WSSAIQNVTDTKAPIDTPTQQLI QDIKENCLNSDVVEQIYKRNPI RYTHHPLHSPLPLPYGDINLN LLKDKGYTTLDQEAIKFNSLQ QLESMSDPIIIGILQTGHDLRP LRDELYCQILKQTNKVPHPGSV GNLYSWQILTCLSCFTLPSRGIL KYLKFLKKRIREQFPGTEMEKY ALFTYESLKKTKCREFVLSRDEI EALIHQRQDMTSTVYCHGGGSC KITINSHTTAGAVEVEKLIRGLA MEDSRNMFALFEYNGHVDKAI ESRTVADVLAKEFLAATSEV GDLPWKFYFKLYCFLDTDNVP KDSVEFAFMFEQAHEAVIHGH HPAPEENLQVLAHAHATSSIMQG DYTLHA/AIPLAEEVYSLQRLK ARISQSTKTFPCERLEKRTSF LEGTLRRSFRTGSVVRQKVVEE QMLDMWIKEEVSSARASIDK WRKFQGMNQEQAMAKYMALI KEWPGYGSTLFDVEVRTGCHV LGWAGCWHLRTWITAKFMWR EDKMEHFALSTSFFRAPKIVPLT PPFSSQFLFSCVNVNASVILGMN

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10624	40992	A	10686	28	561	MDIVQDATFVYATLQTAHYHR DAGLPVYLYEFEHHARGIIVKP RTDGDHGDEMYFLFGGPFAT GAKVPPDPTGCPVSHLWMQT HPSIGWPQGAHQFLICYALPNE SLLLRRKQKQKE*GGRNPNDG NLPWPRYNKDEKYLQDFTT RVGMKLEKKMAFWMSLYQS QRPEKQRQF
10625	40993	A	10687	148	444	
10626	40994	A	10688	1	1531	PLPGARRCLHEFWGQLASMYV STRERYKWLRFNEDCLYLNYY APARAPGDPQLPVMVWFPGGA FIVGAASSYEGSDLAAREKEGL VFLQHRLGIFSFLSTDDSHARG NWGLLDQMAALRWVQENIAA FRGRPREILTLFGQSAGAMSISG LMMSPLASGLFHRAISQSGTAL FRLFITRNPLKVAKKVAHLGAC NHNSTQILVNCLRALIR\AKVM RVSNKMRFLQLNFQRDPEEIIW SMSPVVDGVVIPDDPLVLLTQG KVSSVPYLLGVNNLEFNWLLP YIMKFPLNRQAMRKETITKML WSTRTLAKNSWGAEHGSKSL VGPPLAQLAPRPQNTKEQVPL VVEEYLDNVNEHDWKMLRNR MMDIVQDATFVYATLQTAHYH RDAGLPVYLYEFEHHARGIIVK PRTDGDHGDEMYFLFGGPFA TGLSMGKEKALSQMMKYWA NFARTGNPNDGNLPCWPRYNK DEKYLQDFTTRVGMKLEKK MAFWMSLYQSQRPEKQRQF

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10627	40995	A	10689	138	1898	ICKYIMNDQWARQNCLHSPTY GPSENVLSSAESKPEIQLSPSCPL IFSSQQALSQHVWLSHLSQLFSS LWAGNPLHLGKHYPEDQKQQ QDPFCFSGKAEWIQEGEDSRLL FGRVSKNGTSKALSSPPEEQP AQSKEDNTVVDIGSSPERRADL EETDKVLHGLEVSGFGEIKYEE FGPGFIKESNLSLQKTQTGETP YMYTEWGDSESGMSVLKNPR THSGGKPYVCRECGRGFTWKS NLITHQRTSHGKPPYCKDCGR GFTWKSNIETHQRTSHGLKPY VCKECCGQSFSLKSNLITHQRAH TGEKPYVCRECGRGFRQHSHL VRHKRTHSGKPPYICRECEQGF SQKSHLIRHLRTHTEGKPPVCT ECGRHFSWKSNLKTHQRTSHG VKPYVCLCECGQCFSLKSNLNK HQRSHTGEKPPVCTECGRGFT RKSTLITHQRTSHGKPPVCAE CGRGFNDKSTLISHQRTSHGK PFMCRECGRRFRQKPNLFRHKR AHSGAFVCRECGQGFCAKTLI KHQRAHAGGKPHVCRECGQGF SRQSHLIRHQRTHSGKPPYICRK CGRGFSRKSNIETHQRTSHG
10628	40996	C	10690	160	294	
10629	40997	A	10691	3	82	SWACAIHPTGYLIEQAGG*WVT ARRD

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10630	40998	A	10692	1	1399	MLRRYRPDITSCHGSTAESKGG VVL DVSGRARPLRRTRNSPST SLTSSKMSGLDGGNKLPLAQTG GLAAPDHASGDPDRDQCQGLR EETEATQVMANTGGGSLETVA EGGASQDPVDCGPALRVPVAG SRGGAATKAGQEDAPPSTKGL EAASAAEAADSSQKNGCQLGE PRGPAGQKALEACGAGGLGSQ MIPGKKAKEVTTKKRAISAAVE KEGEAGAAEKKVVKKK VAGGVKEETRPAPKINNCMD SLEAIDQELSNVNAQADRAFLQ LERKFGMRRLHMQRISFIQNI PGFWVTAFRNHPQLSPMISQGD EDMLRYMINLEVEELKHPRAG CKFKFIFQGNPYFRNEGLVKEY ERRSSGRVVPFSTPTLRWHRGQ DPQAHIHNRNREGNTIPSFNWF DHSLEFDRIAEIKGELWPNPL QYYLMGEGPRRGIRGPPRPVE SARSFRFQSG
10631	40999	A	10693	3	441	
10632	41000	A	10694	190	2716	
10633	41001	A	10695	1	793	MARQKKMGQSVLRVFFLVLG LLGHSHGGFPNTISIGKRKRASR RSRLSLTRDHCPGKAFAVAFRA ERSTGGEQEAAGMLQGGEESRLF GSLWTLWPWRACSSWKLQSGD ADCLAAPGRITRARGAQSVVSG CRETGWGLFMRNTVQEHSFR FAVQLYNTNQNTTEKPFHLNY HETSPIPLKSPVVFCCALVVHS TLHRPCLCSVSSLAHRSHIPSPH CHCKNCCCTPLQPTNVLDVYA LFARSREKANVTCLKLPLEVIPF
10634	41002	A	10696	2	2744	
10635	41003	A	10697	2	2740	
10636	41004	B	10698	47	7237	

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10637	41005	A	10699	426	2118	GFGHTVHAAEGGDFGGSWQGD DSVLLCSTVDPGSWAASRGKG SPCRGPLCGCCPGRSS/QPSKVE VAVSCSCGALLGMCMPVVL LEGCPRGVAAKGKGSQAQTV RRSPSADQSLEDSPSKVPKWS FGDRSRARQAFRIKGAASRQNS EEASLPGEDIVDDKSCPCFEVTE DLTPGLKVSIRAVCMRFLVSK RKFKESLRPYDVMVIEQYSAG HLDMLSRJKSLQSRQEPRLPVQ QGTRTGIDMIVGPPPTSPRHKK YPTKGPTAPPRESQYSPRVQDI VGRGPAITDKDRTKGPAEALP EDPSMMGRLGKVEKQVLSMEK KLDFLVNIYMQRMGIPPTETEA YFGAKEPEPAPPYHSPEDSREH VDRHGCIVKIVRSSSTGQKNFS APPAAPPVQCPPTSWQPQSH RQGHGTSVPVGDHGLVRIPPPP AHERSL SAYGGGNRASMEFLR QEDTPGCRPEGLTRDSDTSISI P SVDHEELERSFSGFSISQSKENL DALNSCYAAVAPCAKVRPYIA EGESDITDSDLCTPCGPPPSAT GEGPFGDVGWAGPRK
10638	41006	A	10700	1	774	
10639	41007	A	10701	124	815	HPGTAMDALNSMQNFLRGRPK TFKSLNAIEWSVKSGQIRNLES ARVSMVGQVKQCEGITSPEGSK SIVEGIIIEEEDEEGSESISKRK KEDDMETKKDHPYTWRJELAK TEKYWDGWFRGLSNFLSCPIP KLLLLAGVDRDLKDLTIGQM Q GKFQMQVLPQCGHAVHE/DAP DKVAEAVATFLIRHFAEPIGG FQCVFPGLLVTCCPPLLQHRAL LVNTFAPEAHC
10640	41008	A	10702	69	370	
10641	41009	A	10703	1	224	MCNTPAYCDLGKAAKDVFNK GYGFGMVKIDLKTCSGVEFS TSGHAYTDTGKASGNLETKYK VCNYGLTFTQK*NTPAYCDLG KAAKDVFNKGYGFGMVKIDLK TKSCSGVEFSTSGHAYTDTGKA SGNLETKYKVCNYGLTFTQK
10642	41010	A	10704	2	171	

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10643	41011	A	10705	1	740	MCNTPTYCDLGKAAEDVFNKG YGFGMGKIDLKTSCSAVEFST SGHAYTDTGKASGNLEPECKV CNYGLTFTQKRNTDNTLGTEIS LENKLA KGLKLSLDITLVPNTG KKSSELKASYKWDFSVGSNV DLDFSGPTIYGWAVLVFEGWL AGYQMSFDTAKSKLSQNNFAL GYEAAADFQLHHTVTDTGTEFGG SIYQKVNIGIEMSLAWTA/GSN NTHFGIATKYKLD CRTSLSAKA VVLGTRV GSC
10644	41012	B	10706	1	318	
10645	41013	A	10707	2	100	
10646	41014	A	10708	116	1746	SSVTGRTEKARIWEVTDRTV/R RPWIGEAVAAAAADGVTFSPV VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSSSTEYVTKVF ALDVAARHRNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS CIVSLKIDWIIERYQLPQSYQLY YFELAI PVGYFYPGSGFSTASRL LLHPRGLRAITIAVFGKQNTYIR LEPFKINVLEQITKHIEKLQCGG VVKQLSRRGNNQHSSTYDINR ADTQVRRAVNNYDIIVMSNSFN GQSEHQVWIARLTWVIGTINVV CAADVLI VPTPAELFDYTSALQ FFDMLRDL LKNVDLKGFE PDV RILLTKYSNSNGSQSPWMEEQI RDAWGS MV LKNV VRETDEVG KARLTWIGTINVCAADVLI V PTPAELFDYTSALQFFDMLRDL LKNVDLKGFE PDVRILLTKYSN SNGSQSPWMEEQIRDAWGS MV LKNV VRETDEVGKEPPSTNTFR HSYAMHMLYAGIPLKVLQSLM GHKSSSTEYVTKVFALDVAAR HRVQFAMPESDAVAMLKQLS
10647	41015	A	10709	284	969	RVSGRKWF FIALKRMPAMKK AMNLFGLSNV RTVHPGFTV YISTHISFSLSGYRTGLRSFGLV KQKKSPIRMPCVYTNP CVSIHP LWLRLRSP SARWLCGSPSLG WTRTEPAPSPRGRTEKARIW EVTDRTVRTWIGEAV/AHAA DGVTFSPVTPHTFRHSYAMH MLYAGIPLKVLQSLMGHKSSIS TEYVTKVFALDVAARHRVQFA MPESDAVAMLKQLS

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10648	41016	A	10710	2817	3297	AGCVRHRLSENRLDHRALPAA SKLPAYA*LPPPLPAGRL*RIPH RQFL*HQI/RL/PTERRCLLTRRT EKARIWEVTDRTVRTWIGAV ARLAADGVTFSPVPTPHTRHS YAMHMLYAGIPLKVLQSLMGH KSISSTEYTKVFALDVAARHR VQIFAMPES
10649	41017	B	10711	1	963	
10650	41018	A	10712	1	1296	
10651	41019	A	10713	1	1167	
10652	41020	A	10714	349	3195	
10653	41021	A	10715	163	864	
10654	41022	A	10716	576	754	
10655	41023	A	10717	1	1449	
10656	41024	A	10718	1422	1600	
10657	41025	A	10719	489	726	ISCCSFFSPRPPHTRFRHSYAMH MLYAGIPLKVLQSLMGHKSIS TEYTKVFALDVAARHRVQFA MPESDAVAMLKQLS
10658	41026	A	10720	1	1596	
10659	41027	A	10721	1	1572	
10660	41028	A	10722	2	100	
10661	41029	A	10723	561	804	TLRQTKPDNSADPPHTFRHSY AMHMLYAGIPLKVLQSLMGHK SISSTEYTKVFALDVAARHRV QFAMPESDAVAMLKQLS
10662	41030	A	10724	1	867	
10663	41031	B	10725	1	825	
10664	41032	A	10726	1	942	
10665	41033	A	10727	2	100	
10666	41034	A	10728	39	359	RILGKGAGQTRAESLVWGRGV PARCC*PGGPFLVPGPPP*VR/H LSYARPMML*PGIPLKVLQSLMG HKSISSPEVYRKVFALNVAARH RVQFAMPEFDAVAMLKQLS
10667	41035	B	10729	41	724	
10668	41036	A	10730	1	1023	
10669	41037	A	10731	1	1314	
10670	41038	A	10732	1	1128	
10671	41039	A	10733	892	1611	
10672	41040	B	10734	78	1099	
10673	41041	A	10735	1	936	
10674	41042	A	10736	766	1056	
10675	41043	A	10737	1	1422	
10676	41044	A	10738	1214	1721	

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10677	41045	A	10739	2592	3233	RWGRWRTGGSSRSEPTMELRA PAWPRGRPGQGARGAGSEL GNATAPSPAELCRNLCRMES PNTDGRPETGSGNRKGAGDK WWKIKTGMRDKLMERRNRRT GRTEKARIWEVTDRTVRTWIGE AVAAAAADGVTFSPVTPHTF RHSYAMHMLYAGIPLKVLQSL MGHKVISSTDFYTKVFALDVA ARHRVQFAMPESDAVAMLKQL
10678	41046	A	10740	6323	7130	
10679	41047	A	10741	319	522	RNTRYWVINSISVIPSSALISK SPRLMAKKTAFHFGISRTSVAE FTFTRSGISRDHCYKAGAADR RPNAPPRAEFQSGWFLIMECFA R*VGDPQL/TA/HFDAV/RRE/IM PL/PREG/KTL/QTEVREMPKRC AVFLAINLGDRFDIKADEGGIT DIEFITQYLVLRVAHEKPKLTR WSDNVRILELLAQNDIMEEQEA MALTRAYTTLRDELHHLALQE LPGHVSDECFATERELVRASW QKWLVEE
10680	41048	A	10742	2	640	
10681	41049	C	10743	1	2358	
10682	41050	A	10744	1264	1894	RGDKPQHIVTVHRADVVKAAQL FKQARARHYHAFNMFFGAFEL FNWRHARENFPPAGKQLCQMV VERADIFGNRHIFVVENHQHIR TDIARVIHRFKRHACGNRAIAN DTDGAAIAFAFTAILYGIQFSCAS FYL FVVYEHGSLKT VGCPLQEV /WRTALESCKPAHIQLSGVLAIS SIVMQSVNAMPSSWSGYSQA ASAARWLLARSLGIC

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10683	41051	A	10745	872	3111	VLKPNHLTERKGC/GFACGRYG KLGAWELDYSPDLDIHFLNDCP MNA MTAGERKIDGRQFYRLRLA QRIMHLFSTRTSSGILYEVDARL RPSGAAGMLVTSAEAFADYQK NEAWTWEHQALVRARVVYGD PQLTAHFDAVRREIMTLPREGK TLQTEVREMREKMRHLGNKH RDRFDIKADEGGITNIEFITQYL VLYAHEKPKLTGWSDNVRIL ELLAQNDIMEEQEAMALTRAY TTLREPRFSRSLFWGCSPLGLF DYLA DLFKIDNSHGGRFKTVLL TFLPPALLYLFPNGFIYGIGGA GLCATIWA VIIPAVLAIAKARKKF PNQMFTVWGGNLIPAIVILFVLP WFYFIPPGICTSLVYRASPPIS MPAKAVAYCVLRISGGDGSCD VICRGKVADRSKFVWPNWSKT HTEPTQSQATASNRTSATTAE QRSDEKEGNNRTRHEEQRSQN ATQHKRRERATTTQKTCSETVT PTTMNMCNEPLRRHARVLPP VLYVQRRYDESHLRISISACNV CRTERHAVHTDEIHTSTVADDC KERVAVMRLRLPLCAACRHIG DVIVYSAVYCEHRCMRLLATR RHYVVTLTTHLRRRLFLTEVNA RYVCIYDDEHSRSTVTHAHP DHQSAHYDTYVYDGTVSYMR LNTSVRLIRRAHTCTSRALMD SHSKDGRPMDYASAVVTHPL
10684	41052	A	10746	1577	1668	TINPPELAFVKTVH*SPRICLGF HIFLLN
10685	41053	A	10747	486	674	HWWKNWRCWIPVIWH*RRSR TIWRCKCKWITASTLRSRSPSK LPPCMSGFQPVVAGRKR
10686	41054	A	10748	254	396	ADDQIPHSKTHLKLSEVEENQ Q*EI*RPLLQ*GGMVPRCVHG RSG
10687	41055	A	10749	3	674	ISAEINRPFAIRGDLG/VVWERQ KQETGWRSWVP/WPHVHAEDII LGNPPDI/PEVTMVHLPRVEATL /APLALLTKTVWLPWKIESPRI RFQFSHHVRRAVLCEDAYYKL TLAQVEKLKNGGKVIASDELM TKFRIPNTLEFCAPVMADAPAI ALLRLSLACDLAQAMMPAFH KPISSSFVNDYAGTSFACAASD MDERRMLNAPLSRLTLVEKL RRCWIPVIRH

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10688	41056	A	10750	1	1755	
10689	41057	A	10751	1	1662	MSKPKYPFEKRLEVVNHHYFTT DDGYRIISARFGVPRTVQRTWV ALYEKHGEKGLPKPGVSADP ELRIKVVVKAVIEQHMSLNQAA AHFMLAGSGSVARWLKVYEER GEAGLRALKIGTKRNAISVDPE KAASALELSKDRRIEDLERQAL SKPDKYADVKKRISEIYHENRG RYGYRRVTLSLHREGQINHK AVQRLMGTLSLKAAIKVKRYR SYRGEISSTKLFLTAFRMIVVA IILIAITFDWNRKPTINQKVS AELNRPF AIRDGLGVVWERQKQE TGWRSVWPWPHVHAEDILGN PPDIPEVTMVHLPRVEATLAPL ALLTKTVWLPWIKLEKPDARLI RLSEKNNNWTFLANDD/NKD ANANRRHGRFGWIIFFSIKGG SPLMTNDIHGSLVYTTGKPRPKL EGDVESRQLRLADLGPLIGVDS GKGAEKSKRSEQKKGEKSVQP AGKVL PYDRFETDKWDVMDA DVRFKGRRIEHGSSLPISDLSTH IILKNADLRLQPLKFGMAGGSIA ANIHLEGDKKPMQGRADIQAR RLKLKELMPDVN
10690	41058	A	10752	1	477	SELGHAGLNGDILVWNPVLED AFELSSMGIRVDAADTLKHQLA VGDEDRLELEWHQALLRGEMP QTIGGGIGQSRLTMLLQLAHI GQVQCGVWAAAVRESVPSLPL QLFHFTRHVVRQPLSKIRNHQ RIGIKFPALQAFHNGAKTTGKI GADTKLLA
10691	41059	A	10753	414	794	RPSPLPTGLGDTGLGLPRFIEM EKLPLFDVAEAEQELQEGPLPEY SGPGLALAKWGLG/LKQVVM ASLFVALFLPFGRAQELSLACL LTSLVVTLKKNNSMTAGILVC LVTVVSPGLIKVLIYDQ
10692	41060	A	10754	88	227	
10693	41061	A	10755	26	261	
10694	41062	A	10756	164	361	
10695	41063	A	10757	1347	1656	RVGRPGHRASASGGNPQNHR RLGEPVSARHPAYLSTGSGDAA AARYRRSA*SLRR*SRASSHPPE RAGTPVAPGTIDIFRWRTAARQ HRPRLRYRRLPHSAA

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10696	41064	A	10758	2096	2248	RLIGLHGQNSRSVPQLPMESAS VA*RCTAALDGGVSSTSTRWLF ASCTRL
10697	41065	A	10759	1	2240	
10698	41066	A	10760	1	1082	MEHERYVGISNLMKPELYLA VGISGQIQHMYGANASQTIFA! NKDKNAPIFYADYGIVGDAG ALMSEIDFDAIIVGAGLAGSVA ALVLAREGAQVLVIERGNSAG AKNVTGGRLYAHSLEHIIPGFA DSAPVERLITHEKLAFTMEKSA MTMDYCNCGDETSPSQRSYSVL RSKFDWLMEQAEAEAGAQLIT GIRVDNLVQRDGKVVGV EADG NRVMKKILTTPIKAEDLQDIRV GDVIYL*RHRSLSVG*RAESGG* RSGRIVKRTG
10699	41067	A	10761	987	1191	
10700	41068	B	10762	1	1506	
10701	41069	A	10763	204	527	GPDRCQIGPLAE*NTGNSHKAA LRQQRAGEGRWWQKPHGEWRA ATADGRTYAISAQATAPQSPA GQSTMPRPRLWSTPALPVMIPA VTVDQRITPASVSTTKQAISA
10702	41070	A	10764	1041	3024	
10703	41071	B	10765	1	763	
10704	41072	A	10766	729	989	HLTRQGIPTDLQLRVLVSRRTK NKQKGHPHRKRICTSPSSKTKS R*NHKDGEKTEQKNWKL*NAE HLSSSKGTQFLTNGPKLDGE

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10705	41073	A	10767	89	1755	LSEGLTNRKDIHTKTPSVRRHH HQRPKCWKFPGHSGRRRK*R /CIQVGKEEVKLSLFADDMIVY LENPIVSAQNLLKLISNFSKVSG YKINVQKSQAFLYTNRRQTESQ IMTELPFTTASRKRIYGLQLTR DVKDLFKENYKPLLNEIKEDTN KWKNI PCSWVGRINIVKMAILP KVIYRFNAIPIKLPMTFFIELEKT TLKFIWNQKRARIASLSQKN KAGGITLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEIM LHIYNYLIFDKPEKNQWGWKDS LFNIWCWENWLAICRKLKLDPF LTPYTKINSRWIKDLNVRSKTIK TLEENLGNTIQDIGMGDFMSK TPKAMATKAKIDKWLILKLSF CTAKETTISVNRQPTWEKIFAI YSSDKGLISRIYNELKQIYKKKT NNPIKKVWKDTNRHFSKEDIYA AKRHMTKCSSSLAVREMQIKT TMRVHLTPVEEVVRAGEMAKTR RCQNVKGASEGIRALALFLIN LTVHMEGNHIDGDIETNRSPL QAPGEICESFTALMAMQLLSKL FWS
10706	41074	A	10768	533	760	
10707	41075	A	10769	1067	1225	
10708	41076	A	10770	1080	1250	SSGLHSWDARLVQYTOINKYN PAYKQSQRQKPHDYLNRCRKS L*QNSTTLHAKNSQ
10709	41077	C	10771	55	1842	
10710	41078	A	10772	1575	1745	SSGLHPWDARLVQYTOINKCN PAYKQSQRQKPHDYLNRCRKS L*QNSTTLHAKNSQ
10711	41079	A	10773	2798	2871	
10712	41080	A	10774	601	876	
10713	41081	A	10775	1194	1421	

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10714	41082	A	10776	587	1683	GWKFWPGQSGRRRK*/R/CIQLG KEKVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSQYKINV QKSQAFLYTNNRQTESQIMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLKEIKEDTNKWKNI PCSWVGRISIVKMAILPKVIYRF NAIPKLPMTFFTELEKTTLLKFI WNQKRARIASILSQKNKAGGI TLPDFKLYYKATVTKTAWCWY QNRDIDQWNGTEPSEIMPHIYN YLIFDKPEKNKQWGKDSL FNK WCWENWLAICRKLKLDPLFLP YTKINSRWIKDLNVRPKTIKLTLE ENLGITIQDIGVGKDFMSKTPK AMATKAKIDKWDLIKLSFCT AKETTVRVNRQPTTW
10715	41083	A	10777	1260	2176	SSGLHPWDARLVQYMQINQCN PAYKQNRQKQPHDYLNRCKRG L*QNSTTLHAKNS/AIN*CWKF WPGQLGRRRK*/R/CIQLGKEEV KLSLFADDMIVYLENPIIASQNLL KLISNFSKVSQYKINVQKSQA FLYTNNRQTESQIMSELPFTIAS KRIKYLGIQLTRDVKDLFKENY KPLLNEIKEDTNKWKNI PCSWI GRINIVKMAILPKVIYRFNAIPK LPMTFFTELEKTTLLKFIWNQKR ARITKSILSQKNKAGGITLPDLK LYYKAIVTQNSMVLPLKQRYR PMEQNRALRNNAAYLQLSDL
10716	41084	A	10778	3813	3983	SSGLHPWDARLVQYQTINKCN PAYKQSQRQKPHDYLNRCKRS L*QNSTTLHAKNSQ
10717	41085	A	10779	1312	3348	
10718	41086	A	10780	1636	1815	
10719	41087	A	10781	67	403	KFLCRPPIIRPPKTFNTLIVLARR CIQCFRFFDIACFN RVGKGFGV GHQLRGFRHDIRGFAQWTHLP DGCAFRDRCYAAGAQCENVPA LTACGDNNQRIGACWYPQGEV
10720	41088	A	10782	506	915	WASVKSPPVCWNCWISHRRVR TCRHVRFAPGFNLAKA/VQGAA LVITGKGRIDSQTAGGKAPLGV ASVANQFNVPVIGIAGVLDGCV EVVPQY GIDAVFSILPR LAPAE VLASGETNLFNSARNIACAIGIG QGIGK
10721	41089	A	10783	1	906	

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10722	41090	A	10784	2	597	SILKLVACDNDNPLVGARGAAAVFGPQKGATPEMVEELEGQLQNYARVLHQQPEINVCQMAGAGAAGGMGIAAPVFFNGDIKPGIEIVLNAVNLAAQVQGAALVITGEGRIUSQTAGGKAPLGVASVAKQFNVPDDLGLLAYVGDGVEV VHQYVGIDAGFNILPFLAPLAEV LASGETNLFNSARNIACAIGQG
10723	41091	A	10785	1	1140	
10724	41092	A	10786	13	628	LLIPARPPGINPYWKVSEANLI RYFQQVGDSTVLPMVLYNFPAL TGQDLTPALVKTLADSRSNIG IKDTIDSVAHLRSMIHTVKGAH PIHTVLCGYHDHLENTLLGGD GAISASGNFAPQVSVNLLKAW RDGDVAKAAGYHQTLQIPQM YQLDTPFVNVVKEAIVLCGRPV STHVLPASPLDEPRKAQLKTL LQQLKLW
10725	41093	A	10787	3	1185	EQSGRGARDGGARDGVREGG\ SWTQQHGLPLTKVELATVAEY PVCLWQRLTLSPQYGSIP/RGD QSDGWKVDYNGPFSWKGQH FVINGIDTCSGCKFAIPVCSASA KLLPMSSQNVYHRDILHRIDSE QGTHFRVKEVQQWALGRGPFY WSYVYISHHPEAAGLVEQCNGIL KTPSQFQMGRNTLQGWGKVLPSLEGCAFSSSKSNLCSVVLKVF VPKEGMVPPGDTTMIILNCKLR LPPMPLNLLASKEVTVD/YQG EIGQLLHNRGKEECVWNTGDC LTYLLILPSSVIKVEKPQPHGR RTINGPDPGSMKTWVTPPAGA VFLIGSWLRYDYGQYTWRAAS SQMLDRKGMNLASNLFHIGILG IFVGHFFGMLTPHWMYEAAMY GSCDTDNANV
10726	41094	A	10788	396	504	WKLRLERRAIQGDSPVHKNARA GELDE*AATRAIPG
10727	41095	A	10789	24	611	EILPVPGPVVIAW/AIFRRIAGES WSAIVISGLSIARHAQQRJITFT ASLAARLEIALKIVRNADGTES ASEQLYQVVGAGCKMPWQSE AMKDVLCIDKRRLMRRTGGTE TSKYPEEKKSTEIPVAAASERGG AQLNQCATEAVVLTRVDSHL KVGDSLSTHITSFLKKFAARFGG QLEKALGLGSMQAFSDIRGL
10728	41096	A	10790	212	578	

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10729 10730	41097 41098	A A	10791 10792	1 3	1707 313	NAE/TVKMFTTSSKEDATFGLG WRVNGNATMTPTFGT/LASPT YGHTGSPPLPPICPVRRPPGYLRR LSPRFRLFGISLPQRPPGILERS LQRRRNPSGWRRRNQ
10731	41099	A	10793	1	1992	MDVQSAADDTGMLPVLVVRGPF NVVWQRLPAALEKVGKMTD STRSQGNMAVTVKPLSDSDWQ ELGASDPGLASGDYKLVQVDL DNRSSLQFIDPKGHTLTQSQND ALENAILAVIRHEICLSDVVRIR ASRRFDKTSCTDRQKILKGY LLPAGWLADVDPRLVGMNV WTLVPAALFFGAGMLFPLAT SGAMEPPFLAGTAGALVGG QNIQSGVLASLSAMLPTGQPG VVDLNGIVDRAVLAAGDAD VASGAARLSARHSIVISSMGE RCCFIRSRITRIGFLAAGVGLD QLAPDFATPVIRELLALLCLFS GGGLAMYGYLRWLRNEKAMRL KEDLPYTNLSLILMVAVI VMGLWIPPTCIVDDRMAYIPG LADSPNDTIKGNTRLRISDLLH HSGGFPADPQYPNKAVALY SQDKGQTMELIKRTPLEYQPGS KHIYSDVDYMLLGFIVESVTGQ PLDRYVEESIYRPLGLTIITVFN LLKGFKPQQAATELNGNTRDG VIHFPNIRTSVLWGQVHDEKAF YSMGGVSGHAGLFSNTGDIALF NAETVKMFTTSSKEDATFGLG WRVNGNATMTPTFGTLASPT YGHTGWTGTVIDPVNHMTI VMLSNNKPHSPVADPQKNPTMF
10732	41100	A	10794	2	137	NCLSPVSN*WPAKTGRPLPS ATVTASTRNVLSKHWRIVVST VC
10733	41101	A	10795	271	553	ATQRQDLHFVRSPGDVAVYQTIT PEAADAVVARNPDTAQHLHC/ VYP/HTSNAALAQKYLHIAASP EVMVPLSAFHAASYSMFFMEF NLJAMWANFS

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10734	41102	A	10796	1	747	MLLGLHSLAFLQRESFSGKQS WGCQLAALLQRRITKMTTEAMK ITLSTQPADARWGEKATYSINN DGITLHLNGADDLGLIQAARK IDGLGIKHVQLSGEGWDADRC WAFWQGYKAPKGRKVVWPD LDDAQRQELDNRLMIIDWVRD TINAPAEELGPSQLAQAQVLDLIS NVAGDRVTYRITKGEDLREQG YMGLHTVGRGERSPVLLALD YNPTGDKAPVYACLLGDIITY RNGKKVEVMNTDAEGRVL
10735	41103	A	10797	444	548	
10736	41104	A	10798	951	1648	TTGRFPSPVQDSFVNNESSRMGL PDEFTLQREFERARQQALAQ W/IAAFEGGFTGIVATLDTGRPG PVMAFRVMDALDLSEEQDVS HRPYRDGFASCNAGMMHACG HDGHTAIGLGLAHTLKQFESGL HGVIKLIFQPAEEGTRGARAMV DAGVDDVDYFTAVHIGTGVP AGTVVCGSDNFMTATKFDHF TGTAAHAGAKPEDGHNALLAA /AQATLALHAIPHSEGASRV
10737	41105	A	10799	1495	2282	FDRHVGEFFLNQLETTNSLAKL HALIGVARRIFKGAHRRTVVGE GYQETFMVELFFDAVKAVTFTPT EHVFLVQFHVVKGDFTAAIHTQ TELFKFGHFDARFAHINKPFGV DRFVRRSPVARHHHDVRGVGA AGNKTLLTIKINLTISTGISRFQA THVGARARFGDR*VRTDSTTV GHRDCHITGGHR/HKSFQPGHEA PQAVPLPGRFH*PSHDHCR* LVSLAGAAYSRQDPVPYMPIS PGLDWVRQIVCCVMASDAD
10738	41106	B	10800	1	3618	
10739	41107	A	10801	3	490	TGIVATLDT/GRPGPVMAFRVD MDALD/LSEEQDVSHRPYRDGF /ASCNAGMMHACGHDGHTAIG LGLAHTLKQFESGL/HGVIKLIF QLHRYAAHAGAKPEDGHNALL /AAAQATLALHAIPHSE/GASR VNVGVMQAGSGR/NVVPASAL L/RQPTRSALNTTQQLNAR

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10740	41108	A	10802	1	513	MGIESLQAFLRSAGALGVWVY TFLERLIPTGLHHFIYQQFISGP AAVEGGQIMYWAQHLQEFSL AEPLKSLFPEGGFALHGNSKIFG AVGIYLA MYFAAAPENRVKVA RLLIPTPLAAMLVVIPEPLAEFTF LFISPILYAVHAVLTASMSPPVM YLPGVVGNMGEKID
10741	41109	A	10803	1	4941	
10742	41110	A	10804	1	1083	
10743	41111	A	10805	1	1363	MPVRKNMIMNEGNITPTNGC RIRASCVPMICINQLKDGNNK PSPLTAARMKQKAILFLIRTVR TDTHVVEDTGRKGSRKANSRE RFPDAFPEFHGFADFRVLRQAM IQIWLVSVMVQHVNVCCTDAC RIVQTRIVVTAGFQLSNASLVA MRRWVYRVRRIQYRRTQTAV FHSTHGNRYREGQPVGTLDIDRY KANENVELVHYAQPLLNEADS LAKVMPSPDIPKQRRWLGLQM LEGDIYSRAYAGEASQHLDAAL ARLRNEMDDPALHIADARYQCI AAICDVVSNLTAEPSRFTTAV DKIVLNRFLGLPIFLVFMVLMF LLAINIGGALQPLFDVGSVALF VHGIQWIGYTLHFPDWLTIFLA QGLGGGINTVLPVPQIMMY\ CFSSFLKTPALACREIFVPLMRL RVNLRWYPPVL*RISSWWTNSRI PTTFSTRGSACWRATPAK
10744	41112	A	10806	199	1083	RLFEHPRLGVAAVENGALGKR SAVVLPFGDAVNHKTRFIEFVK SAIEGNRLTVRAIGPQFTTQTPV IVFNQGVSGAQNIAGRAVVLLQ TNSFGTGEIHKETLNILHLRPAPA VD*LVVITDDHHFAGVARQQA DPRVLNVVGILEFVHQDIGKTF AVVLQDMRLVKPQLVSAQQQL GEVHQARAVTRFLIRLIHLLPGL LHRITVALNMMRTQAFIFLAVD VPHCLPRRPLLVEVHGFDQITQ KVAAWRGHRFALFVIAKEVQ RNVHWHRRVKIGWAEKRNAL RQKAGNFQMRQ
10745	41113	A	10807	49	273	DFLGRGAFNVINIGAWASRPVQ GSTVDLSHGLHLVLHLKNNL*F YGFDSHFLKSFYKGTSSISIQVE VGISQGNL
10746	41114	B	10808	91	2183	

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10747	41115	A	10809	8	219	FSLWPL/KKFSNRFLKKKPMEF GSWTTRELIASFAGVRGAITLA GVLSIPLLLPDGNVPARYELVF LAAY
10748	41116	A	10810	84	509	
10749	41117	A	10811	3	163	ENTTWLYAD*NAGRDADFGHA KRKWTWLTWLAIAAVATAMAN RQPAGLFAFLT
10750	41118	A	10812	1	707	MGWRMGIWLRVFTVAKHLQR AESDQIGFRLKEHCWKRYAVR HPVKDVSFGSPVLTVMNRAPQ/ SN/PARTVGVWLRMFRRLKR/ RKPRPLPLSPLHMDV/HAGNLV HSASGLKLIDW/EYAGDGDIAL ELAAVW/VENTEQHRQLVNDY ATR/AKIQPAQLWRQVRRWLP/ WLLMLKAGWFEYRWQ/TGD RQFIRLADDSWRQLHRSNKES RELVARLRVFAQSSGGAVDQE GGRVQCFREGL
10751	41119	A	10813	1	227	SFINVERYRAEPTADAAPLKR GAFGSWLPPEPDHYAED/DHQQ YLHKNPYG YCGGIGGVCQAY KIVQIQYIARTA
10752	41120	A	10814	1	283	
10753	41121	A	10815	315	569	
10754	41122	A	10816	65	580	SDRS*IPVRPTHDRSGNRHDGSS GYCRCYG*HG*HRGIRYRCWPE KSQTRSGLLPLTVNYQERTYA AGRIPGSFFRREGRPSEGETLIA RLIDRPIRPLFPEGFVNEVQVIA TVVSVNPQVNPDIVAMIGASAA LSLSGIPFNGPIGAARVGYNDQ YVLNPTQDELKESK
10755	41123	A	10817	235	1236	TDHDGRNDTQRIGSGERNRPF NANTAHHQCRFAGFALFCGEIF TTNQRRQPHQRRDNTNTHGSD GHHGINTLSNANQHEGIGHFVN RTAHIERQHQTHDHRQHNNAA NSGTEVSQ*AR*HAAY*RYVAE REIHSGDRCGKRNSAHKIMPG WWCALPDTAPSLSKVVFVKGC PHLCPWCANPESISGKIQTVRRE AKCLHCAKCLRDADECPGSAF ERIGRDISDALEREVMKDDIFF RTSGGGVTLYRGEDPAEDARY AHTNQPRQNKAVVDDEATDV GGAGTVKLNRCQIARISRQDVI TVASRCEHGFCPCDTVHRHD GDHTGTEDFVF
10756	41124	A	10818	1	400	

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10757	41125	A	10819	783	1116	SVLHLYEQNTEVHDTRGYRPI KTLDIVPAFEASHLLWQSYENS WEQIFSAVGASWQKHGYTDV LTQLGYGQRHWNIDIDAGATL RWEKRPYDGDREHNLVVEFD MTFRF
10758	41126	A	10820	3	474	TCGEAASIVDRIRGFFEPSSILV STLVLTLRPTGLPLVTDLSLPM RLLPTEIMAGSPIRS/RDISLGDD PGINGQRAQGTWERWTVRADE PQAFHIEGVMFQIRNVNGAMPF PEDRGWKDTVWVDGQVELLV YFGQPSWAHFQFYFNSQTHKV GPRAVA
10759	41127	B	10821	93	786	
10760	41128	A	10822	191	748	GPATPRQPFKVLASLGRVLVQH GRWDAQHLHNAVHLVDLIGAT EEQLSGVHLHKDAAQGPHVNG QVVGCAQEHLR*AVEAALDIL VDPLAKLAGAAEVHNLGGAAL GVAQQDVFGLVAVNDAAEQ AWPERAVPCRAAAPASGSGSA RRRGSCCAGGORTGCRTAAQIP STSGFRNMKCRFRCTI
10761	41129	B	10823	1	2724	
10762	41130	B	10824	116	2458	
10763	41131	A	10825	1	1317	

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10764	41132	A	10826	99	2052	NPADGRTGFTLCATGEALSSAT IAAAERRQALQEGCDDILS/HG DADMVSMAR/PFLADAELLSK AQSGRA/DEINTCIGCNQACLD Q/IFVGKVTSCLVNPRACH/ETK MPILPAVQKKNLA/VVGAGPAG LAFA/FNIAKQIPKKEEFYD/L/ RYYRMIIEVTGVTLKL/NHTVT ADQLQAFDETILAVG/IVPRTPPI DGIDHP/KVLSYPDVLRLDKAPV/ SN/KVAIIGCGGIGFDTAM/YLS QPGESTSQNIAGFC/NEWGIDSS LQQADCDAPAKASKPGQGLGK TTGW/HRITL/LSRGVKMIPGV S/YQKIDDDGLHVINGANQGS DMLRLQGEIDSASRIGRRSAAP KLGLSLNDGRFCFINCHILDRLPY KGLVPACSWNGGSLDPLEGRP DEPHVEVLGIPPAAMLDAQPRL ASTLNGCLGVAOPYEDERTQE GLPGPRDTAAEEVLGVQTTGGA GSRGRVRGPPQADLPSASGPGA ACWSMSPPPDQPPCVLAHGFFR RTPSTQQRPAEQCFHSPAPLEL PLSSTSSILSFAEYGNAMAWLY RGKILPSGTPDDDLKAQSANDGN PDPTMEKAFIQLIHDGIRSIAMS NPILSCRRYGRYQEWCLTIPAV FISAPYVRRYVRFHEHQEGGGV RQEATVREIPLAIAVIPNSRTPC
10765	41133	A	10827	1	525	DAMVSSWNRAAPNTIPTAAKA GGNYLSLLVGSEARRHGYQE GIALDVNGYISEGAGENLFEVK DGVLFPT/PGFTSSALPGITDAI IKLAKELGIEVREQVL.SR/EKS LYLADEVFMSGTAGEITPRRS NGYSGLAKRCGPVTKRIQH ALQGVYSWVTPGYFESVRCTA
10766	41134	A	10828	8	573	REPAGENGPPVCDGAMLDLKA/ WGSECHQQLTGRDNQIQRSIY LLPERAKLAELRLVIPGQVDY LQHIEELAAFIKGLGDVPLRLN AFHAHGVYGEAQSWASATPED VEPLADALKVRGTCTRPDKTRQ ASHQALCANCMRRERLIRPTV RHKPVGMIRDRKRIRHYAPTA GCGVNALSGLRFGTDL

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10767	41135	A	10829	1	479	SNATNGIEPPRGYVSISKASKDGI LRQVVPDYEHLDHAYELLGEM PGNDGYLQLVGIMQKFIDQSSIS ANTNYDPSRFPSGKVPMMQQLL KDLLTAYKFGVKTLYYQNTR/G RR*RRTRRS GAVNPGTMGCESG ACKNPGYLRMPGCRKRTPLIPA LPGFGFW
10768	41136	A	10830	1	443	MDSLMDMLASTQGRMRDDQR VTVSSLPGFQFVGSKAYKPSRR PDKAFTPHPASQYQILHAPLVA AIVSGLTAARVVFVRLQQPSLG VLSNTSGCDATNVVGRQLQDNA SVSPGIVHTDSVIWRSCQVRRS AVHTLRQKTRLFDAVDA
10769	41137	A	10831	1	323	MDLVTGSRKVIAMEHCAKDG SAKILARRCTMPLTAQHAGHML VTELAVVRSFDGKMWLTEIAD GPTSQAQPAATYRIPLSNSRV RRYRHYRYRYNLSIRKKRHRPL
10770	41138	A	10832	526	975	TPYPAYVQHVTGRIJRRGKRR RQCLPVLESRFHNTQKSRGETE GASGFSLQHLHGDSSRAA PGPY RVSTAAADSGGRAGSSAPSAV PRGC*GPSLAPAGRSQR*HRGG GQLSPAAPTANKAAGLGPPA RLNFFIRAQCDSRINDITR
10771	41139	A	10833	1906	2049	PLSIIEADFRIWANAG*RMVAGI KPSIARVPLVLQVSALEVPEQC YRH
10772	41140	A	10834	1	808	MPKPNTRWSAWGLRRLKRW SVARGSNLNRSVQYEFTGRGD RIGWVKGIDDNWHLTLFIENGR ILDYPARPLKTGLLEIAKIHKGD FRITANQNLIAGVPESEKAKIE KIAKESGLMNAVSPQRENSMA CVSFPTCLAMAEAEERFLPSFID NIDNLMAKHGVSDHIVMRVT GCPNGCGRAMLAEEVLVGKAP GRYNLHLGGNRIGTRIPQITRRI EHRANDARTHRKVAEAFTRFA LFRPAPYQFIKRRQDFRLVMFSI YMPVPS

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10773	41141	A	10835	248	830	HHYRKMNIQQSKWLIIVTVCDG KLNWLLSGSKVCCTWMLCVQ/ SEPELAKAWIFANLLAAFLIDDI IQPSLDFPPRRAEITIAADGTISA LNPGDPANTVAPVGRLLKLVKA TGSEVQRGDDGIFRLSAETQAT RGPVLQADPTLRVMSGVLEGS NVNAVAAMSDMIASARRFEMQ MKVISSVDDNAGRANQLLSMS
10774	41142	B	10836	328	481	
10775	41143	A	10837	14	675	FRKLQVCWLPRPHLRPWWTCK PRWFGSCLRVFL/LEIVI/GDV/ WGLRLWSALGVAFFG/WAFITS LQAKRGWMRIVPIILLAAALVS VRPLQDWAFGATHTAQTQTHL NFTQIQTVDELNQALVEAQGKP VMLDLYADWCVACKEFEKYTF SDPQVQKALADTVLLQANVTA NDAQDVALLKHLNVLGLPTILF FDGQGGQEHQARVTGFMDAET FSAHLRDRQP
10776	41144	A	10838	1	1413	GMALTYTALGLVVAAGLQFQ AALQHPYVLIGLAIVFTLLAMS MFGLFTLQLPSSLQTRLTMSN RQGGGSPG/GAILLYIAQSGNM WLGGGTLYLALGMGLPLMLI TVFGRNLLPKSGPWMEQVKTA FGFVILALPVNIAPGSLDKALNQ YAAHSGFTLSVDASLTRGKQSN GLHGDYDVESGLQQLDGSGL QVKPLGNNSWTLEPAPAPKED ALTVVGDWLGDAENDVFEH AGARDVIRREDFAKTGATTMR EVLNRIPGVSAPENNGTGSHDL AMNFGIRGLNPRLASRSTVLM GIPRPLRPLRSAAFTGSRFARQ HGCHCTWYAVVVRVTDTS VGGVVNFVTRAIPQDFGIEAGIL MSDLKHGSLVGACLGRLGPGA VLYLAVAVLGVRRGVVLC PLGGTGLGYSCGGAFQFAAS CFLGRYGVVQGVHVCFGPRSV FLDDCLRFDLPLVWLSCLR

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10777	41145	A	10839	1	908	LLKPFHVIAIATGRSLAVFCMG RLRTICSHA TPPASAI/LLYI/AQS GTWGGGGTLYLYALGMGLPL MLITVFGTRLLPKSGPWMEQV KTAFGYVILALPVFLLERVIGD VWGLRLWSALGVAFGGWAFIT SLQAKRGWMRIVQJILLAAALV SVRPLQDWAFGATHTGQTQTH LNFTQIKTVDELNQALVEAKGK PVMLDLYADWCVACKEFEKYT FSDPQVQKALADTVLLQANVT ANDAQDVPTSAFFISPPNALVAI IVQLRFGDFYNRVSKGSRPTVF GRTLKARRITLSEKSLKAKIH
10778	41146	A	10840	3	808	SSGGHGRRAGRLQHPLLRVH VPVVDTSVPCSRQLQWHHLPL CPGQLQHGHFHGPWCFFPSG*G *GQGGRLPGSAVQERGCARYP GPHEVVCHVPLLPAAALLPLQR L*QLCRGL*PPLPLGQ/PTASGV ETIATSSCSCCHSVHTWWASWP SAWSTC*TTLRGWEPTPPSRIL GSCGPHCRGDVDRGHVHPGE* AFQSLVPCQGT PKGPMAPP*VG RGVSP/PGTRVEAALSCESPFA RQSMCFNLHTHSIDPKQSRRPY SDNVGKE
10779	41147	A	10841	2	646	CSWQPAVPTQPQAPGSAAPRQ LPGHSRGAQPALVSPHKGLTPV PGTPA/PASTPPAPAGGGLPSP AAGAPPAHCPG/HPPAPATAAP VPGLCGPCSLPACQTR/PPTH VNTKKRV/PG/VRPAARRPWPP GCTWRGARTVTFHLQNLPGVN CQMLTVGRSGIRPTCTIASCSV NKLHPQMHPATQPHHRMALSP SHSEGPSHCWGLSLGDISPIR
10780	41148	A	10842	3	550	

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10781	41149	A	10843	2	1132	LCLVMILYTRRRWCKRRRVQP PQKSASAEAAAEIHYPVLIIGG HGRESLRNARVQGHNSGTL RETPILDGYEYDITDLRHHLQR ECMNGGEDFASQVTRTLDLSQ GCNEKSGMDLTPGGDGRKARL MNKYKDNIIATSPVDSNIIQQAT LLSHTSSSQKRINNKAARGMHV *H*GEGDSTGEAENDPQLTFYT DPSRSRRSRGRNDRGGRNKTT LTLISITSCVIGLVCSHVNCPLV VKITLHVPEHLIADGEPVLLRM GSQLDASDWLNPAQVVLFSQQ NSSGPWAMDLCARRLLDPCEH QCDPETGRREHRAAGNCQRDH ARAHSVWLGSPPYHDTSLRWS PMYTTMESAPHAFFPSVTADAE
10782	41150	A	10844	3	3935	HASGPGGLKMLAGLCALLACC WGPAAVLATAAGDVDPKSEKE CKLKSITVSALPFLRENDLSIMH SPSASEPKLLFSVRNDFPGEMV VVDDLENTLPYFVLEISGNTE DIPLVRWRQQLWLENTLLFHHI HQDGAQSLPGQDPTTEEPQHESA EEELRILHISVMGGMIALLLSIL CLVMILYTRRRWCKRRRVQP QKSASAEAAAEIHYPVLIIGGH GRESLRNARVQGHNSGTL SIR ETPILDGYEYDIT
10783	41151	A	10845	184	357	ALQGWSKNLHPEDIQLGKTPP P*QVAQEGGWSRRVSGDWTIL EEQPGSTTRRVSVGM
10784	41152	A	10846	226	609	VILSSFDLIKHGILLEISDSIQFRG CKRSRIPELGGLEELW*PGDCR QPRPWRAGRHLQPGSLGSLVS KHQLRGSRKTL/YSAFRKCHLL SVWEGKPLKI*RGDQVADSSQK KQLAADAHTPYRGGDI

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10785	41153	A	10847	20	1317	SSHQKQMLAPCFLGSLQNQWH HTAGKGK/WVLGTCAFGEQLA ASGHMKETRADRSKKLFRHYT VGSYDSFDTSRGGVRKPYAGF FPDLQDICDEQPRPLHSTLRPAC GGIQPGKQQMPFAKTDTCASD KHVEKKLERLIHQAVSDAPEPS RVVKGIFIGLPCARLWVVPYL MGHVQEVMTAEGYERASQATF REQMQEVPCLQRSTGSSMKT GNKIRRVTDNVLTRSGPLINDIL SVAVDSSSVSLIWMHLFSSHPL GIVRYWCGMGISCKLLLTRVC YLITPLDLERFPFNTQVTFPE RRVSFVLLPLSWCLDTRLPREP GCRSRDSFTHRVPFYSVTPTSG DVPGSHPFCDKPVRRGDDPYIR NDRGTLYSTLQFISTCVQVVG YGHLPGFKSDAQAQVPRLLSQ KRDQNHKEEITDGDERP
10786	41154	A	10848	1930	5781	RAKSPANIHMTGNSHITLTLN VNLGNSPIKRLRLASWIKSQDP SVCCIQETHLMCRDTHRLKIKG WRKIYQANGKQKAGVAILVS DKTDFKPTKIKRDKEGHYMMV KGSIQQEELTLNMYAPNTGAP RFIKQVLSDLQRLDLSHTLIMG DFNTPLSTLDRSTQKVNKDTQ ELNSALHQADLIDIYRTLHPKST EYTFFSAPHHSYSKIDHILGSEA LLSKCKRTEIHTNLYSDHSAIKL ELRIKNLTQSR
10787	41155	A	10849	1	3654	
10788	41156	A	10850	1	5127	
10789	41157	A	10851	209	3816	QGRPTFRFRKYREHHKDPREE QLQDT*SSDSPKLK*KKCK*GQ PERKVKLPTKGSPD*KRISRQ/ KTLQARRQSWFFEKINKIDRPQ ARLIKKKREKNQIDTIKNDKGD ITTDPTETIQTIREYYKHLANK LENLEEMDKFLDYTLPRLNQE EVESVNRNPTGSEIEAITNSLPTK KSPGPDGFTAEPYORYKEELVP FLKLQFQPIKEGILPNSFYEASII LIPKPGRDTTKKGNFRISPLMNI DAKIL
10790	41158	A	10852	1	3663	

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10791	41159	A	10853	1	3210	MVKGSIQQEELTILNIYAPNTG ALRFIKQVLRDLQRDLDSHTIIM GDFHTPLSTLDRSTRQKVNKDI QELNSALHQEDLIDYRTLHPKS TEYTFSSAPHHTYSKIDHIVGSK ALLSKCKRTEIITNCLSDHSAIK LELRINKLTQNRSTTWKLNLL LNDYWVHNEMKAIEKMFFETN ENKDDTTYQNLWDTFKAVCRGK FIALNAHKRRQERSKIDTLTSQL KELEKQEQTTHSKASRRQEITKIR AELKEIETQ
10792	41160	A	10854	1	3354	
10793	41161	A	10855	1	5073	
10794	41162	A	10856	1	3235	
10795	41163	B	10857	1	3300	
10796	41164	A	10858	1	2563	MKAIEKMFFETNENKDDTTNQ LWDAFKAEVEVSLNRPITGA GAIINSLPTKKSPGPDGFTAEFY QRYKEELVPLLLKLFQSIKEE LPNSFYEASIIIPKPGRDTTKKE NFRPISLMNIDAKILNKILANRI QQHIKLIHQDQVGFPGMQG WPNIRKSINVIQHINRAKDKNH MIISDAEAKAFDKIQPFMLKTL NKLIGDGTIFYKIIRAIYDKPTAN IILNGQKLEAFPLKTGTROGCPL SPLLFNILLEVLRAIRQEKEIK GIQLGKEEVKLSLFADDMIVYL ENPIVSAQNLLKLISNFSKVS GYNKINQVKSQAFLYTSNRQTESQ MSELPTTIASKRIKYLGIQLTRD VKDLFKENYKPLKEIKEDTNK WKNIPCSWVGRINIVKMAILPK VIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRAHITKSILSQKNK AGGITLPDFKLYKATVTKTA WYCYQNRDIDQWNRTEPSEITP HTYNYLIFDKPEKNKQWGD KSLFNKWCWENWLAIRWKLKLD PFLTPYTKINSRWIKDLNVRPKT IKTLEENLGITQDIGMGKDFMS RTPKAMATKAKIDKWDLIK LKSFCATAKETTRVNRQPTTWEKIF ATYSSDKGLISRIYNELKQIYKK KTNNPIKKWEKDMNRHFSKED IYAAKHKMKKCSSLAIREMQI KITMRYHLTPVRMAIIKSGNN
10797	41165	B	10859	1	3420	
10798	41166	B	10860	1	4019	

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10799	41167	A	10861	1	1825	MVKGSIQQEELTILNTYAAHTG APRLIKQVLSDLQRDLDSHTIM GDFNTPLSTLDRSTRQKVNKDT QELKSALHQADLTDIYRTLHHK STEYTFSSAPHHIYSKIDHILGSK ALLSKCKRTEIITNYLSDHSAIK LELWIKNLTONHSTTWELNNLL LNDYWVHNEMKAEIKMFFETN ENKDDTTYHNLWDTFKAVCRGK FIPLNAHKRRKQERSKIDTLTSQ KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLOKINESRSWFF ERINKIDRLRLARLIKKKREKNQI DAIKNDKGDITDPTEIQTIRE YCKHLYANKLENLEEMDKFLD TYTLPRLNQEEVESLNRPIGTAE IVAIINSLPTKSGPGDGFATF YQRYKEELVPFLKLQFSIEKE GILPNSFYEAHILIPKGRDOTT KENFRPISLMNIDAKILNKKLA KRIQQHIKKLIHHDQVGFIPGM QGFNIRKSNVQHINRAKDK NHMIISDAEAFDKIQPFMLK TLNKLGIKYLGIHLTRDVKDI.F KENYKPLLKEIKEDRNKWNKIP CSWVGRINIVKMAILPKNILITL QLLLVLPELSTLIPLWLPALAGO
10800	41168	A	10862	1	4449	
10801	41169	A	10863	824	3693	AWKGTDDRSTRQKVNKDTQEL NSALHQADLIDIYRTLHPKSTE YT/FFSAPHHTYSKIDHIVGSKA LLSKCKRTEIITNYLSDHSAIKL ELRIKNFTQSRSTTWKLNNLLL NDYWVHNEMNAEIKMFFETNE NKDDTTYQNLWDFAKAVCRGK FIPLNAHKRRKQERSKIDTLTSQ KELEKQEQTHSKASRRQEITKIR AELKEIETQKTLOKINESRSWFF ERITKSDRPLARLIKKKREKNQI DTIKNDKGDIT
10802	41170	A	10864	1	3297	
10803	41171	A	10865	1	4791	
10804	41172	A	10866	3	3316	
10805	41173	B	10867	1	3415	
10806	41174	B	10868	1	4753	
10807	41175	B	10869	1	3384	
10808	41176	A	10870	1	3345	
10809	41177	B	10871	1	3772	
10810	41178	A	10872	1	3720	
10811	41179	A	10873	1	3894	

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10812	41180	A	10874	1	3335	MVKGSIQQEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDYRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRINKLTQSRSTTWKLN NLLNDYWVHNEMKAEIKMFF ETNENKDDTTYQNLWDAPKAVC RGKFIALNVYKRKQERSKIDTL TSQKLEKQEQTHSKASRRQE ITKIRAEKKEIETQ
10813	41181	A	10875	1	3780	
10814	41182	A	10876	1	3852	
10815	41183	A	10877	1	3345	
10816	41184	A	10878	965	4362	TWKGTTSRCKIMPYRSTRQ KVNKDTQELNSALHQADLIDY RTLHTKSTEYTFSSAPHHTYSKI DHIVGSKALLSKCERTEITNYL SDHSAMKLELRINKLTQNCSTT WKLNNLLNDYWVHNEMKAE IKMFFETNENKDDTTYQNLWDA FKAVCRGKFIALNAHKRQERS KIDLTLSQKLEKQEQTHSKA SRRQEITKIRAEKKEIETQKTLQ KINESRSWFFERINKIDRPLRLI KKKREKNQIDT
10817	41185	A	10879	1	3921	
10818	41186	A	10880	1	3988	MTGSNSHITILTLNINGLNSAIK RHRLASWIKSQDPSVCCIQETH LMCRDTHRLKIKGWKRIYQAN GKQKKAGVAILVSKTDFKPT KIKRDKEGHYIMVKGSIQQEEL TILNIYAPNTGAPRFIKQVLSDL QRDLDSHTLIMGDFNTPLSILDR STRQKVNKDTQELNSALHQAD LIDYRTLHPKSTEYTFSSAPIHI TYSKIDHIVGSKALLSKCKRTEI ITNYLSDHSAIKLELRINKLTQS RSTTWKLNLL
10819	41187	A	10881	2	462	YFTDRLRLARAGTPL/IMFGTIA RSGVRIVSREPLNRRAILIALSL AVGLGVSQQPLIQFAPEWLKN LLSSGIAAGGITAIVFSLAGHPA LATNAQPMFAFLHQTTFFQNL IRVKEAICSDQFNNTMFRGLQG NSACTKCNPRCLNELTPTE
10820	41188	B	10882	16	163	

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10821	41189	A	10883	2	1509	RDEVNGCIRLVYDMYSTFGFEK IVVKLSTRPEKRIGSDMWDRA EADLAVALEENNIPFEYQLGEG AFYGPKEFTLYDCLDRAWQC GTVQLDFSLPSRLSASYVGEDN ERKVPVMIHRAILGSMERFNGIL SEEFAGFFPTWLAPVQVVMNI TDSQSEYVNELTQKLSNAGIRV KADLRNEKIGFKNRSGELSHLP PINQSKPRNFPSAALPQVPQPTH LSQRPRASPKPPPPDPERVELSL EEHREMLEGFYEEISKGRKPTLI LRTQLSVRVNAILASLESVKPL YTMALGLLVKYPDSALGQLRIE STVDGSRLYITGNGVLFQHVKF HAFLLYLGYPQAAREVRIMQF CHTLREFALEYRTCRERVLQQQ QKQATYRERNKTRGRMITETE KFSGVAGEAPSNPSVPVAVSSG PGRGDADSHASKSLTTSRPED TTHNRRSRDRHGPRGCQVCSA QPSLLRAVPVADMRALMTGKD CPPCPGKRLRGAELGPL
10822	41190	A	10884	296	757	ISRRRRALSPKAESSLSILPRE KRSPSRTWILTPRRLFSLAISSKS AGNTLSSRIFK*KA*ACK*RG VSTRCRIFLALFIVTIKHLMMR STASNRQYSISIWTILPCWSARC FSIKIAGIPAEPPRYLLISPGLTG LKINFFTTVSFW
10823	41191	A	10885	1	519	MGLPWQVGMGAIFWGAIGLLL LTIFRVRYWMIANIPVSLRVGIT SGIGLFI GMMGLKNAGVIVANP ETLVSIGNLTSHSVLLGILGFFII AIIASRNHAAVLVSI VVTLLG WMLGDVHYNGIVSAPPSVMTV VGHVDLAGPIGNSLV/GCYPFAI LRRFSDGSGGLGRNQI
10824	41192	B	10886	1	3489	
10825	41193	A	10887	817	1528	WGSRDNRDEIRNTLVLDTLRLQ RVCAQRAFLVLVFLGKVTFEEL NFTFILVIQNVRGDTVEPTVVR DNHRTARELQQGVFQRAQGF IQVVGWVFEQQHVAANLSRCR LVNTPTQQVRFSTATFRVIWV TPTAGKLSGGFLFKMYGLPAA AIAIGTLLNQKTARKWAVL*SP PALTSFLTGITEPIEFSFMFVAPI LYIHAILAALFMWKFVPEKTR KTLLEEALSNRIAAE
10826	41194	C	10888	1	573	

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10827	41195	A	10889	2321	2554	WRKRCVKVRNLSPLCLPDRKL TLPCCSIAIRNCIAKL PVS* LWV ALWGWVTGRLRLNLIFLTRK RQKLSSSQGSRW
10828	41196	A	10890	1	4350	KULELRSKREAGMLERSSSRMV TCSQWAATRNPPVVALPIYGFI RCLVPFGLLHIWNVFQM QIGE YTNAAGQVFHGDIPRYMAGDP TAGKLSGGFLFKMYGLPASAIA IWHFVKPETRAKVGIMIFAAL TSFLTGITIEPIESFMFVAPILYII HAILAGIWHQSQVFFWGCVTVR RSRTV
10829	41197	A	10891	137	686	
10830	41198	A	10892	3	3831	SIGMMGLKNAGVIVANPETLVS IGNLTSHSVLLGILGFFIIAIL/AS RNIHAAVLVSIVVTLLGWML GDVHNGIVFAPPSVMTVVGH VDLAGSFNLGLAGVIFSMLVN LFDSSGTLIGVTDKAGLADEK GKFPRMKQALYVDSISSVTGSFI GTFSVTAYIESSGSVSVGGRTG LTAVVVGLLFLVLPLSLAGM VPGYAAAGALIYVGLMTSSL ARVNWQDLTESVPFITAVMM PFSFITEGIAL
10831	41199	A	10893	6	146	MCSEK VAMCCDDDDDDDDDD DDDDDDDDDYSCSHGFWD FSY TWNTSPQGHGLMGSPHGLVE IRDKLGDRTQRVYIQRITGNGL EFENPCKQFRGLTRMYIRRLTR LSVQWYMALE RPPVLQKYRY RGSKAHETSHSMSTVTSNEKQ DNTRIDTQGTNR/VATLRHRE TVLANEVAPYAATDNVLAAS DVGDVSWKLPVAQCFSPCFAV GTPPLHTWQ/SGLLQECQEHQQ VTDTPYHCPKPNVTPSLK
10832	41200	C	10894	1	1197	
10833	41201	A	10895	1	763	
10834	41202	A	10896	2	412	LFEFTLDVKVRESPI LFRDESM RTACSPDGLCSNGFGLKCPF TSRDFMFKRLGGFEAIKSAYMA QVQYSMWVTGKDAWFFANYD PRMKREGIHHVVVERDPQYMS DFNEMVPEFIEKMDALAEIGL TVRELGI

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10835	41203	A	10897	3	663	ARGKKPPRRGKEDFWDLSIATR VSVNPIKFPVEA*PFLKPLQQV SVGPLGGRLPLPIGNLLQLQVAD GTLSTGTGLEMEMVARVALV QPHEPGATTVPARKFFDICRGL PEGAEIAVQLEGERMLVRSGRS RFSLSLTPAADFPNLDDWQSEV EFTLPQATMKRLIEATQFSMAH QDVRYYLNGMLFETEGEELRT VATDGHRLAVCSMPIGQSLPSH
10836	41204	A	10898	377	1077	WRGQRCLASVFFPRHPGAEGRG RPVFAETIFL**SRRGLAR/TGR RKLPVKLKAADFPNLDDWQSE VEFTLPQATMKRLIEATQFSMA HQDVRYYLNGMLFETEGEELR TVATDGHRLAVCSMPIGQSLPS HSVIVPRKGVIELMRMLDGGD NPLRVQIGSNIRAHVGDFFITS KLVDGRFPDYRRVLPKNPDKH LEAGCDLLKQAFARAAIILSNEK FRGVRLYVSESQSLKSRQ
10837	41205	A	10899	591	871	VRGFPSGAEQLYG*SVSLILLP NLSNSG/RTGFPVAPLPYSKSPS DFMSLLISTVPGSQL*QPIQRAE LVCTTCSPIVSAPTQAPTQGA SH
10838	41206	B	10900	1	1765	
10839	41207	A	10901	1	1177	MKSLIIVNPADICGRTCEVAC VVAHPSEQELNADVFLPRLKV QRLDSIKRFWEQMMRIVTAAV MASTLAVSSLSHAAEVGSGDN WHPGEELTQRSTQSHMFDGSL TEHQRRQMRDLMMQARHEOPP VNVSELETMHFPGMLFETEGEE LRTVATDGHRLAVCSMPIGQSL PSHSVIVPRKGVIELMRMLDGG DNPLRVQIGSNIRAHVGDFFIT SKLVDGRFPDYRRVLPKNPDK HLEAGCDLLKQAFARAAIILS EKFRGVRLYVSENQLKITANNP DQEEAEIILDVPYSGAEMEIGF NVSYVMDVLNALKCENVRMM LTDSSVSVQIEDAASQSIAAYV GMPMRLEGSPLGNPEFQKISSP CALYIALCSKARHHTGRYLGLC
10840	41208	A	10902	527	925	

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10841	41209	A	10903	1	1514	MAFGLFWLIWILMSTITRIGID MSLALFTEMTPPNTEGGGLAN ALAGSGLLILWATVFGTPLGIM AGIYLA EYGRKSWLA EIVRFIN DILLSAPSIVVGLFVYITIVVQM EHFSGWAGVIALALLQVPVIRT TENMLKLVPSYSLREAAAYALGT PKWKMISAITLKSAVVGNMTRI L/LRMAPIVVKTAPLLFTALSNO FWSTDMMQPIANLPVTIFKFAM SPFAEWQQLAWAGVRNLFYY GKFHALKNINLDIAKNQVCVC YNQCTESLVNGLYANAAHLVS VGQRSTGNSSVIKARQSSIRP MIVKYSALCLCRMRSERFIRRT KHKRFDRLQCTCRPDKRSASG NLAFVISLRPVLVAVVFALFA AFPMFSDVSIQLRHIFANFLPA TGDVIQRYIEQFVANSNKMTAV GACGLIVTALLMYSIDSALNTI WRSKRARPKIYSAFVYWMILTL GPLLAGASLAISSYLLSKQWAI DIDSVNRLGAILITALITGDT
10842	41210	A	10904	900	1250	WYACDQCQTCLPDHAPECAVA *AKTCCTA IETGT YRQSGRERK QSAMVL*RVRVLL**RRETACH VRAGLL*S*GTALGGHYRRLQQ *NSTGRHAGSGGTPLQRSSVV SSGVADG
10843	41211	A	10905	626	850	LRFLVFNILSRYSLISTVQKFS AMLNGTLPLENIIH*LRNITAIM NLVIFHGLSA*SVCIYIPGRGSV MSDRV
10844	41212	A	10906	307	858	
10845	41213	A	10907	698	1115	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR *SVTTS/CIMPKPDGLTA AKNLA EAFEHYNEWHPHSGTRRRAR FSVRATYAAGRLATIPGYRGGP LGLMCGQPNRKPTDGANERLT MIRAATAMSE
10846	41214	B	10908	1	721	
10847	41215	A	10909	1	2615	
10848	41216	B	10910	1	1164	
10849	41217	B	10911	1	1930	
10850	41218	A	10912	689	1033	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR *SVTTS/CIMPKPDGLTA AKNLA EAFEHYNEWHPHDGPESVFM PSR*APMTR*KIYSPPPYRSSQR AHRHA

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10851	41219	A	10913	393	686	NPSQLWEAAPQWKWIQGAGK VSCQLSRAADQLGRQHHISDPC FSIVPLIL*FAAYFPINPAVLKLA PVALYADAIRYNARTPLQGSLL PLTRLVWA
10852	41220	A	10914	1313	2370	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR *SVTTS/CIMPKPDGLTAAKNLA EAFEHYNEWHPHRANPDANVV SEDLVRESVGKSVVNLHGVVD MAAIRQLKATHDTSVSSEQVD NVRMLLAMVDDFRCVVIKLA ERIAHLREVKDAPEDEVLAAK ECTNIYAPLANRLGIGQLKWEL EDYCFRYLHPTYEYKRIAKLLHE RRLDREHYIEEFVGHLEAEMK AEGVKADEVYGRPKHIYSWRK MQKKNLAFDELFDVRAVRIVA ERLQDCYAALGIVHTHYRHLP DEFDDYVANPKPNGYQSIHTV VLGPGGKTVEIQRITKQMHEDA ELGVAAHWEI
10853	41221	B	10915	1	1556	
10854	41222	A	10916	1566	1947	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR *SVTTS/CIMPKPDGLTAAKNLA EAFEHYNEWHPH/ECAGLSLAT GISAAAGL*WARRSFIQRDSRD PRYRAPIRIHPLPGANHLRQ
10855	41223	B	10917	1	1571	
10856	41224	A	10918	2024	2589	QDMQNLVLVRETSVKPFYPL KVPEAFR/RIQGRKGEGEGAY VYRSAFSVFQKPRFSCALGGAJ AASWAGGGAPSPCGRAELPW GPGVGVAGTVCPERPRRERRL RGEREEEAADKVMARRWRKSR RRKRKEMEERMSPEETEGTNF DFAGEAVGQAERKGFAPSAAE ESFHEEEKRRRKEQSDLTF
10857	41225	B	10919	690	2724	
10858	41226	A	10920	3892	4338	

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10859	41227	A	10921	2573	3473	ANGARLALPPLGTFQGRQLRRR RPRWRRRRPGEASGPVMRLRG PRPGASAPWDGGGQVAR*WC PFPSQGWDDGSGGGQGDGAR FRTHRAKVQDGDGR*DEADG VHRHAPLQGLVLVQVGVAD REDDAGNEGLQHLQQPGYGGH IASDLAGPGPGHFGGVSHTR DAGEEGGGDGVVPRTAVGQEL DIGGGVDDGGREAEGRGAGEG DGEVAPRQGEAGLEPAQLHDE DDQGHGEAEAPGEHGPVAHGP RPGAHASHQREGHAGRHLQQA AKETQGLCQGPGRPHDHGGPQ
10860	41228	A	10922	819	1274	NPLPRLQLRRLQLHPSVRNCCQ TRRCGR*HRQLRQ*ARRKLVR SVYFGSCLRQLLREEWK*Y*RV *VLGWYSAVSTSSLPFDYCLP NSDGYRRVVDPGSLSGHPFLYQ RYGWQHDDVHQPDGLGPPGS LHPDPAFCRCVLRNCGNLLA
10861	41229	A	10923	720	3546	RDGRKPLQFDAARNCGGSSQSQ RSGSRKRRGDRRI/TLSMLKTRK ANRWA*SFRKMAAISTP/RTDI ACAKYRYETLHADRVLYIDS RQHQLMQAWAIVRKAGYVP ESVPLEHHMFMMMLGKDGKPF KTRAGGTVKLADLDEALERA RRLVAERTRYSAKSWKTVFRL VIGEOMIDVLGPEKRRRRITQE KIAIVQSSFEPMVTSLVARQH GVAASQLFLWRKQYQEGSLTA VAAGEQVVPASELAAMKQ
10862	41230	A	10924	764	1227	RIMVHATGLMKHASSPGCWDL NRRTRRCGVRRVTE*QRAS*KR *SVTTS/CIMPKPDGLTAAKNLA EAFEHYNEWHPHNPTEWFLS HCHIHKYPKSTLIHQGEKAET LYYIGKGSVAVLKDEEGKEMI LSYLNQGDITGDLGLFEEGQER SAW
10863	41231	A	10925	2467	2653	WLPFGLSHHNSPHPTSWGANG GFCQLLSMSVLMHSGTLGAH WDFSPVIGLEANRGVGDGS

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10864	41232	A	10926	1	860	MSHQLTFADSEFSSKRRQTRKE IFLSRMEQILPWQNMVEVIEPFY PKAGNGRRPYPLETMLRIHCM QHWYNLSDGAMEDALYEIASM RLFARLSLDSALPDRTTIMNFR HLLAQHQLARQLFKTINRWLAL GVMMTQGTLDATIEAPSSTK NKEQQRDPPEMHQTKKGNQWH FGMKAHIGVDAKSGLTHSLVT TAANEHDLNLQGNLLHGEKQF VSAMPATKEPQRELAEDVDVD LLIAERPQKVKTLK/TESAQ'G' KRPTSTNT*KPASVPGWSTRA SSSGSSAS
10865	41233	B	10927	754	910	
10866	41234	A	10928	2395	3454	
10867	41235	A	10929	1	1377	MSCMTPASDGTGISIDDEEAKQ FRESVVEWLMTNHPHDCPVCE EGGNCHLQDMVTMTGHSFRY RFTKRTHRNQDLGPFISHEMNR CIACYRCVRYKYADGTDLG VYGAHDNVYFGRFPEDGTLESE FSGNLVEICPTGVFTDKTHER YNRKWDMQFAPSCQCSIGCN ISPGERYGELRRRIENRYNGTVN HYFLCDRGRFGYGVNLDKDRP RQPVQRRGDDFITLNAEQAMQ GAADILRQSKKVIIGISPRASVE SNFALRELVGEEFYTGIAHGE QERLQALQKVLREGGIYTPALR EIESYDAVLVLGEDVTQTGARV ALAVRQA VKGKAREMAAAQK VADWQIAAILNIGQ/HPLFVT/N VDDTRLDDIAAWTYRAPVEDQ ARLGFAIAHALDNSAPAVDIE PELQSKIDVIVQALAVFRLVIGE QMIDVLGPEKRRRTTQEKIAN
10868	41236	A	10930	19	586	IAALLKDKHPAMLLLAATKRG KALAAARLSVQLNAALVNDATA VDIVDGHICAEHRMYGGFAQE KINSPLAIIITLAPGVQEPCTSDTS HQCPTEVVPYV/APRHEILCRER RAIKAASSVDLSKAKRVVGVG RGLAAQDDLMVHELAAVLN AEVGCSPRIAEGENWMERHAQ HKSWNPLSWAPLGSQAHP

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10869	41237	A	10931	1	1364	MLRILCALCSLLTGTRADPGA LLRLGMDIMNREVQSAMDESH ILEKMAAEAGKKQPGMKPIKGI TNLKVKDVQLPVITLNFVPGVG IFQCVSTGMTVTGKSFMGGMN EHVALNITANRLRDEETGLP VFKSEGEVILVNVKTNLPSNM LPKMVNKFLDSTLHKVLPGLM CPAIDAVLVVYNNRWTNLSDP MPVGMGTVKYVLM SAPATT ASVIQLDFSPVQQQKGKTIKL ADAGEALTFP/RGVMPKA/PPQL LVPATFLSAELALLQKSFHVN QDTMIGELPPQTTKTLARFIPEV AVAYPKSKPLTTQIKIKKPPKV AMKTGKSLHLHSTLEMFAAR WRRKAPMSFLLEEHNKGG HSLHENQLQMATSLDRLLSLR KSSSIGNFNERELTGFTSYLEE AYIPVVNDVLQVGLPLPDFLAM NYNLAELDIVELGGMPEADI
10870	41238	A	10932	111	415	VSALSLLHRAPCRRLPPLQ DAGLHGWEHGVQGRGPAAH RDPV*EGWHHSGHLAQGHSEG *PCGDSETPAGREGKTAGHRTG RCGCRQEQTGAQQD
10871	41239	A	10933	2	219	FLGGEGVIFPRGWGGAAMRFV STGSRHTTP*GSEKSAGPHTQW HQNSK*ATSETRLHSCASEGIVP AGCRPY

[illegible]

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10875	41243	A	10937	76	614	PDRRWSSLDTMNHTGQTFSPV NSGQPPNYEMLKEEHEVAVLG APHNPAPPTSTVIHRISETSVPD HV/VLVPVQHPLEHPCCLGFIA FAYSVKSRDRKMVGDTVGAQ/ ALCLHRQVPEHLGPDSDGHPHD HSAHRHPSADLPGLWIDQEASL RPGALPMTICIPRTPTSI PRPAPR GQELCP
10876	41244	B	10938	695	1011	
10877	41245	A	10939	410	5501	EAKTHKSVVMTDPLLDSPASS TGEMDGLCPPELLIPPLSNRGI LGPVQSPCPSRDPAPIPEPGCL LVEATATEEGPGNMEIIVETVA GTLTPGAPGETAPKLPGEREP SQEAGTPLPGQETAEEENVEKE EKSDTKQDSQKAVDKGQGAQR LEGDVVSGTESLFKTHMCPECK RCFKKRTHLVEHLHLHFPDPSL QCPNCQKFFTSKSLKTHLLRE LGEKAHHCLCHYSAVERNAL NRHMASHMEDIS
10878	41246	A	10940	446	1704	GGPDM DARAPAVGGSCHQHOP SGAPGP/CIGRMES/EVGVRDHA IPEGARCNRFRKETT EGPLHCSR CGLLCPSASLRGHTRKQHPRL ECGACQEAFFSRLALDEHRRQQ HFSHRCQLCDFARERVLVK HYLEQHEETSAAVAASDGDGD AGQPPLHCFPCDFTCRHQLVLD HHVKGHGGTRLYKCTDCAYST KNRQKITWHSRIHTGEKPYHCH LCPYACADPSRLKYHMRHKEE RKYLCPCEGKYCKWVNQLKY HMTKHTGLKPYQCPECEYCTN PIADALRVHQETRHREARAFMC EQCGKAFKTRFLRLTHLRKHSE AKPYVCNVCHRAFRWAAGLR HHALTHTDHPFFCRLCNKYA KQKFQVVKHVRHHHPDQADPN QGVGKDPPTPTVHLHDVQLED PSPAPAAPHTGPEG

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10879	41247	A	10941	1	944	MSILLTSIARQSRDKRTRLGHK QRILAGLSNHPIRNLQGLRR FALVDRQLVVQNVVTRWCRM VYQSAANVFIQHRPISHDERVQ QRGTAITMMVQQAQWAERGK SGLSGVAIGPAVDTSALQAQLR ETLPPHMPVPVLLQLPLPLSA NGKLDRLKALPLPELKAQAPGR APKAGSETHIAAAFSSLLGCDVQ DADADFFALGGHSLAMKLA QLSRQVARQVTPGQVMVASTV AKLATIIDAEEDSTRRM/WRNH SAVA*R*WPDVLPFPCVRFCL AVQRALALSRSTMVDYRHSVT APQWPHADGGKPG
10880	41248	A	10942	1	939	MRTILTIDIQLRYPRRPGAFGTH TFLKCAFSNKQRRFTVKRFAPL AARYPASQEMPPVRHGHAVAA AIPCGNVNPANGNTPARYKQGQC GLCSSTLQDALRDFIQVAHTCEI PLMPACFGLADDKLWRWLNE KLPCSLMLLPTLPPSVGLRLQN QLQRKIVLFGGVWMPGDEVKK VTCKNGVVNEIWTRNHADIPLR PRFAVLASGSFFSGGLVAERN IREPILGLDVLQTATRGEWYKG DFFAPQPWQQFGVTTDETLP QAGQTIENTLFAICSMGGFDPI AQGGGGVCVSAALHAAQQIA QRAGGQQ
10881	41249	A	10943	25	479	
10882	41250	A	10944	2	453	APSRTSGSSVGLQGSYVLDVVG REFGCERVKG*FLVHRAGHL/L TLWLFSQINKMEWWSRLVSS DPEINTKKINPENSKVSPGWL ELQQEGEGPRCFQSFTDSCHCL PSLSDLDSETSMVEKMMYDQ RQKSMGLPTSDEQKKQEILKK

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10883	41251	A	10945	3	1110	RDPQERRERGRTRVQSSGTWIGA GAMGGEQEEERFDGMLLAMA HQHEGGVQELVNTFFSLRRKT DFFIGGEEGMAEKLITQTFSHH NQLAQKTRREKJARQEAERREK AERAARLAKEAKSETSGPQIKE LTDEKAEKLQLEIDQKKDAENP EAQLKNGSLDSPGKQDTEEDDE EDEKDKGKLPNLGNGADLAQ *RLNPDPCRELDLAVPF.CVNFR LKGGKDMVVDI/RRQHLGVGL KGQPAIIDGELYNEVKVEESISW LIEDGKVVTVHLEKINKMEW WSRLVSSDPEINTKK\INPENS LSDLSETR\SMVEKMMYDQ\ RQKSMGLPTSDEQKK\QEILK\K FMDQHPMGFFPKAKFTNPNC
10884	41252	A	10946	50	426	
10885	41253	A	10947	1	942	QVWKQCNCFKHYSNETDNSTTQ LVGLQTLQVVVPSLILCEHCMN FSSPHVWCCLVQAVPGQGQT MQVPVSGTQGLQQVSN*KY*A VYQRRGFKE\IITTYQTQIIHQ PQTAVTAGQTQVIPLALSHRSK TDLEESDN*VRYFPVNADGTIL QQGKCTHKLP*DFLGQLFCPLD N*HLSSSGQGTVTVTLPVAGNV VNSGGMVVMVRKICIFQLCL*NF LEHAT*CLLKFEPLYVNAKQYH RILKRRQARAKLEAEGKIPKER RVCITLGR*ERRIAGFYF*NYLL YPKEKDSPHMQVGRHIHIFILLFI TLY
10886	41254	A	10948	24	378	
10887	41255	A	10949	15	658	QRPNAAQTPSRGCOLSAPARA GRFHQPQSCRPSRVGCKGHVCIP GDRSLALWPRLGCGE*TSSAL DSQGILVSNFPHEGS/PTPQSG LKTGRILLNHGRRLKVSQSEG RFLEVGWKQRGPTAHRTHSNR TRRRHALSTGGDTGRARNARS GGGRSPSSLPAASSTPGVCWS PRMSQARQPPSCRRGVPRRPEM LRLSLSPSCQICVCVRFH

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10888	41256	A	10950	1171	1639	PMALWADGRARHKVGTCECECGMHPGLKCSGR TLGSQTM LATTPCDSPT*1/SNKNGLRSV/SYR*CLINALWLFSPHILVRCGTESS*LLPSLVPSWLP*LVRVRPLPTGWC*IPSCCLKPPTWSSHSPQRLP*NPATLVCLQNGTARSHSSTPV
10889	41257	A	10951	2	357	HERLLNPGRETWDATCYSETASCVA*ATVQ*HDHGLS*PQTPGLKWFHSHFSLPSSWDYRHHVPPCPETGCPVTDQGVQWSYHGSL*PQTPRLKQSYHYSLPSSWDYRW EHPVAGKQA
10890	41258	A	10952	15	578	IQITPKGRRTKPCRQKRQRTIVTPRQSTPRSNRGKDTRSKQRDETT E*TTTRAQDTNKEGATQDR TETARRTQSNMEKEKFNQHNKRKRD RDSRKDKGHERETKNTERNRTKRREKRKDNKNHNEAKSQRQTRKKKETKETATRKREEPSNSCSMHPFQISWLHSVGDNGRRDQLLCQGFHLYYLMCFQ
10891	41259	A	10953	2	369	DIDPTGLQSQSGPKGQDPPLMFSEDYQKSLLEQYHLGLDQKLRYVVGELIWNFADFMTNQCPKTTSPVILFLPSCPEEPQANKATLVCLMNN/FYPGILMVTWKADGTLITQSVEKTTPSKQS
10892	41260	A	10954	1	417	FGTGPSASPRTSFRHQCGH*PHWTA/VTVDSQGAGQPKTTSPVILFLPSCPEEPQANKATLVCLMNNFIPGILMVTWKADGTLITQSVEKTT/PSKQSNKNKYVASSYLSLTPEISWRSRRSYSCQVMQEGSTVEKSVAPAECS
10893	41261	A	10955	113	767	GPMRPGTGQGGLEAPGEPGPNLRQRWPLLLGLAVVTHGLLRPTAASQSRALGPGAPGSSRSSLRSRWGRFLLQRGSWTGPRCWPRGFQSKHNSVTHVFGSGTQLTVLSQPQ/ALTPSVILFLPSCPEEPQANKATLVCLMNDYFPGILTVWKADGTPITH/GVEKTTSPSKQSNKNKYVASS/YTSLTPEQWRSRRSYSCQVMQEGSTVEKSVAP

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10894	41262	A	10956	1	344	GSAAGQVQQQQRRHQQGVK TVKYDRKELRRLLVLEEWIVE QLGQLYGCEEEEMPEVEIDIDD LLDADSDEERASKLQEAIVDC YKPTTEFIKELLSRIRGMREN*A PPPKKSV
10895	41263	A	10957	3	349	TMNNMRGQILLFLLIWLWNR YGQLVGSSEKHKIASQLELIQS QFHYCVTLDKLLNFSEPVHVK QEQLLSVCSEKEVTEVKVLALV NHVGSKCCFLFCSGPSP*PKFSV SQVFS
10896	41264	A	10958	998	1383	
10897	41265	A	10959	39	402	TDHIMREYKLVVLGSGGVGKS ALTQVQVQGFVEKYDPTIEDS YRKQVEVDQCCMLEILDITAG TEQFTAMRDLYMKNQGQFALV YSITGQSTFNDLQDLREQILRG* RTREDVPMILVGN
10898	41266	A	10960	25	739	YKKNFIDISLSVKCETCTHMLT SSSL*C*NLCISLFLIDFNL*AG FVI*VGFTAQSTFNDLQDLREQI LRVKDTEDEVISFLCKMLCHLS VAK*KSACFQNLARQWCNCAF LESSAKSKINNVETYNCAWAA QTS AFLVCFKLTA RLLALSITNV SSCTGWGVQRSHQDQGNKSHA ASSVWKVGFGIVRLGTGTCLSS LERGYMCMEKEMFDPYTPSRV LKPRSEALELFGPLKSLT
10899	41267	A	10961	946	1424	YFRFLCVIFCSFLLRCLVSRVLL YPMIAEIPRVQGRGGPSWPL GGRLKELSRLLTFLKVRKLSIL SGWREVP LGQPSL TEPP/PPAPP HPGPGSWLASASAPHL SQPPAA GPAGQPPSPGSPVPGGCSLALP VTSVLCLEPPALKPAAASAPVV AVH
10900	41268	A	10962	1	148	TALQEFGTRSGIPALGCPPDP* PPPGSCPPPEQLLSVGEPSCRS CSP
10901	41269	A	10963	10	233	LGAARRAQLLESWPRA/PPPAR LHACHLP/LPRTPKVHTS*PTQ QQGGFSLCKKKNPVSVEMIC SSARLKLTE
10902	41270	A	10964	1	331	RPLLSLTLCWELRAALSYWRA GRAPPPPARLHAGPAGFWVLT PSGGEGERPRLHWGGGGRRG GGRKKD*GGQGRGAGGFATF SPPANAPRLHTSLTNSSARWIFL CV

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10903	41271	A	10965	4	1023	FPRAGEKPYTCESGRAFNQS* TLTTHMTIHAG*KPYKCEECGK AFYRFSYLTKHMIHTGETFYK CEECGRGFNWSSTLTKNRIHT GEKPYKCEQCGKALNESSNLT AHKIIHTGEKPYKCEECGKAFN RSPKLTAHKVIHSGEKPYKCEE CGKAFSQSSILTTKRIHTGEKP YKCEECGKAFNRSSNLTKHKII HTGEKSYKCEECGICRTPKMAV FSQCHQVLKITNIHYPSSIAIVH GDRAQSHVDICTLGDKASGAIH GTAFTYTQCEQRAYNETAVSR YTISRPPSHHGGDSEITTEFPAI GRCNGVHKSWGNSRCSDRWRS
10904	41272	A	10966	1	290	
10905	41273	A	10967	1	1508	MSWAARPPFLQRHAAGQC GVGRKEMHCGVASRWRRRR WLDPAAAAAA VAGGEQQT EPEPGEA GRDGMGDSGRGEC SRRAGEPVTALSA T P P P P P SSMGSPLPPAPPFGSGPVSS QVRGCDQLTA WPLSFSCFC V LGVRGLHCP P P P P GPGAG CAICGRSSGMWLRG*TERESL GHVSSPVG*DLTYS CRDNKDCT VDKQRNRQC YCRYQKCLATG MKREGKDPPCGVL DHMPFSLI PLRPPEEMPVDRIEAE LAVEQ KSDQGVGPGGTGGSGSSVS GVNPLSFVMGVGGGSLGLWAK RIPHFSSLPDDQVILLRAGQ*P WIPLTS*HLTPL*L PDLFLATGL HVHRNSAHSAGVGAIFDRSVA LG*AGM*IEGVGL*AGPCLRAII LFNPGKRRITFVSQGGN LGAS SSPMETCYCKQKYPEQQR*DG AGGH*GSLGGGECYEDVFLFFF KLIGDTPIDTFLMEMLEAPHQL
10906	41274	A	10968	945	1131	MICTVAISYVLFVDVYISLLSAT CSPKQGS AVFQHD*VSPGI*NG SERCCSRDRHRQFLW
10907	41275	A	10969	37	332	AEGIRTIQGTENIFCKVWGRQ VLSQNTNTLEGQSN DHGCLRL KRTFTISTFAHYSRFFLQRF/VFP YTGFEKCSQSTAW*KPRYLLSHS VKGKRN LHPA
10908	41276	A	10970	137	283	
10909	41277	B	10971	1	624	

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10910	41278	A	10972	3	618	KTQDPAKAPNTPDILEIEFKKG VPVKVTNVKDGTTTHQTSLELF MYLNEVAAQHGVGRIIDLGDN RFIGMKGRGIYYTPTGTILYHA HLHIEAFIMDREVRTIIQGLGLK FAELVYTGFWHSPELCLRHCI AKSQERVEGKVQVSVLKGQVY ILGRESPLSLYNEELVSMNVQG DYEPTDATGFININSLRLKEYHR LQSKVTAK
10911	41279	B	10973	1	1102	
10912	41280	A	10974	748	1396	LYLQRPFFQIRSSLQVLGHRQIF PQSPRCLHLAPPLMRHSHRSPT WY*FSPRRTQSRPVSAQPLGS CGGIQPAAPPVTPQSQLSPPRG R*LGSDGAGTQPRHVQNPCLT CVHM*SPPPCLNLQARCPQSL RAKVVPAAVEQARARVGHVESPG SHCWLEREPEVGSQPQGGQRPL PAGAAD*CLGAFWQTHLDLGD SLISCSHDLQGWQLSQA
10913	41281	A	10975	1	846	
10914	41282	A	10976	2	851	WNSAELGRGGPGAGGAVIGM MRTQCLLGLRTFVAFAAKLWS FFIYLLRRQIRTVIQYQTVRYDI LPLSPVSRNRLAQVKRKLVLVD LDETLIHHHDGVL RPTVRPGT PPDFILKVVIDKHPVRFFVHKR PHVDFLEVV SQWYELVVF TAS MEIYGSAVADKLDNSRSILKR RYRQHQCTLELG/SYIKD/LSLV VHSDLS/GIVIL/DNSPGA/YRSH PGYGGRI/DNAIP/KSWSVTPS/ DTALLNLLPMLDALRFTADVRS /VLRNLHQHRLWYTA CFPLPP
10915	41283	A	10977	25	153	
10916	41284	A	10978	1	741	MMSFDSMSHIQVMLLQEVPS YPASKKNEA/PQTSGGGPGT KGLGE/PAVVPMSPAVGT/PALT QCHGPHAEDDLEELTTDPVA RDCPLDLLMDGKTGAIISSLLHS NCLPAPFCQCSHAVKWLKTV HSCCPLGEVQPORRCVIATKE KGIGVKHHCNIHSDNVNSIITAT VAHQQQQLPQNGNNSGIKNN QNSSENTVTNNSKNISNHIICRN SSKNSKSSSSSSSSNNKNSSNTI NSNNKAR

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10917	41285	A	10979	1	669	MMSFDSMSHIQVMLLQEVPS YPASKKNEA/PQTSGGGPGT KGLGE/PAVVPMSPAVGT/PALT QCHGPHDEDDLEPILTTDPVA RDLTMPTAASQHLKQCLEHH HYFHSYNINSDIIVSRNNISSHIT TPVHHCHISDNVNSHITATVAA HQQQQLPQNGNNSGIKNQNS SENTVTNNSKNISNHIICRNSSK NSKSSSSSSNNKNSSNTINSN NKAR
10918	41286	A	10980	3	980	IESPGFPFGLQRPVPHRGEFL RCTSSEALPCFYSWTVTFSPWT VAAAQGGPRPGPASKRTLLATQ SEIAAAELGPGSWGPPSCPSE QSSHGPPASS*AAPLQTGRRLRS RAS*RSAGPSVAALPAPLSRQPE RHPSVSASRSGHPGCPSPPPP AARPVQPSPCRAPPGSAAGRAR APHA*AAPGSWLSAGAAARR WPFQTAKGSGS*DRPGRPGPDA PAAPPGWHRAPPGSSSGAGTG RHPQPFGRPRRTAPYAAPCA FVATLVFS*LLIFGGAFSPALS HCPTSA*LKRLLEPAPIAFPPG LHPGTLLSRAE
10919	41287	A	10981	1	5229	
10920	41288	A	10982	1	7044	
10921	41289	A	10983	1	3228	
10922	41290	A	10984	10	209	TLSGGEPQRLAERRARLQDEE RRRQQLE*MRKREEDRARQ EEERRRQEERTKRDAAEKVM
10923	41291	A	10985	293	363	
10924	41292	A	10986	3	434	
10925	41293	A	10987	3	1536	
10926	41294	A	10988	315	993	VPVAPIHFHSHFSAPTFTQSR QDSMQCILRQHCHLILSRSSSL VPAGLRGAMAFALAIRDTASY ARQMMFTTLLICPELLALLLS LSHSRSLLLHGYHGPS*YALFFS LSFSLVTWVGAKPGRYQSLIFV VVVGCTFQNGEPLREEDSDFIL TEGDLTLTYGDSTVTANGSSSS HTASTSLEGSRRTKSSSEEVLER DLGMGQKQVSSRGTRLVFPLE
10927	41295	A	10989	3	320	

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10928	41296	A	10990	3	582	GPPTPRRPRPLPSSLPSRRSRDPP RIPLCA*FPQTRKQIARSEPD*T WASQSSSTIPRIWRVFHA*KFST APL.TATPPPGKMCAGCRETVK TT*PPLRGGPAPFLLPSRAVARG TRPGFRSALSFRRPGNRSRGVN LIKLGRLSPPPYPGGGSYTPE NSQPLPSLLHLEKCALRDAE RQLKPPDHHLMAVWLPDVWN GEGEPSPSHTRHSLRASSNYV LRAPEGNLLARRLPRETAINLQ PKACYKTLSPESFSHFYNQFC PRRHQWLPAPPPGHFFLG
10929	41297	A	10991	3	338	NSPSRPRSSQRGVAGRREAGP VAVP*GGPKKGRGC*GNRWG QRPRWMLRASGSGESTTPACSA ENRHAS*RKKRRPGQVSWE TEETRSGHSGPRGHAEP LHRP QRR
10930	41298	A	10992	3	226	TILSS*SSSSSSPSPSPSPSPSP SPSPSPSPSPSPSPSPSPSP PALFPRSLSFSLFPGTGTFPSCP
10931	41299	A	10993	24	489	KEYLVRTK*QKQKGENPLVKIT FRPPPGRLRTYPSAPWSARSTYG RAAAVWRPHSPSAPRRGTHPW PAGHRGQRASGEGVGTHTHAH MSSVCACSTHTCWSRNCCKDPR EDRGRGLTVLLEAAVCNSCLLL VLKTPRNPQLPILYTDSDTKSST GNP
10932	41300	A	10994	1	1491	
10933	41301	A	10995	140	308	RNVIKLKGWSRPSKQQDNPTLR PGPPSPAGGQQLLMRMRPLA GGGKSWGIAHFYKPLQRERRA GAECGLARQVRAEVTKWIGVN RRPRKRRKMEKEEVFEKLLPD QLGLLLEHLLEQKTLSPRTLQS LQRTYHLQDQDAEVRHRWCEL IVKHKFTKAYKSVRFLEQDQA MGVYLYGELMVSEDARQQQL ARRCFERTKEQMDRSSAQVVA EMLF*RGQDRFSLKKCDKVKG MVKTQQATGQPDSPPRALTG RRVPATADADEKAFGGWRKIL GYRTFL

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10934	41302	A	10996	219	688	RRMHAYVSLDPLRPPFFFLF FFFFFFLRRSFALVAQAGVHW RDLGSPQPPPRFK*FSCLSLPSS WNYRHHAPRPANFVFLVETGL QLPTSGDLPASASQSVGITGVS HCAWPGNWLLKETRCSSVGR QITGPITDAWVDPGIPDRYLQ
10935	41303	A	10997	3	298	FFFFFLRQSFALVAQAGVQWRD LCSPQPPPPRFK*FSCLSLPSSW NYRHHGPPHPANF*FLVEMEFH HVGQACLKLLPSGDPALASQS AGITGVSHRA
10936	41304	A	10998	2	438	APSVRSGNERDLARDEEAQETQ VRGCHASGGCTPAATAGASPP AWAGRRGTGQRLRSQPRQTGR QPPRVQPLAPPGAPAPLPNPQ NCRKTRSHPRFWAGTLAPGPC PGLWCLPGLVQVDVLAAGRCD HLSCLPPLCPQAFLL
10937	41305	A	10999	2856	3044	GAATGEGGCCRLPGHPALAST A*AIPCRGPRVQETSPPPVLGW DPGSRAMSRLVFAVVGAG
10938	41306	A	11000	1	908	GLGDPGVPLRSGGLGPPADLK GDQAVAE*LHEASGVTEHHPS AQPGPGGEAAEPAHLIV*EPEG GSPGHPPGGPGHPG*SEGPAAG KPGPAGGSAQGCRRSSEPSGT *SGRSPR*GPHGHPDCRTHPAR EGAQVHSRSLPGGAPVRRGCS QGPEQLRQEDFLRVQQLSAA GPLRPQLYPQVWLCPEHQLE QYPRSYFSEIDVFKPCGVQQG CPVLDRASSKISPEDAAGSVVR LRSLWAASGLQQGASGLATFL QLLTCGVLPWDEELVHLLDE VVASAAALRCPDPVPMPTCG

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10939	41307	A	11001	218	990	VLQLLKAMRLEFLPPGGFMV LLASGVKLQTFATQVPSWLHP VDPSGLEVELPASPVQCAHTP QPLGGRWDVWPWSRQGRSSG RLGPHGSPWRRWEAQAWQPA GPKPCPVGS*GPVNRNGQRRW AGTAGDPVHPPQLAQVLSPL PGADRAGQLLRVQGPSPCPPG TPAGPQGRCAAPVPTGVSPSTP PCKLREQAPALASPERGSHSAA VG*RAPQVLPKW*PELMFRWV RSFFLLVGSWLTSGVKLHPFVV SVTALKGDASGVIPSSRWVHGL AGLRCEAADLRDSGAQLASPS GSLTRTGGGAACQSRVCPHSS AFGWSMGLGAMEQGAALIGEA RASREPMEEVGGSGMAACRSQ ALPRGQLRPSEKSRAPVGWH CWGPSTPSAATGPGAKPLIARG RQGRPAQAQSGAPAKPMPTRNSS WPAKAVRSPGSHWRLSLHTSL QAERAGSGLGQPRKGLPQCSSG LKGSSSAAKVVAQAEAAQRAS EGCEDYLARCHLSIRKMRRRN
10940	41308	A	11002	3	644	EPPGPTGPPSPQSPWHPLGR WSSTHVVFTHLHLAAGPWSCD HRWMGKQLPVSLASGVQGV RFRSQDMYQSSRNKFPSGAAH VPQEWAVPWKNQGNTHQSSRP SESGCCAQAEGSNQCHQREAE AGPSRLSLPDGGRRLTTPRHNP GPWYWNNSPQRLN*WRRGDPS WPEPQGKPHTTGARVPACQRR EICLSFPRGPRRRQKENIYEYL
10941	41309	A	11003	202	438	FHGHAPAGEMRGWPRVTKRSP AQSGKTHFPSPGPGPDTSTESI FRRAWKAPGPGRGRTADPET ARCGAWDEIVEPV
10942	41310	A	11004	520	1094	GPLSQCPPLRLLPPLGVYSKGR APHADTHSPGHRRTAHAQPA AAAATATR*QRRRLPPRRTPF RRPAARPDRRVPAHSSAVLPRP GKPGAFQALRKMDSDVDSGGP GEPGGKLGFARLRRAPPDRLPG CPSSHSFQTQSLSFMAHNVDPE LESATSLGLLRRSWFCFTWQK QTVYWSVTGRIRHSGEK
10943	41311	A	11005	1	138	SISLMNDVKILNKILANQIQQH RKLHHDD*VGFIPCLRILVYI

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10944	41312	A	11006	65	297	NQRLPQFLPTTTPPATRAT*D EEKSPYPGPGSDKKCP TLQ.LPSP PTPSAGGFPLGESGSPGGLVK AQIMEGISM
10945	41313	B	11007	322	6900	
10946	41314	A	11008	3	215	
10947	41315	A	11009	1	234	
10948	41316	A	11010	149	300	
10949	41317	B	11011	28	162	
10950	41318	A	11012	700	861	RRKCIPGRNRNKHGPDGAGRP *VCREQEQEGQCAWTGYPGAQG PDPYCGKGPYS
10951	41319	A	11013	291	744	LKKRTKCDQLKTSFLDLGRGPI LKWLCTSKWGHQQIIRA*GTE YKTTSTFFFFETASRLCHPGWE CSGAISAHS*FLLPGSCHSPASA S*VAVTTDTREHAQLIFF*HFSTR DGFHVVARWLDLLTCDLPLSL QVLGYRNYIIIVRQLPSR
10952	41320	A	11014	139	414	SPKTAPPGFFFSF*LHLMLMKFT PGAIKLVFLQFLLGISFFFLGKP PSSWFRNESC SVFRKESQSWQ GRAHVWG*SDPWSSGRSRAH L
10953	41321	A	11015	5	565	VHTTEATCTTTGAKPCWPWSKL ATRQDHSVLSTSNPRGPTPHKS GSPETAGALSSGDAGSRGEGPR TVSSERSSPGKGGSTLLGTTA*G PGPAHFASAVLGPSSKSLQAAS *EVDSPSSLLKTAVSVLASTVR LSVSFMPFITVSVTSSVISASS PSELASMATLPGASG*AAAVN FELDEE
10954	41322	A	11016	188	515	SQTVSIVGELPIPRKRCEIGIWD AQKR/CPRLTGPWATISVPTISK KATGN/PQHPNHPRARYQINAE *WKVHIF*TNDRPSHECPCTLV VHRTLQDLRHKSSTSGGKTHG
10955	41323	A	11017	80	397	SVQRSVDHL*DHP*TSVDWELY LDGSSFANPCKVTLKTTTSPAS VTPEADWSMHQSQRNLSRDS FSLKFGLIIHDFLPTFNPLENP CGFLTRCCVPNQISS
10956	41324	A	11018	104	392	PSQFHLKLLHMLALLYPVGTG QVKDSSLQKSTSVPPDSPQTG HSLKLGPNPGRFR*RPQCQPGV LPDVELSCHSWNVLWTTAA KTPIFCY

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10957	41325	A	11019	125	1404	NLALGMAMWN\RPCQRLPQQP LVAEPTAEGEPLPTGRELTEA NRFAYAAALCGISLSQLFPEPEHS SFCTEFMAGLVKWLSEAVLP TMTAFASGLGGEGTDVSVQTL LKDDPILKDDPTVITQDLSFSLK DGHYDARARVLVCHMTSLQLQV PLEELDVL EEMFLESLEKEEEE SEMAEASRKKKENRRKWKRYL LIGLATVGGGTVIGVTGGLAAP LVAAGAATIIGSAGAAALGSAA GIAIMTSLFGAAGAGLTGYKM KKRVGAIEEFTFLPLTEGRQLHI TIAVTGWLASGKYRTFSAPWA ALAIHSREQYCLAWEAKYLMEL GNALETILSGLANMVAQEALK YTVLSGIVAALTWPASLLSVAN VIDNPWGVCLHRS AEVGKHLA HILLSRQQGRRPVTLIGFSLGAR VIYFCLQEMAQEK
10958	41326	A	11020	3	1693	CQRLPQQPLVAEPTAEGEPLP TGRELTEANRFAYAAALCGISLS QLFPEPEHR*VLLSCPLGTPVGL HSDAHYGGRLAVAVHVEGTLF FTSSTFAAASVFQKARPWQHPG EQMAFSGKPLVAAVTSAGGS GAPSVGCTELISTSVLGYHTAL EMAGLVQWLELSEAVLPTMTA FASGLGGEGADV FVQILLKDDP LKDDPTVITQVHPTPGVKDGKL IF*ARVLVCHMTSLQLQVPLEEL DVL EEMFLESLEKEIEESE*ES PATKTEGGGEDKDRKHPLMGD KMTESKTDLWIYEMGNAGVLL FRRYLWLQPKKKENRRKWK YLLIGLATVGGGTVIGESS*RCA PLVAAGAATIIGSAGAAALGSA AGIAIMTSLFGAAGAGLTGKVQ KE*VGAI EEF TFLPLTEGRQLHI TIAVTGWLASGKYREDQEDQA ALAHSREQYCLAWEAKYLMEL GNALETILSGLANMVAQEALK YTVLSGKCPHLPWPASLLSVAN VIDNPWGVCLHRS AEVGKHLA HILLSRQQVPGNGCVIGFSLGA RVYIFCLQEMAQEKGEHLL
10959	41327	A	11021	208	324	VSLLKAADNWL VNSYPFCNSV SSEFFFR*IRDFFLFWIH
10960	41328	A	11022	1265	1459	
10961	41329	C	11023	188	730	

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10962	41330	A	11024	64	228	QHLLRRWGRSGLLNDR*VSN EIKMEINKFIELNNNSDTYITL WDTANTVLKFM
10963	41331	A	11025	1	648	
10964	41332	A	11026	26	613	VGAGGRGWRFAAAVRRRAAGG GLRPGPAPGPRAGGGGPRGAH LALLRRAGALRAGKEYGKADA RWVYFDPTIVSVEILAVALDVS LALFLIYAIVKEKYYRHFLQITL CVCEL.YGCWMTFLPEWAHPEA PNLQQPATGWLYWLGFTLFFF* RCVGLIPRNWLLWAVHGPRTS RKWHQKGNQFQWKEVFSGT
10965	41333	A	11027	2	252	ARGRAGVAGGPR*AAELPGL RDPFPASRPLRRSDCLGLIRHK PPDPGAGARVEGEALPSWSPGG ALEEGVT*PGRGPPWE
10966	41334	A	11028	3	637	RQVRRGGQGGEPARIQCPRRL GEGPGAPNRLGPPARDPRCSPW PRADSPRPNRLSSPQLPRPAYL GPACFP*PSWGVSRSLPSLAPW RPHRLPDSQRFPPNGGSRSRATS GSWTWKSKECREWRPSGSRGT RGSSGSGAGSSGSSAGVGRRAG HGRWHLR*GPLFAAPASATCP LWHGWKGASLDLGLQPWATF YPRVTGARGGRTLGP
10967	41335	A	11029	158	462	
10968	41336	A	11030	339	866	QICHSPPGNKAHSHLLPYQTPV PSSQYPPSPSRTLQLPFPTWNP CQWPSRGSCGSPAVGTGPPFPT GIPSV*APSARG*HHSSACGCH PGCAGPQPARSPHGPAPASGCH TVSGCCCHALLQSCLAAGRPSA GTWPHPPGGLPSAPGTETPCTA FEGFQPPCWLSQLPLSPCL
10969	41337	A	11031	621	944	TPOGGTAPSGGRHPWASASPIR LPPL*CSARPGCH/SSRMSPGT RPSGPLQDCHPPRPQTPHAGS HHTSAPQAPAGTF**RQRVAPG SSCWHLPQSWSCSAWLGGC
10970	41338	A	11032	3	257	AGRASKGG*NPSKAVQGSVPG AEGSPPEGCGQGPAGLGLPGA RQDCSRA*QHPPGPGGQVEVY LDISLAPGSTGIQGLEAKHL
10971	41339	A	11033	94	227	SSYVFKSILAFGMTWMRLTII LSEVTQG*KTKHQMFSLICGS

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10972	41340	A	11034	404	894	FVYFFRGELCKISSTLGFKGTGQ GLQPSKVS**VPSRPAGNRP YPETSQPPGPSGG*HWLAGW Q*GGPEPGWTCIWP*GS*GTEIG SPSQGPPEPAGVPSRDAGSAA TGCHTGLAGVWPRLCHRRV TDGRKSMKRCLSRSYCTSSVRA SGGGAGRIT
10973	41341	A	11035	1	408	
10974	41342	A	11036	68	204	SFLWHPGLHFHTHH**NYKS SSK*MVRIRVTFSKFIFVRNNYC
10975	41343	A	11037	5	188	PQCRHLRLQGLALSPKLECSAI TAHCSLELPGSSNPPSASRF*GS RSVAQAGVQQCYHSSLQPTP GVKQSSSLFPFLRLQPKVSSATL PVRLQE
10976	41344	A	11038	1	263	
10977	41345	A	11039	2	283	
10978	41346	A	11040	1	1965	MAAENEASQESALGAYSPVDY MSITSFPRLEPEPAPAAPLRGR KDEDAFLGDPDTGEAR*PRPCP ALGSPRSSFFCVKHGSPLETR KDPFSAAAAECSRQDGLTVIV TACLTFATGVTVALVMQIYFG DPQVRGTNGEGEETGEWVG* CLRNCGKGSSVDAAVAAALCL GIVAPHSSGLGG*GAVEVGVPQ AYFLPPGL*ASCAARALREETL QRSWETKVGTLVRRESSGESLF IALLLTQALIC*VLAQDGFNVT HDLGQWGLGIWERHEVDGEG* NL*DLEPPPLPGSLLRPDLAEV LDVLGTSGPAAFYAGGNLTLE MVAEVSARVVRVGACPKVPIA GHPRPHFGVYRGDLSPGSQGP PSGEASQSMATSFWPNLTSLV SREQUALHWVAEVRRLRLFFPGF KDIRSGEIGYCHRADDMLRWV LGRTWGLQRQRVWVGKGQEK SSYELDGAPTAQVLIMGPDF IVAMVRYASSDSEPGTRDPLNQ EGVGAG*RFSPNRTANHSAPS LVGFASLLSWG*GL*VGGAM AWLPLCGTYLALGANGAARGL SGLTQVRFTPWLAFFSREPSG LDCRCLS*QSNLLQVDSECAE TSWGGHRDR*RKDSQGCPCWV HGSRRITNNFIIVKDRSPDAA

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10979	41347	A	11041	1	363	SSMTTVHATTATQKTVGETLA* LLQNIIPVSTSVAEAMGKVIPEP DKRLTGMAFCVPTHNMLVVVAL ICHLQKAAKYDGMRRFCNATT GITFNGHFVRLLSWDEFGSSNR VVDLMVHTASKE
10980	41348	A	11042	162	303	CLLLKSCSQEAAAALALPALGL VFDVFL*IVFVRTKYLRVGFNRN FF
10981	41349	C	11043	56	118	
10982	41350	C	11044	345	410	
10983	41351	C	11045	7	439	
10984	41352	A	11046	2	80	
10985	41353	B	11047	205	5326	
10986	41354	A	11048	1	813	
10987	41355	A	11049	1	1454	
10988	41356	A	11050	2	1624	
10989	41357	A	11051	1	1185	
10990	41358	A	11052	1	2149	MKEKMLRAAREKGRVTHKGK PIRLTADLSAETPQARREWGPIF NILKEKNFQPRISYPDKLSFISEG EIKYFTDKQMLRDFVTTTRPVLK ELLKEALNMERNWYQPLQKH AKNMPNSIILIPKGRDRTTKEN FRPISLMNIDAKILNKILANRIQ QHIKKLIHHDQVGFIPGMQGW NIHKSINVIQHINRTIDKNHMIIS IDA EKAADFQIQLFMLKTLNKL GIDGTYLKIRIKYLGJQLTREV DLFKENYKPLLNEIKEDTNKW KNIPSCWVGRINIMKMAILPKVI YRFNAISNKLPMFTFTELEKTT NFIWNQKRARIKSIKSNKA GGITLPDFKQYYKATVTKTAW YWYQNRDIDQWNRTEPSEITPH IYTYLIFDKPEKNKQWKGDSLF NKWCWENWLAVCRKLKLDPF LTPYTKINSRWIKDLNVRPKTIK TLEEILGITIQDTGMGKDFMSKT PKAMATKAKIDKWDQIKLSF CTAKETTIRVNRQPTKWEKIFA TYSSDKGLFRIYNELKQIYKKK TNNPIKKWAKDMNRPFSKEDIY AAKKYMKKCSPLAIREMQIKT TMRYLTPVRMAIKKSGNNR QTESQIMSELPITIASKRIKYLGI QLTKDVKDLFKENYKPLLNEIK EDTNKWKNIPCS WIGRINIVKIM AILPKPTNVHVTNLAAQDTTAL EAAQISLEGHPQEKEISVTAMPL
10991	41359	A	11053	1	2031	

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10992	41360	A	11054	1	1188	
10993	41361	C	11055	1	353	
10994	41362	B	11056	151	1608	
10995	41363	A	11057	1	373	
10996	41364	B	11058	1	488	
10997	41365	A	11059	1	1257	
10998	41366	A	11060	2	3527	
10999	41367	A	11061	1	2373	
11000	41368	A	11062	1	1755	
11001	41369	A	11063	1	1599	
11002	41370	B	11064	220	1286	
11003	41371	A	11065	1	1826	
11004	41372	A	11066	1	1645	MDFKFLDTYTLPRLNQEEVESLN RPITGAEIVAIINSLPTKKSPGPD GFTAIFYQLISNFSKVSQGYRIN VQESQAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGRINILKMAILPKNW KKTTLKFIWNHAKACIAKSILS QRNKAGGITLPDFELYKATVT KTAWYWYQNRDIDQWNRTEP SEITPHIYNHMFIDKPKDNKKW GNDSLFDKWCWENWLAICRKL KLPFLTPYTKINSRWIKDLNV RPKTIKTEESLGNITQDIGIK DFMSKTSKAMTTKAKIDKWDL IKLKSFCTAKETTIRVNRQPT WENIFAIYSSDKGLISRIYKELK QIYKKKTNNPIKKWAKDMNRH FSKEDIYAAKHKMKCSSLAI REMQUIKTMYHLTPVRMAIJK KSGNNRTRENYFKIHESKKSQ NSQGNRKEQSWRRHATRLQ TIVQGYTVAKTACYWYKNRPT DQSNRTENQEIRLHTYHNLI FKPDKNGETTPYSINGARITG
11005	41373	A	11067	1961	2588	KLAQDRDALSPPLLFNIVLEVL ARAIQKEIKIGLQKEEVKLS LFADDMIVYLENPVSAQNLLK LISNFSKVSQGYKINVQKSQAF LYTNRRQTESQTMSELPFTIASK RIKYLGIQLTRDVKDILFKENYK PLLNEIKEDTNKWKNIPCS WVGRINIVKMAILPKVNIYRFNAIP IKLPMTVFTELEKNYFKVHMGT KKEPASPSQS
11006	41374	A	11068	2	278	
11007	41375	A	11069	3	274	

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11008	41376	A	11070	261	1382	LELSFPAGQRGVLSGDPQNLCTCPSGSWHVPRCWAVEQRPNLPRTVTQLVAEDGSRVYVVGTAHFSDDSKRDVVKVSAATHIIPDTGWCKLLPGSRDGLVRFPTYRVSMCLKMDESTLLREAEQLSLEKLQQA VRQVRSRGQSGSGSGSKPPHITEQLGMAPGGEFREAFKEVGTG*GRGWPGCGSQAVTFKRAIAALSFQKVR LAWGLCFLSDPIR*GCPDRDPGRPAGWSVGMAEMIGEPDLHRTIVSERDVLTYMLRQAARLELPRASDGDGRPQAWDPL*G*GPRGHVPGIEKNWSTDLNIQEIMT*VPAPCKPHPTSPQVAFFGLLGYSLYWMGRRTASLVLSLPAAYCQCLQR
11009	41377	A	11071	3	506	KDCQF*VGPEQKKALYKVHAPIQAALQLGPYE*ADQKRTCVRFRGHTCETAFTFWKSLGLDKVTKPRSSSSQLLALAIRSSPGSTTDACLLDSFSGKSRISSWFGS
11010	41378	A	11072	2	374	IRRESTHLQALGTTTPQDR LTC TGHS AQPPACASPLPPGPP*SSAWPLPPSTRLARQKQAAATAQP*PLTTQTTLGPWSSASTWTSAHKQPGAAAQEWSTAGSRQLLAGASGSSPSSCSVWTN
11011	41379	A	11073	3	553	
11012	41380	A	11074	239	547	GHHFQMNNVCRCSVWMLSLEPHVPGQIHSC**ERAKLCGKEFRMHNLMMGHMLHSDSKPFKCLYCPSKFTLKGNLTRHMKVKHGVMERGLHSQVSRPSLEA
11013	41381	A	11075	1	267	MAISMVTTKSTTIRITTAAGCHYENDMAHNHSDRGGGLPKVVLVLTPTFLTPPGKGGGAAGALERRTEGDRDAGGAAQEGGLTPTSPVPSS*HTLWLR TVDPEASTSPSTRHPYPNRRGGGGRALPHPRR*V*AGCHYENDMAHNHSDRGGGLPKVVLVLTPTFLTPPGKGGGAAGALERRTEEGDRDAGGAAQEGGLTPTSPVPSS
11014	41382	A	11076	1	1707	
11015	41383	A	11077	1	1407	

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11016	41384	A	11078	1	1275	MVKGSIQQEELTLKIYAPNTG APRFIKQVLSDLQRDLDSHTIM TGDFTNPLSTSDRSTRQKVNKD IQELNSALHQADLIDYRTLHPK STEYTFFSAPHRTYSIIDLIGGSK ALLSKCKRIEITTNCLSDHSAIK LELRIKKLTQNRSTTWQLNNLL LNDYWVHNEMKAEIKMFFETN ENKDDTTYQNLWDTFKAVCRGK FIALNAHKRKQERSKIDTLTSQL KELEKQEQTSHKASRRQEITKIR AELKEIETQKTIQKISESRSWFF EKINKIDRLLARLIKKKREKNQI DAIKNDQGDITTLERVVLEEDP TLHLNNTYTPRKVLYRWNRQSS TSVIETNKTSVELSLPFDEYDIIIE IKPFSDGGDGSSEQIRIPKIS/NK KTK*PNPWRQK*G**LAVADA YARGSGASTSNACLTSAISTI
11017	41385	A	11079	1	426	MLHTKQHLSMGTEDMDDKLH FSDCSAASLVSLSTTTGGHVL NMSADIARYLPVLYRWNRQSS TSVIETNKTSVELSLPFDEYDIIIE IKPFSDGGDGSSEQIRIPKISNA *ARGSGASTPNACALSAISRIMI SLTARSSL
11018	41386	A	11080	3	620	DRTLAEAPHTAPARSGHRGWC PRPHRRRRNRGRQLLAPGRGA DPGAGEAATVQWRLLRGQPAA ALHVQQGAGDAANAGLQRGA HADSHDRAPAGHAPGPVAAA GRGHDGQVPAALG*AGGPVGL RRPEPPLQTRGKGR LAPATQQV GQARRLPTRGQQLLRPPQFAA HHGPRPRLGGRGRGGSHKSPPH GIWPRLAGWRATLE
11019	41387	A	11081	335	640	PLGVLWSLVKSLVHSDAGAGE L*EVITGSTWPNP**QCCLVPNV DDEEEGEEQDDDDDEEEGL*D IDEEGDEDEGEEEDDDVVEEG EEDEGEDDWKFAKE
11020	41388	A	11082	2	204	

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11021	41389	A	11083	3	1471	SKDTRKRDVDSKSPGMPLFEAE GVLSRTQIFPTTIKVIDPEFLEEP PALAFLYKDLYEAVGEKKKE EETASEGDSVNSEASFPSRNSDT DDGTGIYFEKYILKDDILHDTSL TQKDDQGGLEEKRVGKDDSYQ PIAAEGEIGWKGFTICREKSL PKGVYGEGRISRPCGDRW* AEESHHIRGRQSGYPENKLCGF LLKTPHHVLERADEAGSHGNE VGNASPEVNLNVPVQVSFPEEE FASGATHVQETSLEPKILVPPE PSEERLRNSPVQDEYEFTESLH NEVVPQDILSEELSSESTPEDVL SQGKSEFEHISENEFASAEQST PAEQKELGSEKKEEDQLSSEVV TEKAQKELKKSQIDTYCYTCKC PISATDKVFGTHKDHEVSTLDT AISAVKTVIRDSOKTKSGEGAY GREMKSPHKFPEGKIHNDKEH DRIVQEFLAETGPKVTRFNEQC RFRPRIVYYENNQTQIMVEEPP
11022	41390	B	11084	148	235	
11023	41391	A	11085	30	420	VSGTRGPSPCLGTSWASGAWR PPLGGLPPSAGANGPRVRSAA GCSLVAGCKVLGSWVSFGAGR SHVACAGSSGESVVRARCPGTA* AAGGPGPQAFQAA*YQGSRMH RAPPRPNRQVQTWWEAGAGTG
11024	41392	A	11086	2	73	ERLRMPGVAKGRPR*GNPRRG RG
11025	41393	B	11087	1	1412	
11026	41394	A	11088	39	427	PPYWGHHFSSAAASAALKGKD GGSSRSLVPPAQ*HSHSPSKTHC VHTPSRSCAQLTHTLTQSPPSL KIAQSPSFDARAHARLRWQIPS APRVPPLSALSPTRTAGSVRFE SQSTKTSRSHRFLPRT
11027	41395	B	11089	1	813	
11028	41396	A	11090	3	365	RTPSSKGCGRPPRGMGAQGS GCGRRRSPRRSQARRWSHPC* PPSPPPWPRPARSPPGCSHRAAL SSPSPSSFLARHSARPLALAL GPPPWCSGSCASSAPFDLQHPE QSQNQDARG
11029	41397	C	11091	295	412	
11030	41398	A	11092	21	164	GAVTENDFYDLVRTIGGDLVE KVDLIDKFVHPK*VKSFLILPLT SV

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11031	41399	A	11093	1	1373	GISTMVGSA LRGAHAYVYLV SKASHISRGHQHQA WGSRPAA ECATQAPG SVVELLGKSY PQD DHSNLRKVLTRVGRNLHNQQ HHPLWLIKERVKEHFYKQYVG RFGTPLFSVYDNLSPVTTWQN FDSLLIPADHPSRKKGDNYLYN RTHMLRAHTSAHQWDL LHAG LDAFLVVG DVYRRDQIDSQHY PIFHQLEA VRLFSKHELFAGIKD GESLQLFEQSSRSAHKQETHMT EAVKLVEFDLKQTLRLMAHL FGDELEIRWVDCYFPFTHPSFE MEINFHGE\WLEVLGC GVMEQ QLVNSAGAQDRIGWAFGLGLE RLAMILYDIPDIRLFWCED\ERF LKQFCVSNINQKV KFP LSKYP AVINDISFWLPSENYA E\NDF*Y LVRTIGSDLVERVDLIDKFVLPK THKTSHSYRIMYR\HMEPTLSQ\ REVRHI/HIQAQEEAAVQLLG V
11032	41400	A	11094	8	119	
11033	41401	A	11095	2	475	QAGPSGGIPEGIAITGDDSSMHA IAPEDLPVGGQDVEA EDSDTGDL DPVLT VFRRGVEREFFSNWYKT A WSFSKLAQKGLSS*PSSLSSS SSSSDKAVTAGTELFASSLSSSS DPRRSISSSSLLFVA PLPVVSSL AGPYLPTAFFTPGRLA FFS
11034	41402	B	11096	677	696	
11035	41403	A	11097	1	357	STMIEAHVDVRTTDGYFFLLFC VGFTKKHNNLIPKTSYA*HQYQ ICLPHQDDRVTHQNPSLPDGSIA RVL SIYYLISRRMNSIISQGL QKVHIHIVPGSLMNQELDDL I TVFFKA
11036	41404	B	11098	1	541	
11037	41405	A	11099	14	671	PAPWRLGKNKRLTKGGKKGA\ KKKG VNPFSKKEWY\DV KAPA MFNIRNIGKTLVTRTQGT KIAS DGLK/GVRVFEVSLADLQNDV AFRKVKLIT\EDVQGNCLTN\F HGMDLY/TRDKMCSMVKK\WQ TMIEAHVDVKTTDGYLLRFLC VGFTKKRNQIRKTSYA\QHQQ VVRQIREGRWMEIMDPRRWQD QMDLEE VGHELIAGSIWKHRH KGLPIYLSSP

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11038	41406	A	11100	1	217	RQGLTLSFRLECPGVISAHCSLN LPGSSKPPASAPQVAGTTGVYH HAS*FFIFFVEMGFHHVAQPL CNFVF
11039	41407	A	11101	2	442	LDVQIQEAQRTPGKFIKRYSP RHFVIRLSKLTKERILRAVRQ KHQVTVYKGPRLAADFSTETL QARRDRGPISLLKQNNYQPRI LYPEKLSIIYEGKIQSFSDKQML REFAIRKPPQLLELLKGSLNLETN PGNT*KQNFFKA
11040	41408	A	11102	2	545	EPRPGKTAHVYGPDCLCGSCV QLSFGSAFFSTRWVSYEQANCK GEQFVFEKGEYAHWDWWTSS QRT/DLSSLRPIKVDSEHKILY ENPNFTGKKMEIIDDVPSFHA HGVYQEKVSSVWLRSGTWVGY *YPGYRGLQYLLEKGDYKDSS DFGARHPQVQSVRCIHD MQGH QCGAFHPSK
11041	41409	A	11103	2	389	EIIIDDDVPSFHAHGYQEKVSSV WVRSGM*VHCQPWLTLPQELR LWGPRSGETLALTAPVSKTCD FGARHPQVQSVRCIHD MQGHQ CGAFHPLGTQEEEEAGQKEQM EQVPFWLARGDICELSGKKS
11042	41410	A	11104	1	446	MEEEELEFVEELEAVLQLTPEV QLAIEQVFPSPDPLDRADFNAY EYINTLFPTEQLPMPSAHGGVSS CGNAGGPVSFATRENARCGIW GSGGVCDGVFGA/GAAGWGGV *GGGALGWMLSGRRIVLRS AIF TSPVSRAGSPERGWS CDC
11043	41411	A	11105	1	210	SSDGRHLAFDQGS PG*VLGHVG KQRAVDVQPSVAVRVRQPLLL LSTIMSGLLGWEQGIDILNSIEI CSI
11044	41412	A	11106	2	287	AAESPGRSTRTDGAGLTRSLPR GSR CAGAWVAAGGLSWARGG GRQEAGWRNDG*GGTGARGG AGSRAAAHARGAAGHRASVSK PGPSRSSRFQCC
11045	41413	A	11107	150	389	GEEIAWLGAA RPKPTPSRIPL* PSLFPWRPHKFPERSVFAQSOP ASQSPPLRP PPSHPEGSCLSGR LPPPGYLLPLR
11046	41414	C	11108	43	213	
11047	41415	A	11109	3	246	SSFPAPAREGALAPCRCLAGISV TLQGNP*GRCHHHHHHHHHHH HRCYDSQESGKLPRPGPKAELE GPPAWLLVGP GAHP

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11048	41416	A	11113	1	726	
11049	41417	A	11114	2	251	LSCGRSLHQGSVTSCKTINALT LTVDITWRGCAW*GCACTFHCR SATNMIRAYVVFSTISVLSLQEI RLSLRAILADLRSLICF
11050	41418	A	11115	1	1041	
11051	41419	A	11116	1	398	MGPNSTLENLLKGATSVFYNR DQEEAQKKERKLGRGTKALAA ALQ/SWQSPGAPRCIH*LLSVW QARVF*RGMPRQQDEATSLSI QWQKPVETELSPDMEVTGFRA SLTDERVHLEPVLPEQYTEQRR QGHL
11052	41420	A	11117	5	137	
11053	41421	A	11118	5	272	
11054	41422	A	11119	2	211	WNQPRCPSTVNWIMKIWIYIT MEHYAAIKRNMIMSFATWME LEAIFLSKMPQ*QKNKYCVFLH ACLES
11055	41423	B	11120	1	1560	
11056	41424	A	11121	1	588	
11057	41425	A	11122	80	574	EPAAQGNVLVDLLC*MKNRNR WLPNELSQLVHTQSQFSKTG MSAKHTAFAMRMSPAQMIDIV VGLSTGQSPFMVLMQGGHSA MQETRIASLPVTAIPAGMKIPCV TAGSACMVGPSVRVNEWFSAY GMAGMAYSRVSTFVRGLSPRY LTTREAPGCGSSAGH
11058	41426	A	11123	48	131	
11059	41427	A	11124	1	1195	
11060	41428	A	11125	2	1028	
11061	41429	A	11126	1	1008	NMMEQVLDIPSL*VISKDNANV TIDAVCFIQVIDAPRAAYEVSNL ELAIINLTMTNIRTVLGSMELDE MLSQRDSINSRLRIVDEATNPL ALKIAARMIEDGELDKRIAQRY SGWNSLGGQILKGQMSLADL AKYAQEHHLSPVHHQVAEWM RARNGQLFRLRSNHLTLLEQN NFIYARGAKIYPDIHIDRSLLKCP SDLFAANARCGICQSDERCLR YQPRRERGLYRIDITYPGKSYTT TALPSRFVWFVTGKAQSTQAS ALSYSIDLLYHHLDLVYQRLGH LDDGTDSDWNHVPTLNGQCTLV LIHEYVDTRGPEIKTILVISWWN ILVFH

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11062	41430	A	11127	3	333	DIQIGEEENRKRWLRTGKCSFLP KEREWMDRLMSWGLVDVTRFH ANPQTADRFSWFDYRSKGFDD NRGLRIDLLASQPLAECCV*T GIDYEIRSMKPSDHAPVWATF RR
11063	41431	A	11128	2	136	YCKLACLQVDSRGSQVVALDV AARHR*QFAMPESDAVAMKLH LS
11064	41432	A	11129	3	431	GVFGRVSEKQRPAAAPAGERPL PRPRPLPCGAAARTGPFAAQAA *RAAAAAPRSERRHHGAEEGH QRCIYRHAADRALGEAARRTG YALRPAGEPELAAAARRR*RAP DPGPRVPRHLGLLATRACPPGG AHCSPERGAISW
11065	41433	A	11130	64	2436	RRQGLEGWWAIGLEGLTGKAL AWLFTVPGVRGLQWSPRFFLTR LRTLCKVLGVLFVAGGKKG PTCILQILKGQRREQA*CISGWA ERVWASGQA*WEVWLHWAKS RNWLFWKQHVHALRVRLDTT LFSLEEGSSFWNQLTWKVVVR RTFSFSINHTPRITLGVPSVHSF QLPGLLNFGFEKVCVLSPRIFN LTHENFLSSEGPEIGLLGATFN CLNKRKLAKYMRNRNVHPKPLV RYLHSLRPPEAAAP*AWCGPR HLSCROMSSSSQIGNDSFQLQV TPVHLLPLSHITRKNPEMYDLP LLFFNPQESAILQLFHQDGECLH CSPVIGDWCHLGHSQACPSFSV PSGLFVPSLLCGAAFGRLVANV LKRYSVCVRVCAHVHVCAVRV VYACVWVRMTISLTVLIESTN EITYGLPIMVTLMVSTLPPGPCQ AQGHVVRPTGPIFRSLEWETE EMDK*GHDFAHVLVSECISSEA *GMLFCGPGDRSLFSTFRAVW SLSRLLDSVIAAGKQ*A*RT*SV GYSLLCPDLKGDPSAVSILRTT VHHAFFPVVTENRGNEKEFMKG NQLISNNIKFKVKTA*EERQV RDKRSRLTRL SALELRNMCD E HIASEEPAEKEDLLQOMLERR* EPGGAPTARRATQRWGEPLAQ MFPLTFHGLILRSQVLTVLLVRG VCYSESQSLSSEAEISQARPDE
11066	41434	A	11133	3	80	

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11067	41435	A	11134	2	958	LKCELSVDQGLAPAIQTVRLTHE SLTALEIPNALLQTIQDLILDLR VRCVMATLQHTAEIEIKRLAEK EDWIVDNEGLTSLPCQFEQIV CSLQSLKGVLECKPGEASVFQQ PKTQEEVCQLSINITQVFIYCLE QLSTKPDADIDITTHLSGDVSSP DLFGSIHEDFSLTSEQRLILVLS NCCYLERHTFLNIAEHFEKHNF QGIE*ITQVSMASLKELDQRLFE NYIELKADPIVGSLEP*YAGYF DCKDCLPPTGVRYNLYKEALVNI IAVHAEVFTISKELVPRVLSKGI EAVSERAQSTDAVCFILOQKWS
11068	41436	A	11135	52	1053	MDEEERVYRACYLICISLLSSPG NPGHSPMLDLNDNTRPSVLG HLSLFLIQKYNHSLFFSPLAWR YKTPHRVAFVEKLTCLVLSQLP YF*IIISNMFFVFLIFKTAESNP INHI*TRLCLFLVF*KMIQEVMMH SLVKLTRGALLPLSIRDGEAKQ YGGWEVALRSHSAHFCLDVFFV RRLTHESLTALEIPNDLLQTIQD LIFRPGSQL*PVSRIFFSAGTFRF KNHLHDFTGFHTCLTGAPRGPV GGCASDDGQAAADTSQWLS*I VLYL*LFLASMFSLSDVDVFL AP*R*FSKHLFCF*EQRLILVLSN CCYLERHTFLNISHGSP
11069	41437	A	11136	50	426	
11070	41438	A	11137	2	949	QQVWKQNCFKHYSNETDNSTT QLVGVTQLQVVVPSLICEHCM NFSSPHVWCCMVQAVPGGQGO TIMQVPVSGTQGLQQVSN*KY *AVYQRRGFKE*ITTGQTQIII QQPQTAVTAGQTQVIPLASHR SKTDLEESDN*VRYQPVNADGT ILQQGKCTHKLP*DGLGQLFCPL DN*HTTSSGGQGTVTVTLVAGN VVNSGGMVMVRKCFQLCL*N FLEHAT*CLLKEPLYVNAKQY HRILKRRQARAKLEAEGKIPKE RRVCITLGR*ERRIAGFYF*NY LFSPKEKDSPHMQVGRHIFILL FITLY
11071	41439	B	11138	26	80	

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11072	41440	A	11139	203	797	HRHARHLFRTTPT*LSWQGS *TPRWKGVRAVVTQPRKERRA ESEQFQATKPRSQL*LQPPTPSL VSSCQLKTTAASRPLT*PSKSVY PSAPFHPWLPC/SKPERSVSPES NDSISEELNHFKP/IVCSPCTPPK RLPDGRVLSPLIJKSTP/QPKQK PAEADFL*GQSTDPQKVGTDLS GAADQKDPFKSHSYLSGS
11073	41441	A	11140	33	379	EATSNFKQPPSLPFWCLKSRSTL KPRQSKVCSSFPVI*GKTGNEL ALQIP*FKSSCGPRFPD***PAGR /SAPSLGPPSPQSCAHQ*EHWWQ VCIKHGITNAEPPAEHLKVLVR E
11074	41442	A	11141	248	622	SESSGRFWLCGLGPGTSPILLSL KFPHELLPASGRSPSPRPVR GKATQVVWAWGYRCVDEDP RCLGTPGRTD/PHCGQGLLCPL GKSCSTSQPLSQDGRGTSWDR SHACSPGGHPHRCIGCM
11075	41443	C	11142	1	1311	
11076	41444	A	11143	452	1286	
11077	41445	A	11144	2	299	GLPLAHGLGRFGMDRIYEGQ VEMTGD*CDVESIDGQPGAFTC YLDVGLARTITGNKVFGALKG AVDKGCSVPHSTR*FPACDSAE FALGIPYFVQPN1
11078	41446	B	11145	49	832	
11079	41447	A	11146	1	1074	
11080	41448	A	11147	1	360	
11081	41449	A	11148	1	1155	
11082	41450	A	11149	75	266	
11083	41451	A	11150	2	222	
11084	41452	A	11151	1	549	
11085	41453	C	11152	453	665	
11086	41454	A	11153	1	1962	
11087	41455	A	11154	1	295	ASTAGVSYYYAAGLKLGLS LSKCRDPRCEPPCE*MSLYKV MAMARKAMSL/YIYFFLDEFM YFAGTWKLETIILSKLSQGQK TKHRMFSLVGGN
11088	41456	A	11155	1	363	
11089	41457	B	11156	1	375	
11090	41458	A	11157	1	197	
11091	41459	C	11158	1	270	
11092	41460	C	11159	1	146	
11093	41461	C	11160	1	268	
11094	41462	C	11161	1	301	
11095	41463	A	11162	1	289	
11096	41464	B	11163	19	240	

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11097	41465	A	11164	2	253	
11098	41466	B	11165	1	978	
11099	41467	B	11166	1	316	
11100	41468	A	11167	191	319	
11101	41469	A	11168	608	763	
11102	41470	A	11169	274	437	
11103	41471	A	11170	1	417	
11104	41472	C	11171	1	792	
11105	41473	A	11172	3	449	IYLTKEIKDLYKEKCKTLLKEIT DDTNKWKHIPSSWMGRINIVK MTTLPKAIYKFNAIPFIPPSFFT ALEDTILKFIWNQKR/CPHSQCK IKQKEQIWRHHTT*FQAIL*GHS HQNS/IGTWMKLENIILSKLLQG QKTKHCFSLIGGN
11106	41474	A	11173	1	441	
11107	41475	B	11174	1	597	
11108	41476	A	11175	5	265	
11109	41477	A	11176	3	280	SIYPNTCTRMFIVALLTIAKTWN QAICPTMIDWIKKMWHIYSME YYAAIKNDEFMSFVGWTWMKLE TIIFSKLSQGQK\TKHRMFSLIGG ELEQ
11110	41478	A	11177	590	747	KAYQPEKAQDQVDSQPNSRTRG TWMKLETHLSKLTQEQTCKHC IFSLISGS
11111	41479	A	11178	3	274	FYYKDTCTHMFIVALTIAKTW NQPKCPSVIDW/IMKNMWHIYT MEYYAAIKNDEFMSFSGTWMK LETHLSKLTQEQTCKHCFSLI SGS
11112	41480	A	11179	1940	2061	
11113	41481	A	11180	493	743	KATRSVNC/WWDHL*RPFWGS PH
11114	41482	B	11181	1	1248	
11115	41483	B	11182	50	8445	
11116	41484	A	11183	40	125	
11117	41485	B	11184	1	1896	
11118	41486	A	11185	1	624	
11119	41487	A	11186	1	357	
11120	41488	A	11187	1	304	
11121	41489	A	11188	681	834	
11122	41490	A	11189	3	2128	
11123	41491	A	11190	175	402	

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11124	41492	A	11191	46	790	NPGAVKMPAYHSSIMDPDTKLI GNM/AHLLPIRSQFKGPAPRET KDTLDIVDEAIFLPSGPNVFFKN YEIKNEADRTLIVITLYISECLK KLQK/CQFPKAQGGGKEMFYA GESTNFSHFLGEPGFPTLTAILC PNPANK/QEDEVMRALFTNQ KGRRLGLRLCEKSFSDP/QNG* T PAKWVWDLAFVKRQFMNKSLS GPWTVESGPGQPTVSRGPGAAF FQQDVTQSFLYLKFKYRDERR ACLYLKNS
11125	41493	A	11192	1	828	
11126	41494	A	11193	1	525	
11127	41495	A	11194	43	1826	THVRLAGARASPRAPRLRPRKP RPQGLPCLPGLRRARLEGGARG RADEMFLPLPAAGRVVVRRL AVVRSGRSLSLTADMTKGLVL GIYSKEKEDDVP/QFTSAGENFD KSLAGKLRITLNISSGPPKAGK TRTFYGLHQDFPSVVLVGLGK KAAGIDEQENWHEGKENIRAA VAAGCRQIQDLELSSVEVDP CG DAQAAAEAGVGLGYEYDDLK QKKKMAVSAKLYGSGDQEA W QKGVLFASGQNLARQLMETPA NEMTPTRFAEIIIEKNLKSASSKT EVHIRPKSWIEEQAMGSFLSVA KGSDEPPVFLEIHYKGSNPANE PPLVFVGKGITFDSGGISIKASA NMDLMRADMGGAATICSATVS AAKLNLPIIIIGLAPLCENMP SG KANKPGDVRVAKNGKTIQVDN TDAIEGRLLADALCYAHTFNP KVILNAAITLTGAMDVALGSGA TGVTFTNSSWLWNKLFASIE TG DRVWRMPLFEHYTRQVVD CQL ADIVNIGKYRSAGACTAAAF L KEFVTHPKWAHLDIAGVMTNK DEV PQSTGKA*LGRPTRTLNEF L LIRFSQDNCLVQILKNVHFSVL NWTVELKKVFE
11128	41496	A	11195	1	273	

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11129	41497	A	11196	2996	8256	LPTRRSWAVFFKGGESGAHTLR RKARKKKKKQVKGGSPKKGEE AKKVEAPRLPKLAAPGGGAGA KGGAGGTSMDRLWSWVLHLG LLSALGCGLAERPRRARRDP AGRPPPAAGPATCATRGPRPP RLAAAAAAGRAWEAVRVP RRQQREARGATEEPSPPSRALY FSGRGQLRVLRADLELPRDAF TLQVWLRAGGQQRSPAVITGL YDKCSYISDRGWVVGIIITSD QDNKDPRIYFFSLKTDARQV
11130	41498	A	11197	75	266	
11131	41499	B	11198	1	363	
11132	41500	A	11199	1	649	PRIRHEVIEEVRIMMLEIINSLT NSLHHNPVLVYALLYKRDLE QFRTHPSQDIMQNDLVISFSS SRLLQAGAEISVERVLEISQGV ALRCPKDRLKEISQKLKFKYVE EEQPRGVF*SPYVWSLVQLQ SALYWEFHRTQLFHPWDSRLR GRDASSPGTPSSQGRPFQSSFIS GVTEVGGTGYLVYLLKEDCT SVFSSHTLIWRIGC
11133	41501	A	11200	108	210	
11134	41502	A	11201	53	259	
11135	41503	A	11202	1	2679	
11136	41504	A	11203	1	675	
11137	41505	A	11204	834	1077	KGLWTVPPSFGDTVSGPPVPTG GSAGHTVPPPPR*CRQPPPSPP WRLFLPQLRSRSSQPPAGPAR HLPPPAARPECFCA
11138	41506	A	11205	1	681	
11139	41507	A	11206	1777	1940	VPILPQPLLLHPHLLS*VPILPQP/ PAPPYPNPFITSPPHTWGLQFH SVTSPPPAQOFTLKRVAEAKGI VK
11140	41508	A	11207	3	547	
11141	41509	A	11208	1	578	
11142	41510	A	11209	194	379	
11143	41511	A	11210	1	927	
11144	41512	B	11211	1	916	
11145	41513	A	11212	1	441	RRKLQKQALGPEQNLETLNL ATSVFYNRDQEEQVQKEKRDQ RKAALVMAIRQTNLGGSERT EHEAGQSPGKACYQCGLLGHF KKDCPMRNKLPPR/RVSTMLRQ SLEGALPQRMKVPWVRSPOPD DPTTLGRVPGASASSCHHPH
11146	41514	A	11213	164	359	
11147	41515	C	11214	157	189	

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11148	41516	A	11215	13	399	VEAFPTGSEKATAVISSLLSDIIP QSRLEPTISIPSDNRRAFISQISQAV FQALSIIP*NLIPYIPGPSSRKH/T LTKLSHLKDDWTILLPLSLRLI QACPRNATGYSFVKVLYRHSFL LRPSLIPDTRPT
11149	41517	A	11216	2	152	WYGEIMGDVQSQCIFER*WAMF LRAASSGIRGGVGT*SGRH*AE GRFYGDFRGNRAASVFSR
11150	41518	A	11217	1	1143	
11151	41519	A	11218	28	453	
11152	41520	A	11219	275	1128	DISTPSLATDHMPITIPNLIT/TY PTQRQYPIPPHALKGLKPVTDDL LQHRLLKPINSPYNSPILPVQKP DKSYRLVQDLRLTNQIVLPIHP VVPNLYTLLSSIPSTTHYSVLH LKDAFFITPLHPSSQPLFAVTWT DPDTQQSQQLTWAVLPQGFRD SPHYFSQALSHDLSFHPASHL IQYIDDLCSFESSQDDTL LLQHLFSKGYSQDDRPFTSQI TQAVSQALGIQWNLHIPHPQS SGKVEWTNGLKLLLLLLTANI DDTSYLQIPHKGLO
11153	41521	A	11220	1	606	
11154	41522	A	11221	713	835	LSQWRSDNGPAFISQITQAVSQ APGIQ*NLIPYIPHPQSSGK
11155	41523	A	11222	1	1133	AEALPQFYFHLSDIRGMLLHE PDLQKGKAVSQEDPQWSYQA DSPGIARRDYMVSRLVEGLKK AAYKAVNYDKLKKTTQVTIVP GPDFNLASHIIPDTPDPHDCYL SDTPGIHSISHISFAIPHPDHTW FIDGSSTTPNRHTPAKAGYAIVP STSIIEAALPPSATSRQAKLIAL TRTLTLAKELCVNIYDSKYAF HILHHHAVIWAERGFLTKQGW SNINASLIKTLKATLLPKEAGV IHCKGKHQKASDPIAQGNTYAD KIAKEAASGPTSVPHGQFFSFL VTPTYSPTKTSTYPSLLTQGKW FLDQGGYLLPASKAHSILPSFH NLFHVGKPLAHLLEYLSFLS WKSILKEITSQ*SICYSTTPQG
11156	41524	B	11223	1	1156	
11157	41525	A	11224	1	4991	
11158	41526	A	11225	3	590	
11159	41527	A	11226	203	1772	
11160	41528	A	11227	1	1669	
11161	41529	A	11228	1473	1604	
11162	41530	A	11229	82	159	

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11163	41531	A	11230	1	1323	
11164	41532	A	11231	377	631	LLKGKLTNRKDIHTKTPSVRRHH HRRPKPGRDITTKIILNQYPW* TSMQKSSIKY WQTESSTSKLS TMIKLASSLGCKNWKKL
11165	41533	C	11232	1	1677	
11166	41534	A	11233	753	966	FVFLWSLMMVTYRWGFGVDV LSVC*FSFQSQSEPQLQVCWSLL EVHS*PCLPGYQQRNCSWPRG SCDVTIT
11167	41535	A	11234	1253	1459	LSDSPKLK*KKKC*GQPERKVG LPTKGSPSD*QQISWQKLCCKPE ESGGQYSTFLKKRIENPEFHIQ
11168	41536	B	11235	1	924	
11169	41537	A	11236	299	436	
11170	41538	A	11237	259	536	FQKEWYQLLVPLV/EIWL*IH VLDF*LVNY*LLPQFQSMMLV SSEIQLLPGLVLGECMCQGIYPF LLDFLWSLMMVTYRWGFGVD VLCVC
11171	41539	B	11238	79	1587	
11172	41540	A	11239	1608	1763	
11173	41541	A	11240	1	2001	
11174	41542	B	11241	1	741	
11175	41543	B	11242	1	1368	
11176	41544	C	11243	1	3924	
11177	41545	A	11244	470	619	KVTRGWGSPHQDAG*SPCQSH QDQTP*GILKEHQEKARRK*RQ LCVLQL
11178	41546	B	11245	1	3546	
11179	41547	A	11246	363	476	
11180	41548	A	11247	1	759	
11181	41549	C	11248	376	986	
11182	41550	A	11249	556	821	MSIRSTWRRAEFNSWVSFLTR LVDLSLVFDDGDVQVGFWCGC PSCLLVFL/ISQDPQLQVCWSL QEVHSRPCSPGYQQRLQYSEY
11183	41551	A	11250	119	340	
11184	41552	B	11251	1	942	
11185	41553	A	11252	436	732	LHIWPFLLPCKAQNVHCSKFC PLGRFPFMAVLQGCPRKGL*CC SCPLGGIWIISCRICAFRTYLRP IMYIPLPFADGMLLCTAHSMAR CFGYCSLVV
11186	41554	C	11253	1	1878	
11187	41555	A	11254	720	1535	ILPEVQGGAGTI*LSLFLIE*PLF LSPA*LPWPELPTLC*IGVVRDG TPVLQCFSGKMLPVFAHSV

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11188	41556	A	11255	2	1059	WLLAASPLWLCRIRP/LILAAFM GWQSRSA LGTQSESGKGS PD QVLVPQDCGPWLGSVELVSP GSQAGEEPILSENKGRVTQMKI PEERSGSNICCSAIFAVLQPPLLI PRQTRSGVDLQQNPDTLQRLVL TVRRKTNKEKGHPHQNPCTCTSP ASKTKGALRFIKQVLRDLERLAL DSHTIMGDFNTPLSTLDRSTRQ KVNKDIQELNSALHQVDLIDY RTLHPKSTEYTVFSAPHHTYSKI DHTVSGKALLSKCKRIEILTNC SDHSAIKLELRICKLTQNHSTTL KLNLLNDYVWHKETKAEIK MVFEIDENKDTIYQNLWDTFK AVCRGKFIALKAHKRKKQERV
11189	41557	A	11256	82	159	
11190	41558	A	11257	820	1358	HTDGLVWMPFLFVSFSPNSQD RQLQVCWRLLLEVHSRCPFGY QQRWLQNNRY/SVNRKCCCLIV PLEVLSQRSTHQHVGEWLCLL GRKFPA GMEACTAMLCSSSVL EAATLSFSVQHRCTGGS*KPQ QGRVYPSEGREHNGAAAFGPF CSSECPASCPDPGTQPCAPGTYI PFFSCQT
11191	41559	A	11258	2435	3261	QVRGYRCRFVTWVNCMSLRFG VQRIPSPSLTGTQPPVGD*HLT RPGTPLR*NFORNDQAVTFVH VHIFVQPLLLIPMQTSGGVDLR QTPTDLQLRVLTVRRKTNKQK GHPHRNPICMSPSSKTKARQAN IQJQEIQRTPQRYSSRA TPRHII VRFTKVEMKEKKLRAAREKGR VTHKGKPIRLTVDLAETLQAR REWGPFI N LKEKNFQPRISYPA KLNFISEEEIKSFTDKQMLRDFV TTRPALQELLKEALNMERNNQ YQPLQNHAKL

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11192	41560	A	11260	1439	2544	VSSTTKEKALSVPPRWICILQKK NPPNHQPVSLPEVFLPQILKFSG PPHWRRIEYKVMRLNIGDM KTKKKMLEKYEQLEIRHQQKS RT*KAVCCIT*LSRHILLGQAPL VQQSM*QPESHQVNPPTS YGIHQTPKLS*IGIK*RPWIM/MSEV KGYKVGNNFFAKAPNRAPPLL KPRQTGSGVDLQQTAPDLQLR VLTVRRNTNKQKGHPHNPICIT SPSSKTKEVENLEKRLDKWLTR LTNVEKSLNDLMELKTMAREL HDEGTSFSSQFDQLEERVPMME DQMNEMKQEEKFREKRMKRN EQSLQEIRDYVKRPNRLIGVPE SDGENGTKELENTLQDIHQENPPS LARQANIQIEIQRMFPQR
11193	41561	A	11261	2772	3111	QSGPSAAGLLEFAGGFLQTLFA WVSAAEVGGCKGSGSSLS*PK KGVMDGTWIKGSLPPEYCAFPPT G*KNGAP/LRLYPTPGSEGPPTT ESP*/FASTAVGDQATARQQRGW GRGARH
11194	41562	A	11262	248	597	DRCPAAWDRHPAGIQSSRREPS KATWTLRSKLSVQDGRDSSL RLNCKVAARLGAGHPMLRLG LRC*YPGKQGLEWTSKLLQQTIC H*GS*LLKGKLTNRKDIHSKTPS VRHYHQR
11195	41563	B	11263	1	2250	
11196	41564	A	11264	1298	1681	GVSVPLLWGASQLGYLGVMDDP LAEAVCPFSDQLHSGRTSTVF KAALGQSGAHCPERCVAQS* AD*RALREHKQ*FGSTLCGPVM VVAMELGSSTMVELVSSPANS VKVFLFLHIFSTCCFLTFS
11197	41565	A	11265	1272	1497	SGLLPIKVAFTKQFLFILLRIWL *RGYVFCWSKVVTTPREQPQCIT DGYQIFIMQKTLSCLSILGKRT MSLMQ
11198	41566	A	11266	1	1071	
11199	41567	A	11267	788	1286	
11200	41568	A	11268	3	455	
11201	41569	A	11269	1	711	
11202	41570	A	11270	225	525	GGGENFSYPWYLLVGCGWFSS SPIVPDVPFSLLLPAQKKKPAP PKVPEPKPKAPAKKGEKVPKG KKGKADAGKEGNNPAENGDA KTAQAQKAEGAGDAK

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11203	41571	A	11271	914	1261	TAKPKTNWCCRAPTSLASTFA TMPFKKAECVGDAPATVKDE PQRISARLSAKPAPPKPEPKPK KAPAKKGEKVPKGGKKADVA GKEG\NNPAEN\GDAKTDQAQK A\EGA\GDAK
11204	41572	A	11272	3	359	
11205	41573	A	11273	440	642	WKAEREIEIPR/PKKAPAKKGE KVPKGGKKGAEGQDGDNPTE NGDAKTDQGGKAEGAGDAKR TVSHQN
11206	41574	A	11274	499	723	
11207	41575	A	11275	147	459	STYVPLSPSPSPMPKRKAEGHA MGDKAKVKDEPQRRFARLSA KPAPPKPEPKPKAPAKKGEKV PKGGKKGAD\AGKEGE*PLQKN GDAKTDQAQKA\EGA\GDAK
11208	41576	B	11276	179	400	
11209	41577	A	11277	24	601	
11210	41578	A	11278	266	441	
11211	41579	A	11279	17	570	HQPKKDLTGFVKWPYIRLQR QRAILYKRLKVHLAINQFTQAL ARQATATQLLKLHAKYRPETKQ EKKQRLARAEEKKAAGKGDVP TKRPPVLRAGVNTVTTLVENK KAQLVVIADVGPIELVVFLLPA LCRKMGVVPYCIKKGARLGR LVHRKTCTTCRFTQ\VNS\EDK GALAK\LV\AIRTNYNDRYDEI R\RHWWG\NVLPKPSVARJAKL\ EKAKAKELAH*TTGGSYQDQLQ
11212	41580	A	11280	175	289	RPCVKESGKPHLKSSTMWTTL KLLRI*PRRTTCSPLS
11213	41581	A	11281	205	361	
11214	41582	A	11282	144	396	CLEVLHKILFFEMESHVSVTQAG VQWRDLGSLQPLPPG\SSNSPTS ASQVAGIRSMRQKGRANFFVFL VEMGFHHVGGADLELL.TL
11215	41583	A	11283	241	550	
11216	41584	A	11284	2	106	
11217	41585	A	11285	2	447	PPLSRLLCPRHPHSGWPEGYSPE HLRCGLRSGTLRSRQALHCQVS SNP*PPSLWF*GCGNVL*ELCLF VLVPSVNLVQVLLSEIWEFHRT

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11218	41586	A	11286	1	2172	PAGRCRTAWAVAAQQLMLSA ALRTLKHVLYYSRQCLMVSRN LGSVGYDPNEKTFDKILVANRG EIAACRVIRTCKMGIKTVAIHSD VDASSVHVKMADEAVCVGPAP TSKSYLNMDAIMEAIKKTRAQ AVHPGYGFLSENKEFARCLAAE DVVFIGPDTHAIQAMGDKIESK LLAKKAEVNTIPGFDGVVKDA EEAVRIAREIGYPMIKASAGG GGKGMRIAWDEETRDGFRLS SQEAASSFGDRLLIEKFIDNPR HIEIQVLGDKKHGALWLNRECE SIQRRNQKVVEEAPSIFLDAETR RAMGEQAVALARAVKYSSAGT VEFLVDSKKNFYFLEMNTRLQ VEHPVTECITGLDLVQEMIRVA KGYPLRHKQADIRINGWAVEC RVYAEDPYKSFGLPISIGRLSQY QEPLHLPGVVRVDSGIQPGSDISI YYDPMISKLITYGSDRTEALKR MADALDNYVIRGVTHNIALLR EVIINSRFGKRNLT*FLUSKGF PEAFKGHILTKSEKTFQLAIA SLFVAFQLRAQHFGQNSRMPVI KPDIANWELSVKLDHKVHTVV ASNNGSVFSVEVDGSKLNVST WNLVASPLLSVSVDEHSEGLFQ CLSREAGGNMSIQFLGTVYKV NILTRLAELNKFMLEKVTEDT SSVLRSPMPGVVVAVSVKPGD AVAEGQEICVIEAMKMQNSMT
11219	41587	A	11287	62	2600	
11220	41588	C	11288	277	508	
11221	41589	B	11289	94	1440	
11222	41590	A	11290	57	237	FLHAENKAHRPGISLCGLRAQP RQPASRHAW*SMRSEQRPLWT ASGRSSGQTRSSRLG

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11223	41591	A	11291	3	1968	EFDYSEDKSSWDNQENPPPTK KIGKKPVAKMPLRRPKMKKTP EKLNDTPASPPRSPAEPNDIPIA KGTYTFDIDKWDDPNFNPFSST SKMQESPPLPQQSYNFDPDTCDD ESVDPFKTSSKTPSSPSKSPASFE IPASAMEANGVDGGLNKPAPK KKKTPLKTDTRVKKSPKRSPL SDPPSQDPTPAATPETPPVISA VHATDEEKLAVTNQKWTCTMT VDLEADKQDYPPQSDLTSTFVNE TKFSSPTEELDYRNSYEIEYME KIGSSLPQDDAPKKQALYLMF DTSQESPVKSSPVRMSPTPCS GSIFFETEALVNTAAKNQHPV PRGLAPNQESHQVPEKSSQKE LEAMGLGTPSEAIETAPEGSFA SADALLSRLAHPVSLCGALDY LEPDLAEKNPPLFAQKLQREAI VHPTDVSTSKTALYSRITTEVE KPAGLLFQQPDLDSALQIARAE IITKEREVSEWKDYEEESIRE VMEMRKIVAEYEKTIAQMIEDE QREKSVSHQTVQQLVLEKEQA LADLNSVEKSLADLFRRYEKM KEVLEGFRKNEEVLKRCQAEY LSRVKKKEEQRYQALKVHAEK LDRANAIEIAQVRGKAQQEQAA HQASLRKEQLRVDALERTLEQ KNKEIEELTKICDELIAKMGKS
11224	41592	A	11292	63	2203	
11225	41593	A	11293	27	586	
11226	41594	A	11294	89	288	
11227	41595	A	11295	1	522	HERFETTYFKKFP*GYVYTGDD CQRDQDGYWITGRIDDMNLN SGHLLSTAEEVSALVEH*RLQ EAAVVGHPHPCEGVNASYCFV TLCDGHTFSPKLTEELKKAIVM RKRLAPFATPDYIQNAPGLPKT RSGKIMRRVLRKIAQNDDHDLG DMSTVADPSVISHLFSHRCLTI
11228	41596	A	11296	2	569	
11229	41597	B	11297	1	990	
11230	41598	A	11298	1	252	
11231	41599	A	11299	39	174	RHIISSNEVH*KEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEE EEEEEIPLSSL

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11232	41600	A	11300	16	379	ILDTSMPMRWTQKNFSMILAQPE QQCKTLSQNKNDRIKKKEE KKKKKKKKKKKKKKKKKKKK KKKKK*EKEKEKEKKKEKE EEKKK/QEEEEEEEEEEEEEE EEEEEEEEEEERRR
11233	41601	A	11301	1	249	
11234	41602	A	11302	1	353	
11235	41603	A	11303	1	847	
11236	41604	A	11304	3	224	QEKRRRKEKKKVKEEEEEEE EEEEEEEEEEKKKKKKKKKK KKKKKKKKKKKKKKKKKK KKKKKKKKKKGRKTDLAVDPV
11237	41605	A	11305	1	417	
11238	41606	A	11306	1	1314	
11239	41607	B	11307	1	133	
11240	41608	A	11308	45	266	
11241	41609	A	11309	35	313	FLQMEDTYIVTKLLLLRFAWL YLDLVFVLI*YRKKRRKKRRKK KEKEKEKEKKKKKKKKKK KKKKKKKKKKKKKKKEMALQS CSLWYLYA
11242	41610	C	11310	240	391	
11243	41611	A	11311	1	579	
11244	41612	A	11312	141	410	PEPILTMESKGMWQLFELTL/H NSKVNTLSKELHSEFSEVMNEI WASDQIRSAVLISSKPGCFIAGA DINMLAACKDPSRSNTAITRKH RE
11245	41613	A	11313	1	358	KWFTPMFEIKGGYA*SKNWR LSVRCGGWPLRRLMEEGSLPNP SRIYYRNKLRLKSQNNSSVDPC MRNLDECEVCRDGLWELFCCDT CSRVFHDDCHIPPVESEKMKES AGSQCCQES
11246	41614	A	11314	1	921	
11247	41615	A	11315	108	2765	

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11248	41616	A	11316	98	2418	AKLMAQQGQQGQMASGDSNL NFRMVAEIQNVFGQNLQEQVC PEPIFRFRFRENKVEIASITRPF FLMGLRDRSFISEQMYEHFOEA FRNLVPVTRVMYCVLSELEKTF GWSHLEALFSRNLMAYPDLNE IYRSFQNVCYEHSPLQMNNVN DLEDRPRLPYGKQENSACH MDDIAPVQEALSSSARCEPGFS SESCEQLALPKAGGDAEDAPS LLPVSKCLAIQIDEGESEMPKL LPYDTEETFDLKTPQVTNEGE EKGCLLPGEGEESDDCSEMC DGEERQEAASSLARRGSVSSEL ENHPMNEEGEELASSLLYDN VPGAEQSAYENEKSCVMCFS EEVPGSPPEARTESDQACGMDT VDIANNSTLGKPKRRKRKRKRG HGWSRMRMRQKNSQQNDNS KADGQVVSSEKCANVNLKDL KIRGRKRKGKPTRFTQSDRAAQ KRVRSRASKKHKDETVDFAKAP LLPVTCGGVKGILHKKKLQGGI LVKCIQTEDGKWFTPTFEIKG GHASKNWLRSVRCGGWPLR WLMENGFLDPPRIRYRKKKRI LKSQNNSSVDCMRNLDECEV CRDGGELFCCDTCRVSFHEDCH IPPVEAERTPWNCIFCRMKESPG SQCCQCESEVLERQMCPEEQLK CEFLLLK VYCCSESSFFAKIPYY YYIREACQGLKEPMLWDKIKK
11249	41617	A	11317	1	1210	
11250	41618	A	11318	1	743	MRYKKEQLFLPKYDLGADAA ILQPQEEDCGSTQVRGGHHRK TEETGLLVTSLNQGIKPHDSVT KLLSPQRSSVLFLLLITSGVHTD SSKAVLESRRSLGYEASFLEYF QSFYKLPVDRLYAWHCSHDH NTTVAINTDRPGLLLTLTLVTI GQGSKKAPSGFHSHPAPTVMKQ QPILCDDRDFSPSFPSTNTPSQF ATNEVLTTGPPPGAG/CCQYSTI TRKTGPNCAQAGCGGARPAK
11251	41619	A	11319	314	486	
11252	41620	A	11320	3	122	
11253	41621	A	11321	1	289	
11254	41622	A	11322	1	399	
11255	41623	A	11323	3	259	

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11270	41638	A	11338	1	503	MKHQHFAALLVPEKFLIAQSTAS RVDRRQIWRDVSERGEISQCL KVGTSLSNSTDVS AVEAVRATV LGSGLTPTVLRNAGPYTRIST VPACLLGQEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEK/EEEE/EEE EEEEEEEEEEEEEEEEEEEEEE EEGEEEEERRKS
11271	41639	A	11339	1	651	MNIDANIPNKILENRIQQHIKKL IHHDQVGFIPGMQGWFNIRKSI NVIQHINRTKDKNCMIISDAEK AFDKIQQCFMLETNLKLGIGG I YLKIIIRAIYDKPTANIILNGQKL EAFPLKTGTQGCPLSPLLFNIV LEVLAIRQEKEIKGVQLGKE EVKLSLFADDMIVYLENPIVSA QHLLKLISFSK VSGYKINVQK SQAFLYTNNRQTENQIMSELPF TIASKRIKYRGQLTRDLKDLFK ENDKPLLKEIKED/DKEMEEHS MLMGRKNQYRENSHAAQEELE KNYFKVHMEPKKSPHYQVNP PKEQSGRRHVT*LQTILQGYSN QNSMVLVPKQTYRSMEQNRSL RNNATYLQLSDL*QTQEKQAM GKGFPPI**MVLGKLASHM*KPE TGSLLPYTLKYNQFKVD*RLKR* T*NHKNQRRKPRHYHSGHRHG QGLHV*NTKINGNKNQN*QMG SN*TKELLHSHKRNRYRQSDQATY KMGENFHNLLIRQRANIQNVQ* TQTNLQEKKNQPHQKVGEHGE QTLKRRHLC SQKTHEK/NSPSL AIREMQIKTTMRYHLTPVRMAI IKKSGNSRKHQKKEEEEEEEEA EEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEE EEEEKCSLKHTEAPCVKGIEITFW NKFSLCDITKSYLSGVQKLEER AHKVKLALKFKKEIKMALHGG
11272	41640	A	11340	1	2184	
11273	41641	A	11341	1	870	GSTISCARCAELRGSASRFRPLP AAAMKWMFKEDHSL EHRCVE SAKIRAKYPDRVP/LTMGQLYE KEKDEDGFLCVAYS GENTFGF
11274	41642	A	11342	2	259	

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11275	41643	A	11343	1	461	GCRRCRRRRCCCARCAELRGS ASRFRPLPAAMKWMFKEDR WLEHRCVESAKIRAKYPDRVP VIVEK/VSQGSQIVDIDKRKYAL VPSDITVAQFMWIIRKRIQLPSE KAIFLFVDKTPVQSSLTMGQLY EKEK\DEGFLYVA\YSGRGLTF
11276	41644	A	11344	1	966	
11277	41645	A	11345	1	1037	RPPFPVPGVQKCLPTRGGGLHIG RWLRDRAGPPEAQDGTGGRSR SRRRPPALPNSRPSVASGREM VVLSPVAEVTIVLLD\EGTTTP IAFVKG/DILFPYIERKMLKIEYL QTHW\EEEEFQ/QDVSLEFENK A\EEADHLDGAVPIPGKHLGIG VDDLLQMM\QAVVDNVCWQM SLDRKTTALK/QLQGH/MWRAA FTAGRMKA\EFFADVPA/VR/K WREAGMKVVIYSSGSVEAQKL LFGHSTEGDILELVDGHFDTKI GHKRRRVKVKTRKVIADSI/GCST/ NKHFVFWTDVTSRRASAGLRE AGCCTLAVVVRPGNAGINR*L RKTYYSLITSFQWNYLPSST
11278	41646	A	11346	346	858	
11279	41647	A	11347	1	234	
11280	41648	A	11348	1	1696	
11281	41649	A	11349	1	234	
11282	41650	A	11350	1	1696	
11283	41651	A	11351	1	211	
11284	41652	A	11352	1	417	
11285	41653	A	11353	1	1458	
11286	41654	A	11354	219	329	
11287	41655	A	11355	132	451	
11288	41656	A	11356	1	996	
11289	41657	A	11357	1	867	MARLWGAISLWPLWAAPVWG GAAAVGVRACSSAAPDGVGE PALRRSYWRHLRRLVLGPPPEPP FSHVQCVQDPPVLRGVAAPVER AQLGGPELQRLTQRLVQVMRR RRCVGLSAPQLGVPRQVLAL PEALCRECPPRQALRQMEPPFP LRVFNPSRLVLDRLVTFTPEG CESVAGFLACVPRFQAVQISGL DPNGEQVWVQASGWAARIQIH EMDHLQGCFLFDKMDSRFTFN VYWMKVND*SFATGAEDSGY QDANTFTLSWANLTHWQLGW LAYDRKLDCCQGMAD
11290	41658	A	11358	3	226	
11291	41659	A	11359	1	756	

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11292	41660	A	11360	35	142	
11293	41661	C	11361	151	484	
11294	41662	A	11362	1	1245	
11295	41663	A	11363	2	1464	CQAKFIMNRLKK/NERQKVQDI KEVKQNIHLIRASFAGKGKQLE EKMQPLEPEAIMLSELMQEQT KCRMFLSLISGKHGVHMDSKTG ATDSGAYLRVEEIQTIREYYK HLYANKLENLEEMDKFLDKYT LPRLNQEEVESLNRPIGAEILAI ISSLPTKKSPGPDGFTAEFYLR KEELVPFLKLSQSIEREGILPNS FYEASIIIPKGRDITKKENFRP ISLMNIDAKILNKILANRIQQHI KKLIHHDQVGFIPGMQGWFNL RKSINVQIHINRAKDKNHMISI HEEKAFDKIQPFMLKTLNKL IDGTYLKIIRAIYDKPTANIILNG QKLEAFPLKTGRQCPLSPLL FNIVLEVLARAIHQEIKGIHL GKEEVTLSLFADDMIVYLENPI VSAQNLLKLISNFSK VSGYKIN VQKSQAFLYTNNRQTESQIMSE LPFTIASRRIKYLGQLTRDMKD LFKENYKPLLSEIVTVF
11296	41664	A	11364	41	559	
11297	41665	C	11365	63	370	
11298	41666	A	11366	3	211	
11299	41667	A	11367	47	358	PDMGLEDEQKMLTESGDPEEE EEEEELVIGLRLSVHTGNLGRP GM*NFPLLSIQN*MGDPHSAIS GGQCGSASWPSARIPLQQVREQ CRASWKKCVKARERLEL\CDE R*SSRSHTEDCTEELFDFLH A\RDHCVAHKLL*QLAFCTDPP TTSERAMPSQLEEMCKRPGSG
11300	41668	A	11368	1	2082	

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11301	41669	A	11369	1	2013	MKHLKRWWWSAGGGLLHLTL LSLAGLRVDLDLYLLPPPTLI QDELLFLGGPASSAYALSPFSAS GGWGRAGHLHPKGRELDPAAP PEGQLREVRLGVFPVPTSV DAWLHVSVAAGSADEAHGLL GAAAASSTGGAGASVDGGSQA VQGGGDPRAARSGPLDAGEE EKAPAEPTAQVPDAGGCASEE NGVLREKHEAVDHSSQHEENE ERVSQKENSLOQNDDEENKI AEKPDWEAEKTTESRNEGISLG DIPLPGSISDGMNSSAHYHVNF QAIQDQVNLHEAILCPNNTFR RDPTARTSQSQEPFLQLNSHTT NPEQTLPGTNLTGFLSPVDNHM RNLTSQLLDLYLDINIFDEINLM SLATEDNFDPIDVSHLFDEPDS DSGLTLDSSHNNTSDIKSNSSHS VCDEGAIGYCTDHESSSHDDL EGAVGGYYPEPSKLCHLDQSDS DFHGDLTFOHVFHNHTYHLQP TAP*ESTSIEFPWP*GGRSQEG RE*DTLKDTRNLSRDEQRAK ALHIPFSVDEIVGMPVDSFNMS LSRYYLTDLQVSLIRDIRRGK NKVAAQNCRRKLDIILNEDD VCNLQAKKETLKREQAQCNKA INIMKQKLHDLYHDIFSRLRDD QGRPVNPNHYALQCTHDGSILI VPKELVASGHKKETQKGRRK
11302	41670	A	11370	3	255	
11303	41671	A	11371	1	1611	
11304	41672	A	11372	109	207	MLCLQRFYMFVDFQSRPQF*L KSCQHHSCHQ
11305	41673	A	11373	1	666	
11306	41674	A	11374	1	1254	

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11307	41675	A	11375	33	1458	KLPLKAKMGKEKTHINIVVIGH VDSGKSTTTGHLIYKCGGIDKR TIEKFEKEAAEMGKGSFYAW VLDKLKAERERGITIDISLWKFE TSKYYYVTIIDAPGHRDFIKNMIT GTSQADCAVLIVAAAGVGEFEA GISKNGQTRHALLAYTLGVK QLIVGVNKMDSPEPPYSQKRYE EIVKEVSTYIKKIGYNPDIVAFV PISGWNGDNMLEPSANMPWFK GWKVTRKDGNASGTTLEALD CILPPTRPDKPLRLPLQDVYKI GGIGTVPVGRVETGVLKPGMIV VTFAPDNVTTEV*SVEMHHEA LSEALPGDN/VGAFNVKNVSVK DVRRGNVAGDSKNDPPMEAA GFTAQVILNHPQISAGYAPV LDCHTAHIACKFAELKKKI ^{DR} RF ^{IG} KKLED ^{IG} PK ^{IF} WKS ^{GD} AAI VDMVP/GK ^{IF} MCVES ^{FD} Y ^{PP} L GPFAVHDMRQTVAGGAHQKQ VDKKAAGA/GK ^{IF} VT ^{IS} AQKAQ
11308	41676	A	11376	1	880	
11309	41677	A	11377	1304	2340	KETE ^{AQ} RKRLRRNEPEEQEIRT RKTRSPQTPDQQT ^{YK} KG ^{RN} ER LCGISQPTKEPTRGGFCFRNPP SNRIFACWGKPAWTACCN ^{SL} R ARRMLMERNARAAGSRKRMG RMD ^{CW} ARVLD ^{IN} LAAEAKSEP EKKAGVKRICKRRCTGSSFD ^{LA} DY* ^{LF} NGDY ^{YD} RMYSY ^{PI} ARV ^P PPPIARA ^{VVP} SKRQ ^{RV} SGNTS RRGKSGFNSKSGQ ^{RG} SSKSGKL KGDD ^{LA} QAIKE ^{EL} TQIKR ^{KS} GF LFLGKT ^{WE} KIEKEQSK ^{QA} AVEM KK**SQKEEQSSQLR*KKDET* ^C *RLEVLKGA ^{ED} SA ^{EG} DL ^{LD} DDD ^{NED} RGDDQLELIK ^{DD} EKE ^E AEEEE ^{DDR} DSAN ^{GR} DDSL ST

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11310	41678	A	11378	80	1141	ETQNRISSPSPCEIFLIFSIFRL CEKPYHQTRSASNVTKTDPRS MNSRVFIGNLTLVVKSDVE AIFSKYGKIVGCSVHKGFALSF SMLMKRNARA AVAGVEDGRMI AGQVL DINLAAEPK VNRGKAG VKRSAAEMYG/SQ*QNTLLRPL YFSSFDLDYDFQRDY YDRMY SYPARVPPPPPIARAVVP SKRQR VSGNTRRGKISGFNSKEWNSG VSSKFWKR*KGDDLQAIKEEL TQIKQKVDLSLENIKEIEQS KQAVEMKNDKSEEE\QSSSS\K KDETNLKMESEGGCRLTLP EE GDP\LD**YDE**RSGGNDPAGS *SKDDEKVEAEE\GEDDRD\ SAN GVEDDS
11311	41679	A	11379	1	1134	
11312	41680	A	11380	1	642	
11313	41681	A	11381	397	898	
11314	41682	A	11382	1	663	
11315	41683	A	11383	44	398	ATMLGLNIIRKWFYKSSEKSL GLRGGGLGRPLAFTLYSLQAAL LCVNAIAVLHE/ERRISSKNICA GGTRTIGIGWIWEKEPGIKSQL MNLIRSVRTEM RVPLIIVNSIAI VLLLLFG
11316	41684	A	11384	3	754	GLYYRKCQLISKEDVTHDTRLF CLMLPPSTHLQVPI/GEHVYLKL PITGTEIVKPYTPVSGSLSEFKE PVL PNNKIYIFLIKIYPTGLFTPE LDRLQIGDFVS VSSPEGNFKISK FQEEDELFLLAAGTGFTPMVKI LNYALTDIPSLRKVKLMFFNKT EDDIIWRSQLEKLA FKDKRLDV EFVLSAISEWNGKQGHISPA LL SEFWKRNLDKSKVLVCICGPVP FTEQGVRLLDHLNFSKNEIHSFT
11317	41685	A	11385	1	1785	
11318	41686	A	11386	95	369	
11319	41687	A	11387	511	728	
11320	41688	A	11388	1	100	
11321	41689	A	11389	1	777	

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11322	41690	A	11390	2	707	PNPKCR*VFPVFLFYRP1*FPFSS PA/SLIARPS*VPILPQPPLL/TPY NPPTTSPPHTRSGLQFSSATSSSP PAQQFPLREVAGAEGIVNAHV FSLSDLSQISQHLGSFSSDPTKYI QEFRYLTLSYNLTWSDNLNVL T STLSPDERERVFPVSQSH/V**P/ SGFMSQTSRKALEQFPERIPQW NYQANS PGKNFKN*NLALKPH NRN*STLPSCTIHERKQPDGNA FLSYNYLPP
11323	41691	A	11391	2	339	LLLFRSLPAKLNQAPILWPPL/PP PPYNPSITSPVHTWFLSQFHSET SPPPPPAQQFPLRAVAGTEGIVR MNGKEFFLQPNLTLITAGFKSQ TSRKALEQFPERIPNGTIRIQIPQ
11324	41692	A	11392	1	993	
11325	41693	A	11393	3	1127	TKETRFIHKPKTPAPVTDWEGS LPLVFNHCRDASLIHSRFGKGV PHRDTCLGSPPLAASPAFLGKG QAAHCQAE LSPNSSASTPPPY NPSITSPPHTRSGLQFSSATSSSP PAQQFPLREVAGAEGIVRVHVP FSLSDLSQISQCLGSFSSDPTKY TQEFQCLTLSYNLTWSDNLNVL TSTLSPDEWERVSSLAQSHADN VPGFTSQTSRKALEQFPE/TDPQ WNHQANSPIARRDYMVSCLV EGLKKAA YKAVNYDKLKTETQ GEDENPAQVVARLAATLRFT ALDPEGP EGRILNMHFITQSAP DITKKLQKLESGPQTQQELINL TFKVHNNGEETDAARSPWKPP GFSRTPSFRACFPCHNFCGY
11326	41694	A	11394	1	312	
11327	41695	A	11395	1	244	MFADR*LFSTTHQSIVPLYL/LF GA*AGVLATALSLIRAE LGQP GNLLGNDHIYNVIVTAHAFVIF FIVPIIIGFGN*LVPLIIGAPDM AFPRINNISF*LLPSSL LLLASVA IVEAGAGTRLNKSYPPLAGNY SHPWKPPVDLTIFSLHLAGVSSI LGAINFITIINIKPPAITQYQTPL FV*STTHQSHRTTPIYSAHELA SSPQPLSLIRAE LGQPGNLLGN DHIYNVIVTAHAFVIFFIPIIIG GFGN
11328	41696	A	11396	1	1287	
11329	41697	A	11397	3	583	

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11330	41698	A	11398	3	419	ILSISKLRSLTSLAGEGSDVTPKAS GVTRHIKGPVAAEMSAFILPL PG*VSPGWEEAASAVNLGLRT TLALRRGVCLIRSRPGTLGLD GASPRTESLHTGTACKGAVDGS SEVDEKLKRIALDFGLHGGDD PRSSWH
11331	41699	B	11399	1	1242	
11332	41700	C	11400	504	755	
11333	41701	A	11401	155	710	ETETTGEREGSLSNHSPNPTAA GLSLDTMKSCHPCNHSSLLSTAA SPPKLWRCFKEEHVELAVLGAP PKPLLPPTSHRDPTASVYLKAP THVWWSLFKHPLS*TPCCMGFI AFAIVSVKSRDRKIGCERDPGI AYASTAK\CLNIWALILGLLHD HSGSSSPVLI\VPGLWDRSGGIT GGQELCP
11334	41702	A	11402	1	1158	
11335	41703	A	11403	80	996	LKGFSLMSGALDVLQMKEE DVLKFLAA\GTHLGGTNLDIFH MEQYIYKRKSDGIYIILMRTW EKLULLAARAIVAIENPADVSAI SSRNTGQRAVLKFAAATGATPI AGRFTPGFTTNHQAAREPRIL LVVTDPRADHQPLTEASYVNLPL TIALCNTDSPRYVDIAIPCNNK GAHSVGLMWWMLAREVLRM RGTISRHPWEVMPDLYFYRDP EEIEKEEQAAAEKAVTKEEFGQ EWTAPAPEFTATQPEVADWSE GVQVPSVPIQQFTEDWSAQPA TEDWSAAPTAAQATEWVGATTD WS
11336	41704	A	11404	1	819	
11337	41705	A	11405	1	1032	
11338	41706	B	11406	63	344	
11339	41707	A	11407	49	281	FFKSTVCSFQKQFQTLVPVIGGS IMY*DISDHRGQR**NVGPCGH
11340	41708	A	11408	985	1213	TQCVTINY*GMKWGSFGYVVFH KDGICALIDKRHFTFCVSFKGSQ IQSSAFLIPDVQVHQRLQKDF QGLMVPIVGS
11341	41709	A	11409	1	774	
11342	41710	A	11410	3	249	
11343	41711	A	11411	3	619	
11344	41712	A	11412	3	493	

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11345	41713	A	11413	3	292	DALPRWPSPSGDGGAVREAGQ QGTRLERPAAVLIRAADPGRRRT QALA/GLPRG*PHPRMDPPESFQ ATGGTQMTSTAPSWLTM*LR SVSGW*ELKD
11346	41714	B	11414	190	315	
11347	41715	A	11415	227	545	
11348	41716	A	11416	1	1896	
11349	41717	B	11417	52	1822	
11350	41718	A	11418	1	458	
11351	41719	C	11419	196	327	
11352	41720	A	11420	258	375	TRALSKFGSSRVEQS*AGYSGP GTP*EGGSGLGETVC
11353	41721	A	11421	3	854	
11354	41722	A	11422	1	434	MTVSKNKCHTKGGKKGTEKK VVASFSKIYWYNVKAPAMFSIR NIGKALVIGHTGTFVSDGFKG GLIEIPDSIGKDKKACRSIYPLH DVFVRKVKMLKKPKFELGKLM ELHGEGRSSGKATGNESGA/KV E*ADGYGSPAQKSF
11355	41723	A	11423	1	642	
11356	41724	A	11424	260	534	
11357	41725	A	11425	1	438	
11358	41726	C	11426	391	750	
11359	41727	A	11427	786	926	AQGGQRQETIQGGRSLRSTLYL* GRSGTSLSQKLAQLSSLTGDST
11360	41728	A	11428	488	649	VLQLLKVAHPFLFIPPGGFVFSL TSGVKLHT*ALQLLKVAPELL IPPGSWSH
11361	41729	A	11429	1	2028	
11362	41730	A	11430	1022	1417	SLMGTTSSALGMHVPRAITRD VLSAPVIVSGNTAKFCTMLGHF LKKTRTERRDIQAP*SFISLPKS TWEKLSAAMVSTLR*GASDQ K/C*LLGGNDRVSLIVIQVEG/PL QDPGTLGRLLQSLTVKRISV
11363	41731	A	11431	1	535	
11364	41732	A	11432	3	1186	
11365	41733	A	11433	201	458	QVDGCIPELKV*F*KKRGRRRGR RGRRRRRRRGRREEGGGGGGG SFWRTHHTKPKDQHKDDTMG HFRSCAFQEGFVVHVPLSSEK
11366	41734	A	11434	1392	1532	AQGGQRQETIQGGRSLRSTLYL* GRSGTSLSQKLAQLSSLTGDST
11367	41735	A	11435	1253	2820	
11368	41736	A	11436	1504	1718	VIGIWALALGILARPQGFHV HLQDVGGA*AAKGLLRNVV R**VDQVQVSGAQGIAGVVVT VGGEEDF
11369	41737	B	11437	1	1383	

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11370	41738	A	11438	3	310	VHGRASSLGVG/TPIPKGHGQIK P/DRLKPPVYGACKLLDMELEM AFFVGPGRNLGEP/IPISKAHEPI FGMVLMAWSARHIQKWEYV PLGPFLGKSGFTVPVKSS
11371	41739	A	11439	1	1337	MSFIPVAEDSDFFPIHNLPGVGF TRGDPRPRIGVAIGDQILDLSIHK HLFTGPVLSKHQDVFNQPTLNS FMGLGQAAWKEARVFLQNLLS VSQARLRDDTELRRKCAFISQAS ATMHLPATIGDYTFYSSRQHA TNVGMFRDKENALMPNWLHL PVGYHGRASSVVSGTPIRRP GQMKPDDSKPPVYGACKLLDM ELEM AFFVGPGRNLGEP/IPISKA HEHIFGMVLMNDWSARDIQKW EYVPLGPFLEGEFVGHCLLPW VVPMDALMPFAVFNPKQGRG PCRYLCHDEPYTFDINLSVNLK GEGMSQAATICKVQILKYMY WTMLQQAHSPTLSNGCNLRP GDLLGFLGPISGPGAQKNFGS MLELSWKGTKPIDLGNGQTVR KFLLDIGDEVITAMATRDFFW YS/QGQDGYRIGFGQ/CAGKVLP ALLPIMRFFLLF
11372	41740	B	11440	100	383	
11373	41741	A	11441	1	263	MEYYAAIKKDEFMSFVRIWMK LETIILSKLSQGQKTKHRRFSLI DG/IHHRSFTRTENSQRTRGRKC WN**PTCGLARSWFGKTWSGN
11374	41742	A	11442	2	160	
11375	41743	A	11443	150	308	CLHR*GRGSPRPGPGGSGTGA GPGAGPSLAPPLPAQNAEGLGG RRRGNKYL
11376	41744	A	11444	1	372	
11377	41745	A	11445	49	177	SQQGLYAKPTSSQAL*GDGQAS AEMGRILSYE*EHAVFGFSSL
11378	41746	B	11446	1	420	
11379	41747	C	11447	1	334	
11380	41748	C	11448	1	268	
11381	41749	C	11449	1	564	
11382	41750	A	11450	1	264	
11383	41751	A	11451	33	194	
11384	41752	C	11452	1	309	
11385	41753	A	11453	1	738	
11386	41754	A	11454	1	2028	

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11387	41755	A	11455	3	1008	LKDAVFSIRISPESQKLFQFQWE DPESGVTTQYTWLTQTQGFENS PTIFGEALARDLQKFPKDLGCI LLLYMDDLLGHSTAVRCAKG MDALLQHLEDCGYKVSKKKA QICRQVTKWGDWERFEWEPL QQQAFCKLKEKFMSAPALGLP DLTKPFTLYVSEREKTA VGVLI QTVGPWPTPVAYLSKQLDGVS KGWPPCLRALAATALLAQEAD KLTLVQNLNIKAPHAVG TSAQ KPELIALTRALELSEGTWMKLE THLSKLSQGQK/DQTLHLVTGIS RST*ACSCLASLQVGLTGSQSL SLENPLRVGIQRRRCFTCAVDG EGFLLGV PMA
11388	41756	A	11456	677	879	KRRNHQILIRSHLQSVEDNLK SGLGSTASL*MSWTQPRNGAE VGFLILGYIKETPRNAETPSMV
11389	41757	A	11457	1	624	
11390	41758	A	11458	3	130	VEEEQGHFSRNAR*IIISW*RNEN GLDRMDCSCRNGERDKGHG
11391	41759	A	11459	1	1477	MADPPWSSVQVKNKYDSGLSS VSAEPLASSASSHPGMSDNAPA SLESGSSSTPTNCSTSSAIPQPGA ATKPWRSKSLSVKHSATVSM L SVKPPGPEAPRPTPEAMKPA PN NQKSMLEKLLFNSKGGSKAG EGPGSRDTSERLETLP SFESE ELEAASRMLTTVGPASSSPKIAL KGIAQRTFSRALTNKSSSLKGN EKEKEKQQREKDKEKSKDLAK RASVTERLDLKEEPKEDPSGAA VPMPKKSSKIASFIPKGGK LNS AKKEPMAPSHSGIPKPGMK SMP GKSPAPAPSKEGERSRSGKLSS GLPQQKQQLDGRHSSSSSLASS EGKGGPGGTTNLNHSISSTVSGS VGTITQTGNTSVVQLPQPQQQ YNHPNTATVAPF*EGFHLP*HA *VITF*TANYASSDNDLNVGYT H*LTASEFFQSRLLSLEAVGLH AHTC*A*LGSNIPFSVRLRPVPA ASAEDLRGHQGLIKDRAQVS
11392	41760	A	11460	1	327	LLLMLGLKHNVKLPRGPMVTL RESVWETLNLFLK*SFV*LNMLIF KKSS*RLQ*VRFHFLCPRVLIVQ LPFMSENMRCLVFCSCVSLLRM MVSSFIHVPPFKVLSFFALG
11393	41761	B	11461	119	203	
11394	41762	B	11462	1	677	

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11395	41763	A	11463	2	74	
11396	41764	A	11464	1	1256	MSASQDSRSRDNGPDGMEPEC VIESNWNEIVDSFDDMNLS ESL LRDIYAYGFKEKPSAIQQA ILPC IRGVNVIAQARSQTKMATFA I SILQQIELDLKATQALVLA PTRE LAQQIQKVVMALVDYMGAS C HACVVRGTNMRAEVQKLQME A PHIIVGTPSRVDFDMLYR YRLAP KSIRMLVLNEADEMLSRGFK G QIYDISKRLNSTTKVVL LSAT MPFDVLEVTKKFMRGPH/ IRIL VKKEELPLEGIRHFYINVE PEEF NLDTLCDWYEP*PITQAVIF HQ PPGGKVDW/LSPEKMHARD ST VPPMHGDMTKKERD/VIM REF RSGS*PEF*ITPLTPGQR PLMC QPGFL*SFKMLTLPPTRG KLLI HRNRSRVDRFGKGVAIN NMVT EEDAKRTLARDIETFYNT SIEEMP
11397	41765	A	11465	1	402	KSRGRGLPYTMDAFMLG MGM LKYPNFVAT*ARGYPGFAP SYG YQFPGFPAAYGPVAAAA VAA ARGSGSNPARPGFPGAN SPGP VADLYGPASQDSGVGN YISAAS PQPGSGFR/HTGIAGPL IATAFT NGYH
11398	41766	A	11466	226	486	
11399	41767	A	11467	2	432	
11400	41768	A	11468	1	834	
11401	41769	A	11469	205	570	
11402	41770	B	11470	61	939	
11403	41771	A	11471	96	269	
11404	41772	A	11472	123	593	VAVLEARLLSPVRASKMT KKR RNNGRAKKGRGHVQPIR CTNC ARCVPKDKA\KKFVIRN IVEAA A\VRDISEASVFDAYV LPLKIYV KLHYCVSCAIHSNVVME SISVK ARKDARTPPFRPPGGCW PHVP PPKPNVRELEFFKDLKDR LISS WEEK
11405	41773	A	11473	1	228	
11406	41774	C	11474	187	423	
11407	41775	A	11475	1	546	
11408	41776	A	11476	1	1254	
11409	41777	A	11477	1	1386	

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11410	41778	A	11478	1	1445	HLKAKMGKEKTHINIVVIGHVD SGKSTTTGHLIYKCGGIDKRTIE KFEKEAAEMGKGSFKYAWVL DKLKAERERGITIDISLWKFETS KYYVTIIDAPGHRDFIKNMITGT SQADCAVLIVAAGVGEFEAGIS KNGQTRHALLAYTLGVKQLI VGVNKMDSTEPPYSQKRYEEIV KEVSTYIKKIGYNPDVAFVPI GWNGDNMLEPSANMPWFKGW KVTRKDGNASGITLLEALDCIL PPTRPTDKPLAALPLQGVHKL GIGTVSSAPMETGFSNPGMVV TFAPSPR*QRKVKSVEVMHHEA LINEALSGEQGLSMSKKVSVK ECFVRGNVAG*PAKNDPTQWE ASWLSLLQVILEPSQAQISAGL CPLYWDCVHTGSHLHAKFAELK EKIDRRSGKKV\EDGPKIL/RS LGDAAIVDMV\PG/RPMC VESFS DYPPLGRFAVRDMRQTVAVGV IKAVDKKAAGAGKVTKSAQK
11411	41779	A	11479	1	996	

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11412	41780	A	11480	1	1875	MPSDLAKKKAACKKEAAKAR QRPKKGHEENGDVVTEPQVAE KNEANGRETTEVDLLTKELEDF EMKKAARAVTGVLSHPNST DVHIINLSLTFHGQELLSDTKLE LNSGRRYGLIGLNGIGKSMLLS AIGKREVPPEHIDIYHLTREMP PSDKTPLHCVMFVDTERAMLE KEAERLAHEDAEEKLMELYE RLEELDADKAEMRASRIHGLG FTPAMQRKKLKDFSGGWRMR VALARALFIRPFMLLLDEPTNH LDLDACVWLEELKTFKRILVL VSHSQDFLNGVCTNIHMHNNKK LKYYTGNYDQYVKTRLELEN QMKRFHWEQDQIAHMKNYIAR FGHGSAKLARQAQSKEKTLQK MMASGLTERVVSDDKTLFSYFPP CGKIPPPVIMVQNVVSFKYTKDG PCIYNNLEFGDLDTRVALVGP NGAGKSTLLKLLTGELLPTDG MIRKSHSVKIGRYHQHLEQEL DLDSLPLEYMMMKCYPEIKEKEE MRKIIGRYGLTGKQVSPINRL SDGQKCRVCLAWLAWQNPMM LFLDEPTNHLDIETDALADAIN EFEGGMMLVSHDFRLIQQVAQ EIWVCEKQTITKWPGLIAYK EHLKSKLVDIEPQLTKELPTTC
11413	41781	A	11481	194	418	YGLASVSPTQISSSSCNPWME GGTLVGGDWIGSHDSEGVLTR SGCLISVWHFSCAVSPATL*RRCL LLLLRLPP
11414	41782	A	11482	1	675	
11415	41783	A	11483	1	1125	
11416	41784	A	11484	1	711	
11417	41785	A	11485	673	796	
11418	41786	A	11486	3	570	RLQEFGRNRHLPVNSPKLTNT KGKRRGTRYMF/SRPFKKGHV VPLATYMRIYKKGDIVDIKGM GTVQKGMPHKCYHGKTRVY N\VTQHA/VMGIVVYKQA*GQR FLPKRI*CCVIEH\KHS/KSRDSF \LKRVKENDQKKKEAKEKGT WVQL\NRQLAPPREAHFVRTN GKEPGACWNPIPEYFHHNR
11419	41787	A	11487	1	2091	
11420	41788	A	11488	1	2208	
11421	41789	A	11489	430	1032	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hud	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
11422	41790	A	11490	3	1158	EDQIDRLDFIRNQMNLLTL.DVK KKIKVETEEVANKVSCAMTDEI CRLSVLVDFECSEFHPNPDVLKI YKSELNKHIEDGMGRNLADRC TDEVNALVLQTQQEIIENLKPLL PAGIQDKLHTLIPCKKFDLSYNL NYHKLCSDFQEDIVFRFSLGWS SLVHRFLGPRNAQRVLLGLSEPI FQLPRSLASTPTAPTTPATPDNA SQEELMITLVTLASVTSRTISM GIIIVGGVIWKTIGWKLLSVSLT MYGALYLYERLSWTHAKERA FKQQFVNYATEKLRMIVSSTSA NCSHQVKQIATTFARLCQVQ DITQKQLEEEIARLPKEIDQLEKI QNNSKLLRNKAVQLENELENF TKQFLPSSNEGSVTIEIALVTLLG GNNRL
11423	41791	A	11491	132	381	SKAESVFPPTLPRQRPAAAAGP HWGAG*GQDEAGLHPGPEDRG FLRETPADPGLQAGLGQVHPPR SRADPPAPYQVPPRMGT
11424	41792	B	11492	129	470	

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11425	41793	A	11493	1	1955	FVSCQAPWSHPPAQLSPVGADA MTLTLVSLICGLSVGPRTCVQ AGTLPKPTLWAEPA SVIARGKP VTLWCQGPLETEEYRLDKGLP WARKRQNPLEPGAKAKFHIPST VYDSAGRYRCY YETPAGWSEP SDPLELVATGFY AEP TLLALPSP VVASGGNVTLCQDTLDGLLTF VLVEEEQKLPRTLYSQKLPKGP SQALFPVGPVTPSCRWRFRCCY YYRKNPQVWSNPSDLEILVPG VSRKPSLLIPQGSVVARGSLTL QCRSDVGYDIFVLYKEGEHDL VQSGGQPPQAGLSQANFTLGP VSRSHGGQYRCYGAHNLSRW SAPSDPLDILAGLIPDIPALSVQ PGPKVASGENVTLLCQSWHQID TFFLTKEGAHPPCLCKSKYQS YRHQAEFSMSPVTS AQGGTYR CYSAIRSYPYLLSSPYQELVV SGPSGDPSLPTGSTPTPGPEDQ PLTPTGLDPQSGLGRHLGVVVG VSVAFVLLFLLLFLLLRHRHQ SKHRTSAHFYRPAGAAGPEPKD QGLQKRASPVADIQEILNAAV KDTQPKDGVEMDARAAASEAP IQDVTY AQLHSLTLRREATEPPP SQEREPPAEPSIYAPLAIHLAHG GPRSHTQQKETQRLQKARELPP VDTNEPQPAWDP

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11426	41794	A	11494	22	1991	GLIPLQSAQSPEGDAMTPALTA LLCLGLSLGPRTRVQAGFPKPK TLWAEPGSVISWGSPTIWCQG SLEAEQYQLDKEGSPEPLDRNN PLEPKNKARFSIPSMTHHAGR YRCHYSSAGWSEPSDLELV MTGAYSKPTLSALPSPVVASGG NMTLRCSGQKRYVHFVLMKEG EHQLPRTLDSQQLHSGGFQALF PVGPNPSHRWRFTCYYYMN TPRVWSHPSDLEILPSGVSRKP SLLTLQGPVLAPGQSLTLQCGS DVGYDRFVLYKEGERDFLQRP GQQPQAGLSQANFTLGPVSPSN GGQYRCYGAHNLSEWSAPSD PLNILMAGQIYDTVSLSAQPGP TVASGENVTLLCQSWWQFDTF LLTKEGAHPPPLRLRSMYGAH KYQAEFPMSPV TSAHAGTYRC YGRSSNPVLLSHPSPELLEVV GHS GGSSLPPTGPPSTPGLGRYL EVLIGVSVAFVLLFLLLFLLR RQRHSHKIRTSGLRLCPSSPRPE K'AD FQRPAGAAETEPKDRGLL RRSSPAADVQEENLYAAVKDT QSEDGVEIYTRQSPHDEDPQAV TYAEVKHSRPRREMA SPSPLS GEFLDTKDRQAEDRQMDTEA AASEAPQDVTYAQLHSLTLRRE ATEPPSPQEGSPAVPSIYATLAI
11427	41795	A	11495	1	1818	
11428	41796	A	11496	3	574	IRCSSVDPRVRPRVRGASGAA YCCRHNVSIPRDHTTHNQSRKW HRNGIKKPRSQRYESLKGVDPK FLRNNRFAKKHNTKGLKKMQ ANNIAKAMSARAEAIKALVKP KEVKPKIPKGGQPINLIRLAYIA HPKLGKRARARIKGLKLCRP KAKAKAKAKADQTKAQAA APASVPAQAPKRTQAPTKASE
11429	41797	B	11497	45	331	
11430	41798	A	11498	1	1779	
11431	41799	A	11499	1	837	

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11432	41800	A	11500	3	557	ERGYSFTTTAERDIVRDIKEKLC YVALDFEQEMATAASSSLEES YELPDGQVITIGNERFRCPEAL FQPSFLGMESCGIHETTFSIM KICDVIDIRKDLYANTVLSGGTT MYPGFADRMQKEITALAPSTM KIKIAPPKYSVWIGGSILAS LSTFQQMWISKQEYDIESGPSI VHRKCF
11433	41801	A	11501	1	1188	
11434	41802	A	11502	1	684	
11435	41803	A	11503	1	1398	
11436	41804	A	11504	22	1239	
11437	41805	A	11505	837	971	
11438	41806	C	11506	1	3018	
11439	41807	A	11507	23	368	
11440	41808	A	11508	1	816	
11441	41809	A	11509	1	441	
11442	41810	A	11510	195	293	IKVSPSGRDPVRDN*ITW*FLPY CSSTTGSLH
11443	41811	A	11511	56	372	MELPASPALFARTPQPLGGRW DWAPWSRGWRSSRRLLGPHRSP RRGSEAQA WRAAGPEPCPAGR QLRPVNIWLFALILTHFTGTFQ VLA*TSQALI*NPRVLYPD
11444	41812	B	11512	108	326	
11445	41813	A	11513	3	326	GSKKKFH*HSRILERSRWRTS YQGRPQPSWLHPVDPHRGCR WSCLPVPCRAPSTPQPLGGRWD WAPWSRGRRLSGRLGPHRSPR NRGRLRHGGLQVPSRASQEGS
11446	41814	A	11514	3	619	VRDIHGSPTHHRPGGLRGKNGF VGEARDPRYSGHCFRECRTO ALVAFT*C*SCGFTVEKN*GLSC LPAGQGSGPAARHV*ASHPLHG LPCGSLP/NRAPPTPRPVPT TQGLRNASARRGTGRQLHLQP WCGIH*VKPAGLLSLLHGQAC GDPATPSRERLSQPAVPTALGS RRRLLGAGSPGSSLPSPQPP GGRRRPP
11447	41815	B	11515	1	1524	
11448	41816	A	11516	1	1365	
11449	41817	B	11517	1	654	
11450	41818	B	11518	1	795	

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11451	41819	A	11519	486	929	QKQEEWPEPTYPRALAAFR GRARDLQPAPEPPITLSMGS APEPPRGAPPAPRRRIPSTTQG LRSSGAGRRTCRQLHLQPCRRI HWVKPAGLLSLWLFQMHSASC WWNYHSGAWRMVALFSWLH* ECPSGESGAPILHFFPALP
11452	41820	A	11520	35	473	VLQLLRHVWWSGFPPGVVVS LALAVKLQTFVTQEPSWLHPVD PAPGLQVELPASPLQCTRSTQPL GGRWDWAPWSRGRSSGRLGP HRSPWRG*EAQAWRAAGPEP/ WPRGKA/C*GPARNRAKRRFP CTF*EEVTVCSPPKRGDD
11453	41821	A	11521	23	229	RSWNPTLFVGMYNATAAWK PI*QFLKKNMKNLP*DPGREPLN QTG*KGKRGQEAFLKGISSR MSQ
11454	41822	B	11522	152	901	
11455	41823	A	11523	1	3063	
11456	41824	A	11524	242	263	VLQLIKAVWTQRTQEPSWLHP VDPALGLQVELPASPACTP QPLGVLPLPGLPLWRHLRSPSVH HCTVGAPFWAGQGRSPLPQR CALFLAGP
11457	41825	A	11525	1584	2082	QRAGSPHSRSLSPVPLPGLPLW RHLRSPSAHRCTMGAPFWAGQ GHSRLPQLAGRRGGGASGNR CCVQRLQASWSSRWAWAWRA PHSEQPAGPAGPQQ*GTWHPG QRLQRMYYWVLQCCRLTGAVL DFSPGLSCLPAGQGSPPAARHA *AFHPLHGLLCGRSLPD
11458	41826	A	11526	1293	1558	CIQHCHHCCCYRCRASAAGAA SLQGSTHYRIQHCTPCPVLLTP SVRLRDVCTRSIWPLVVTGLPS AMNVSSWCSTSSPAFGVLVLWI
11459	41827	B	11527	179	1031	
11460	41828	A	11529	1	342	
11461	41829	A	11530	1	3081	
11462	41830	A	11531	1	371	
11463	41831	A	11532	1	501	
11464	41832	A	11533	1	836	
11465	41833	A	11534	88	573	
11466	41834	A	11535	1	675	
11467	41835	A	11536	1239	1556	FLSLPTFLFVIFSGEEELLVLALV FLSLFFFFFLRWSFAVVAQAV VQWHNLSLPGFKQFSCLSLP SSWDYRCPPPRANFCIFTRDG VSPCCPGWSRTSLDR

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11468	41836	A	11537	2	375	ASIEIDSLYEGIDFYTSITRARFE ELNADLFRGTIDPVEKALRDA KLDKSIQHIDIVLVGGSTRIPKIQ KLLQDFYEAAYGA AVQAAIL SGDKSIENVQDLLSDVTPFP LGIE TAGGVMTVPH
11469	41837	A	11538	2	295	NRMGNHFAEFKRKHKKDISEN KRAVRRLRTACERAKRTL/SSST QASIEIDSLYEGIDFYTSITRAPF EELNAWGISWWWLPPVPGAS SGPTIEEVD
11470	41838	A	11539	1	1659	
11471	41839	A	11540	1	810	AGKPHCGGEFCTPNVHHFFR*F *ANPKRTII/ENKEALTPPTV/C* RAKPTLSSAPRAVI/EIDSS*E/GI GLYTSITPPRFEELNADLFLAPL TPVEKALRNAKLDKSIQHIDIVL VGGSTRIPKIQSFLQDFFNGKE LNKSINPDEAVAYGA AVQAAIL SGDKSIENVQDLLSDVTPSLG IETAGGVMTVLIKRNTTPTKQT QTFTTYSIDNQPGVLIQVYEGER AMTKDNNLLGKFELTGMPGG MPGGFPGGAPPSGGASSGPTI EEVD
11472	41840	B	11541	848	2399	
11473	41841	A	11542	1	876	
11474	41842	A	11543	16	1203	SIPHEPWPVSLLLFQE QVPGKK ELRKGLALLEAIISICGSLDKVL KEKRKLFHSMGEGTINGLLDE LLQTRVLNQEMEKKVRENAT VMDKTRALIDSVIPKGAQACQI CITYICEEDSYLAETLGLSADQT SGNYLNMQDSQGVLSFPAPQ AVQDNPA MPTSSGSEGNVKLC SLEEAAQRIWEQKSAEIVPIMDK SSRTRVALIICNEEFDSIPRTG AEVDITGMTMLLQNLGYSVDV KKNL TASDMTELEAFahrPE HKTS DSTFLVFM SHGIREGICG KKHSEQVPDILQLNAIFNMLNT KNCPSLKD KPKV IIIQACRGDSP GVVWFKDSVGSQNLSPTE EFEDDAIKKAHIEKDFIACSSST PDNVSWRHPTMGSVFGRGLIEH
11475	41843	A	11544	2	654	
11476	41844	A	11545	3	291	LIPPLLRPLVQSGGIPMGKFMK PGKVVLVLAGRYSGRKA VIVIR YSVDIPLDKTVVNKDVFRDPAL KRKARREAKVKFEERYKTGKN KWFFQKLRF

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11477	41845	A	11546	157	386	
11478	41846	A	11547	2	531	FWQESASGHLWLSGFLSGPFSLSAEMGKFMKPGKVVLVLAGRYSGRKAVIVKNIDDGTSRPPYS HALVAGIDRYPRKVTAAMGKK KIAKRSKIKSFVKVYNNHLMPTRYSDIPLDKTVVKNKGFTDPALKRNARMEAKVKFEERYKTGKNKWFQKLRVLDAFVLII KNYKE
11479	41847	A	11548	1	414	LGGKGTWGETKPAMAAAEEDGGPEGPNRERGGAGATKTLITYGNHLFSPQWLETRPERQECPVCKAGISREKVVGEKSLTFSLHFLRLKTPQICRLPV*LFLPP*GFQPFQDGGFHFSFGVGAFFPGFFNPSPY
11480	41848	A	11549	1	654	
11481	41849	A	11550	3	663	RQGEVVSGLLGRVYVYLGGKGTWGETKPAMASAEESGAPNVPNRERGGAGRPKTPFECNICLETAREAVSVCGHLYCWPCLEH QWLETRPERQECVPCKAGISREKVVPLYGRGS/QRSPQDPRIKNSPRPPGGRGPAPE/SRGGSQPF GDTGGFHFSFGVGAFFPGFFTT VFNAHEPFRRGTGVDLG/QGHPSLQLGKEFLPGFSAIFFLFWL
11482	41850	A	11551	3	369	
11483	41851	A	11552	375	851	
11484	41852	A	11553	1	927	
11485	41853	A	11554	104	845	

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11486	41854	A	11555	200	1496	ETIQAVVFMSLHFLYYCSEPTL DVKIAFCQGFQDKQVDVSYIAKH YNMSKSKVDNQFYSEVGDST FTVLKRYQNLKPIGSGAQGIVC AAYDAVLDNRNVAIKKLSRPFQ NQTHAKRAYRELVLKMCVNH KNIISLLNVFTPQKTLLEFQDQVY LVMELMDANLCQVIQMELEHE RMSYLLYQMLCGIKHLHSAGII HRDLKPSNIVKSDCTLKILDF GLARTAGTSFMMTPYVVTYY RAPEVILGMGYKENVDIWSVG CIMGEMVRHKILFGRDYIDQW NKVIEQLGTPCEFMKKLQPTV RNYVENRPKYAGLTFPKLFPS LFPADSEHNKLSAQARDLLSK MLVIDPAKRISVDDALQHPYIN VWYDPAEVEAPPQYDKQLD EREHTIEEWKELIYKEVMDSVEE KT*KWC*LKGQSPSAQVQQ
11487	41855	B	11556	56	1564	
11488	41856	A	11557	1	970	
11489	41857	A	11558	1	903	
11490	41858	A	11559	237	479	PVGTNTECEIPFQPMETGHSSR VDASGYK*PCLLCVSYSRGKTA GECTLF*VHHFLSSLCPVNLGA NNQLHYIPWFSTDG
11491	41859	A	11560	1	477	
11492	41860	A	11561	125	1133	
11493	41861	A	11562	1	837	
11494	41862	A	11563	2	708	CQHYKFRYHQGGEGQEEPPLN PHGAARAAYVLRKCTFDMFNF LASQHRVLPEGATCDEEEDVQ LRSTRATSLELPMAMRFRHLK KTSKEAVGVYRSIAHGRGLFCK RNIDAGEMVIEYSGVIRSVLTD MRKKFYDGGKIGICYMFSMDD FDVVDATMHGNAARFINHSCE PNCFSGVIPGGGPENKIVIFGLR RILGGEEVNLRTKKFPIEDAKIN KLPCNCGAKRCRRFLN
11495	41863	A	11564	2	136	
11496	41864	A	11565	1	551	AILYAKRASVFKLQKPNAAIR DCDRAIEINPDSAQPYKWRGKA H/RAQKIAEHRKRYERKREEREI KERIERVKKAREEHERAQREEE ARRQSGAQYGSFPGGFPGGMP GNFPGGIPMGGGMPGMAGM PGLNEILSDPEVLAAMQDPEVM VAFQDVAQNANMSKYQSNPK VMNLISKLSAKK

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11497	41865	A	11566	1	804	
11498	41866	A	11567	64	1215	PPSFAIHLPTMDPRKVNELRAF VKMCKQDPSVLYTEEMRFLRE WVESIGGKVPPATQKAISEENT KEEKPDSSKVEEDLKADEPSSE ESDLEIDKEGVIEPDTDAPQEM GDENAEITEEMMDQANDKKVA AIEALNDGELQKAIDLFTDAIKL NPRLAILYAKRASVFKLQKPN AAIRDCDRAIEINPDSAQPYKW RGKAHRL/LGHWEAAHDLAL ACKLDYDESDASAMLKEVQFRA QKIAEHRKRYERKREEREIKERI ERVKKAREEHERAQRE/EEARR QSGAQQYGSFPGGFLGGMPGN FPGGMPGMMGGGMPGMMG/GM PGLNEILSDPEVLAAMQDPEVM VAFQDVAQNPAINMSKYQSNP KVMNLIJSKLSAKFGGQA
11499	41867	A	11568	1	265	VKAKIQDKEGIPPDQQRILFAG KQLEDGRTLSDYNIQKESTLHL VLRLRGGIIEPSLRQLAQKYN DKMICR/KCCGHTNNLRPKKK
11500	41868	A	11569	3	318	
11501	41869	A	11570	7	57	RFFNFLGGIP/P*SGPKGMTL/DQ TQGSKSKIQWPALTFFKPLVER NIPSSVTAVEFLVDKQLDLTE DSAFQPYQVRNFRLLFKIKG*L NFIDIQTFFKQYSLNISSNF*LC EKPNECSQLILLIG*TVY*FFNFL GGIPLNLGQKE
11502	41870	A	11571	1	2109	
11503	41871	A	11572	50	251	
11504	41872	A	11573	1	1922	
11505	41873	A	11574	2	479	
11506	41874	A	11575	1	909	LILTSVLLFQRHGYCTLGEAFN RLDFSSAIQDIRTFNYVVKLLQL IAKSQLTSLSGVAQKNFYNILD KIVQKVLDDHNPRLIKDLLQD LSSTLCILIRGVGKSVLVGNINI WICRLETILAWQQQLQDLQMT KQVNNGLTSLPLHMLTNILY RFSDBGWDITLGGVTP/TLYML SEDRQLWKKLCQYHFAEKQFC RHILSEKGHIEWEVGCNFATF RKHYPAKEQYGRQHCIFCRHCS ILFWKDSGHP/CTAADPDSCTFP VSSQQFIALFQVLRAPCHPY WRFVNPAPVACGLIVSVL
11507	41875	A	11576	1	1035	

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11508	41876	A	11577	63	606	FAKNERTQRGKRRG\TRYMFSSR PFRR\HGVPV\PGPHICRIYRK DIVDTQGGVLFKKGMPHKCY PWPKLEGVLQLLPQHA\VAIVV NQPVLGQSFFPRE*IVRIEHIKH SKSPR*ASLK/RVLKENDSEKER SPNEKGTWGSNLKRHLAPPQK KHTL*RTNGKEPEL\LEPIPYEFH GHNRC
11509	41877	A	11578	1	490	
11510	41878	A	11579	150	536	NCKISFLHFCYIFVKALKRISAL SRGKILAKRINVRIEHIKHSKSR DSFLKRVKENDQKKKEAKEKG TWVQLKR/QGKNLVYISLVLR L*G*DLTHHII\FPFFFL**PAPP REAHFVRTNGKEPELL
11511	41879	A	11580	336	476	GMGTVQKGMPHKCYHGKTGR VYNVTQHAGIVVVKQVK*VV LCG
11512	41880	A	11581	1	626	WAFRPEPPSSSKFAQNDGPQRG KRRGTRYMFSSRPF*ENHGVPV LAHFMRVYKKGDI\VRHPRGM GYCSKKGMPPTSCYPWQKLGR VYNVTPAMLFIVCKQTKLK NDSLPRG/ILMWRI*AHLRHF*G ARD/RASLKTGRENGSRKKER KPKGGKVTWGFQLKRRHLGFP PQEEATFLLEPIGGREP*ACLE PYFPYWISWGINRC
11513	41881	A	11582	499	723	
11514	41882	A	11583	96	411	PAPTSRRCRRRAPLPPKKKAEGD AKGNKAKVKDEPQRRSARLSA KPAPPKPEPKKAPAKKGEKV PKGKKGKAD\AGKEGE*PLQKN GDAKTDQAQKA\EGAGDAK
11515	41883	A	11584	3	493	
11516	41884	A	11585	588	759	GEGCGWAEVGRCRPGPPDPAG PAGAAGP/GAARGGLFRGVLS SSRCGGGSSSSRSGR
11517	41885	A	11586	213	626	
11518	41886	A	11587	1	645	
11519	41887	A	11588	1	739	
11520	41888	A	11589	327	676	NPNPSWNLAHVWMDRK*EQ RGIV/V**SNINKS*KEKMSMQC LEMPRNPDI*GRIDVSFQNLMR LTR*SQMGYLPWDLKQLETF KLS*KQVMLS\VVTVFVRNMLQ LRFLTSFSG
11521	41889	A	11590	11	328	

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11522	41890	A	11591	1	378	LFIVTVCPAFLRFSSAICDSFLIC PQVGCGVRRVLVTVGVLLSIS LDMAATGVSLGSSWSLFLGIW LMIRFQVS*WYPNWLILSWRN ISITSTPSYYFTYFPTFCYQISPPN QLFCFLCSWFL
11523	41891	A	11592	1	780	
11524	41892	A	11593	1	1461	MVTLMGHAALCLHYVMQLGT TGGAWYFPRASSQAREMPQCP TLESQEGENSEEEKGDSSKEDPK ETVALAFVRENPGAQNGLQNA QQQGGKKRKKKRJIISGKVLED FLALAMHFADEETGQKRCSLN QTIQLLITPDGTGSIWHQAFSSIV RRAAQYGFREGGEDDDWTL YWTDYSVSLERVMEMKSYQKI NHFPGMSEICRDLARNMSR MLKMFPKDFRFPRTWCLPADP AQLDLWSQTFWPRPTAPDGT GADGLGLRLGSLGK/VSFWFPA CHGLG*PEASYYTAS/MACGSLP/ WKLSTFSAYLEDHSYVNEQIW RDIEDVVIKTLISAHPIIRNHYHT CFPNHTLNSACFEILGF DILLDH KLKPPWLLTEKMQTAGALFISP ALPSYSNFPLOVARREFQTSVV SRDIDTAAKFIGAGAATVGVAG SRAGIGTVFGSLIIGYARNPSLK QQLFSYAILGFALSEAMGLFCL MVAFLILFAM
11525	41893	A	11594	1	2301	
11526	41894	A	11595	3	381	
11527	41895	A	11596	1	729	
11528	41896	A	11597	1	1006	MVKVKARVNEFGYTGCGLVTRA AFNSGKVDIVAINDPFDLNYLA YMLQYDSTHGKFGHTIKAENG KL VINGNPITIQE*DPTKIKWG DAGTEYVVESTSIFTAMEKVGA HLQRGAKRVMIFAPSTEAIMFM MKVNYEKYDNSLKIIISNASCTT NCLAPLAKVIHDSNGIVERLMI TVHVITTTQKTVDGPCRKLRPD GHRALQNIIPASTSTAKAMVKV IPELNKKLTGMASHVPTAKVLV VDPTCHL/EKPAKYDIDKMM KQASEDPKIGILGYTEHQIVSSD FNSDTQSTFDAGAGITLNDHF VKLISWYDNEFGYSNRVVDLM AHMASKE
11529	41897	A	11598	3	508	
11530	41898	B	11599	1	5068	

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11531	41899	A	11600	58	659	PVATTCECIFIHLGEADVWIGN AA/WELYLYLEQSIQHDSMPMSD KTTG*GDN*FYASS/GAGKFVS RAVFINLEPIVTDEVCTGTYHQ LFHPEQLITDKEDAAHNYAWG HHDIGKIIGCYSTNKTCTIQQV DWCFTSLKVGINCQLPTVVPAG NLANIKRAACMLSNITIAIEAW VCLGHKSDLSYANCSFVHQFFN KSIH
11532	41900	A	11601	511	1173	
11533	41901	A	11602	3	497	WCDGPQNRYALICQQC/YSHNG MALKEEFYIAFRCA YCFFLNP ARKTRPQAPRLPEFSFEKRQVV EGSSSVGPLPSGVLSSDNQFNE ESLEHDVLDNDTEQTDKIPAT EQTNQVIEKASDSEEPKQET ENEEASVIETNSTVPGADSI PDP ELSGESLTAE
11534	41902	A	11603	2	764	
11535	41903	A	11604	1	444	
11536	41904	B	11605	44	1748	
11537	41905	B	11606	1	1134	
11538	41906	A	11607	1	549	
11539	41907	A	11608	212	548	
11540	41908	A	11609	1	905	ESVAAAAARFPPTAPKELERQQ RRRFRFHHLFLFSLRTPCRVSV SLQPWLWKATEVMAMFEQMR ANVGKLLKGIDRYNPENLATLE R/YVETQAKENAYDLEPNLAV LKLYQFNPAFFQTITVTAQILLK ALTNLPHTDFTLCKMIDQATI QERNGPIDQIFVPSGTLLEDPA HFGPFWQTPGNGRACQKAWD ENHWLFGKVLTFG*RLLVVRK FIC/HVVGYHLP SHIDR/WLLAE MLGD/SDKPAKRCWMSKIRLR EDDRRQGFUCS/QE*EHLNPRN/ IVEKIDFDSVSSIMASSQ
11541	41909	A	11610	186	209	QLWPN*LLSRNKEATLRYSQLP TCHSICY*MPAF*HTISDLSFNK NINCKSYHLRVFYKYV*IVCHF *VPKYVWTKYYQTS CRT*WR* SGVE*PPII SSSSACCLLRRLPT EGTCPEIFWNPRLGISAECRDSC GPTSF
11542	41910	A	11611	2	2948	
11543	41911	B	11612	1	999	
11544	41912	A	11613	1	657	
11545	41913	A	11614	1	707	
11546	41914	A	11615	1	297	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, /-possible nucleotide insertion)
11547	41915	A	11616	1	1287	
11548	41916	A	11617	242	540	LTNEKKVQDQMDSQPNSTRGT RRSLYPFLLLKLFQLEKEGILPNS FYEASIIIPKPGRDITTTKKEF* TNIPDEHRCKNPQ*NTSKPNPA AHPKAYPP
11549	41917	A	11618	193	916	
11550	41918	A	11619	1	2169	
11551	41919	A	11620	1	615	
11552	41920	A	11621	39	568	NSAWARRPLVLPMLSLVSPWK SSQHFIRVLNPPNLDGRRKNNSP LPITCHLRVWARRYAHVVLRLK ADVIDLT/RAGEL/TEDEVERVI TILQINPRQYKIPD/WFLNRQKD VKDGKYSQVLANGLDNKLRED LIERLKEDSAPIEGLRHFWGLR/ VRGQHTQDQLGRRGRHRGAS GARR
11553	41921	A	11622	1	378	
11554	41922	A	11623	1	222	
11555	41923	A	11624	2	367	
11556	41924	A	11625	2	376	QTYSLRRATPRHIVGFTKVM KEKVLRAA/NKPIRLTVDLAET LQARKEGGPIFNILKEKNFQPRI SYPAKLSFISEGEIKSFDTKQML KDFVTTTRPALQELLKEALNME RNNQYQPLQKHAKW
11557	41925	A	11626	1	633	
11558	41926	A	11627	164	714	IGVNRHLIQESPSWNLGAPLE QIFQRKEQAAIFAILQPLLVISRQ TGSGVDPQQITPADLQK/SGSDS REQNKTENEFDELTEIGCRRWV ITNSSSELKEHVVTQCKEAKNLE KMLQELLTRITSLKNNINDLME LKNTAQELREAYTHINSQTDQA EERISEIEDQLNEIKGEDNIREKT VKRNE
11559	41927	A	11628	504	936	TESSSININKDDHAKTP/PKDH NSSPAREQNK TENEFDELTEIGC RRWVITNSSSELKEHVVTQCKEA KNLEKMLQELLTRITSLKNNIN DLMELKNTAQELREAYTHINSQ TDQAERISEIEDQLNEIKGEDN IREKTVKRIE

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11560	41928	A	11629	1949	3232	PGKQDLEWTSKKLQQTCTRRGT LLVEGKLTNRKE*HQHQKQLR PHGNLIQRDHNCSAPAREQNWMM ENEFDKLTVGFRRWITITNSSK LKERVLTQCKEATNLAKRLEK LLTRITSLKNNKNDLMELKNATA QELREAYTSISGRINQAEQRTSE IEDQLNEIKRRGVSVCPQPS EDT PRSTARVPKGMVPPRPRVPLVT PPREKKEAPWLACLRTRALRLI DPSPQVWDIVSCDAENETKLEN TLQDIIQENFPNLAQANVQIQ EIQRTPQRYSSRRATPRHIIVRFT KVEMKEKMLRAAREK\GQVT HKAKPIRLTADLSAENLQAR/R TEWGPPIFNILKEKNFQPRISYPA K\LSFISEGEIKYFTDKQMLRDF VTTRPALK\ELLKALN\MERD NRYQPQLQNHAKFVKTIAREE TCINLMCQITS
11561	41929	A	11630	1	421	
11562	41930	A	11631	2	415	
11563	41931	A	11632	59	492	GHIGVRPSLHPVTSTTSGNVSP LARAMASISELACVYLALILHD DEVIIIEVNTILIKAAASVNV/ PFWPGFLFGKALANVIGSLICN VGAGGPALAAAGAAPAGGPAPSI AAASAEKKMEAKKEESEED DDMGFLGFTKPVL
11564	41932	A	11633	100	527	PPRTGQRQPLHSARRHGSPVS/E LACIYVSA LISARTDEVTVTEDK INALIKSSPL*MLSPFWPWLCLQ RPLANVNVIGSLICNVVGPVPEA ASQPGA\GPARKVLPSTAAAP S*RRRKLEAKRRKNPKEVLNDE HGLLVFLN
11565	41933	A	11634	1	675	
11566	41934	A	11635	1	1032	

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11567	41935	A	11636	3	976	HEAKHQMADDAGGS/AGGPEG PGGPWDGK\TPLL\SGEVFGIVIR GRGSRP/RGRGRGR\GRGARGG KGPRIK/WIGMPVHVQGAALVK DH*RSKFPWKEIYLFSLP\KGIK DS*FSFLA\GPLSKDEGFEGCLPV QKQTRAGQAQVSRPFVAIGG LQMAHVGSGVLSAPKEVATG HPVGAILAKLSIRPRAQKGIWG TKY\WQSPNTVP\CKV\TGRCGF VVVRLIP\APRGS\GIVSAPVA\K KLLMMA\GIDDCYTSAPGCTAT LGNFAKGHPLIAIFK\TYKLP*P PDL\WKETVFTKV\VPYQ\EFTH LVKDHPPESSVQRDLRLQLVAT
11568	41936	C	11637	279	322	
11569	41937	A	11638	1	107	
11570	41938	C	11639	69	134	
11571	41939	B	11640	223	950	
11572	41940	B	11641	1	684	
11573	41941	A	11642	1	564	EFGTRDNRVLLPLVNPTVFDDI AVD/GVYPLGRVSFELFADKVP KTAENFRALSTGEKGFGYKGS\ CFHRLFP\GFMCQGW*L*SHHN GTGGKSHLWGRNLKDENFIIL KHTGPGILSMANAG\PNNTNGSP VFLTCTA\KTE\WLDGKH\AGL GKVKEGMNI\VEAMER\FGSRN GKTSKKIISIA\DCGTTN
11574	41942	A	11643	1	877	MSGALDVLMQKEEDVLKFHA AGTHLGGTNLDFQMEQYIYKR KSDGIYIINLKRTWEKFLLAAR AVVAIENPADVS\VISSGNTGQR AVLKFAAATGATPIAGHFTPGT FTNQIAAFREPRLLVVTDPR DHQPLTESSVYNLPTIALCNTDS PLRYVD\ICNNKGAHSVGLMW WMLAREVLRMRGTISRGPWE VMPDLYFYRDPEEIEKEEQAAA EKA\VTKEEFQGEWTAPAPEFTA TQPEVADLSEGVQVPVPIQQF PTDDWSTQPATENWSAAPTAQ ATEWVGATTDWS
11575	41943	A	11644	1	1674	

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11576	41944	A	11645	1	1121	MLEAVLEESPREEA AFSWVMK GNLAAAGKTIQAQDRDAVGLSS RTGESMENLQKNLLPKQRRRT RETFTMSGALDVLQMKEDVL KFLAA\GTHLGGTNLDFQMEQ YIYKRKSDGIYIINLKRTWEKLL \LAA\RAIVAENPADVSVISSRN TGPEGLCLKFAAA\TGATPIAG\ RFTPGVFTTNQIAAFREATGF LVVTWTPGLDHQPLTEA\SYV YLPTIA\LCNTDS\PLARYVDIAIP CNNKGAHSGVLMW\WMLARE VLRMRGVTISREHPWEVMPDL YFYRDPREEIEKEEQAAAEKAVT KEEFQGEWTAPAPEFTAQPEV ADWSEGVQVPSVPIQQPFTED WSAQPATDWSAAPTQAQATE WVGATTDWS
11577	41945	A	11648	1	396	
11578	41946	A	11649	1	567	
11579	41947	A	11650	1	226	
11580	41948	A	11651	3	377	
11581	41949	A	11652	19	450	PDRRWSSLDTMNHTGQTFSPV NSGQPPNYEMLKEEHEVAVLG APHNPAPPTSTVIHIRSTSVDP HVVWSLFTLTMNCCLGFIAP AYSVKSRDKMVGVDVTAQA YASTAKALNIWALILGILMTIL LIVIPGLIFQAYG
11582	41950	A	11653	210	2206	
11583	41951	A	11654	450	644	SLRLWVWVTERAVTNLPSSRGV GDKPPVGPSPHLFLSLVVAFNPL QSTRNPASASQPQPCSAEQPAR RG*AEPA\RTVLP\HAEMWLPR LHEFEHRLVHRCFTLTFVDET DHCAVLPRGAGSGQGQGFERIL SQSPGSLWESC*PGLWNLNSNP PPCPLPAPLGRTAQ
11584	41952	A	11655	66	157	RGTWSIIA*KSQGISWDRFEET LCREPFT
11585	41953	A	11656	1	2538	
11586	41954	B	11657	68	1602	
11587	41955	B	11658	1	1464	
11588	41956	A	11659	587	1081	ILSWLTLWSILRLYIVTLTGKIC SLTSEASEATSPPRGTNNRSVA LA\VVTLVWRVCSFIDSKAFIL AFAFFFSHWFSILFPFPHGATL WYFWGDFECRSRGRNIHTDDR ARLVPMTERGGPPQGGEPART RSPRQGGRGGMEGGE*YPCPPH LGGQERKPG

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11589	41957	A	11660	180	583	YTEVLKGPDGAENHGTRTT** MHKPH*PIRSTGRKADKQLQQS LRINKINVQKSQAFLYTNNRQT ESQIMSELPFTIASKRIKYLGIQL TMDVKDLFKENYKPLLKEIRG YKQMGHEHSMMLGRKNQYSEN GHATAQ
11590	41958	A	11661	82	159	
11591	41959	A	11662	2	1008	NAAPLQQRNKAGCR/YDLDEL REEGFRRSNFFKLKAEVRTQCK ETKNLEKTLDKWLTRKTSVEK SLNDLMELKTMVQGLRDKCTN FSNGFDQLEERVSVIEEQMNEM KQEKKYREKKDRSMTQKVNK DIQELDSALHQEELIDYRTVHP KSTEYTFFSAPHRITYFKIDHIVG SKALLSKCKRTEIITNCLSDHSA IKLELRIRKKLTQNRSTTWKLN LLLNDYVWHNEMKAEIKMFFE TNENKDTTYENLWDTFKAVCR GKFRALNVHKKRQERSKIDTLI SQLKELERQELTHSKASRMQEI TKIRAEQKEKETEKNIQKNQRI QELFLKDKQQN
11592	41960	B	11663	1	1529	
11593	41961	B	11664	111	1350	
11594	41962	C	11665	1	2127	
11595	41963	B	11666	1	1350	
11596	41964	A	11667	1	1506	

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11597	41965	A	11668	1	1855	MIHIVPLYSSLGDRVKSCCKRE RERERRKKERKKERKKERKK RKKASSKEREEGRKKERKKL RKKEEKERKKKKRREGRKE RKKEKERKEGKKERKNIPGKR RESTDPLKEMDHRCLLPEMLK GTWWTTPARASGPAVPLCE RQWTVDTTSVVPSTHMPGQM TQPIPADSHNMDEAGGHYPK QTNTRPENQILHVFTDKWELNT EYKDPKKRTTDRAYLRVEAT LAADWMVPTQIEGRSSFVLATL AADWMVPTQIEGRSSFVLATL AADWMVPTQIEGRSSFVLATL AADWMVPTQIEGRGRMTPHM AGYSSETKLPEERSGSSICGSPIS AVLQPPLLIPRQTGSGVDLQQT PTDLQLRLMERSSSPATEQSW MENDFDEMDEGFRRSNYSEL KEEVQTYCKEVCGRGKFKALNA HKKRQETSKIDTLTSQLEKELEK QEETHSKASRRQEITKIRAELEK IETQKTLQKINESRSWFFKEKINK IHRPLARLIKKKTEKNQINAIKN DKWDITNNLTIQATIREYYKK LYANKLENLEEMDKFLDTYTL PRL*/N/CRQSLIAYYQIKVQDQ MDSQSNSTRGTRRSWYHSF
11598	41966	A	11669	2678	2897	PDGAKKHGKRTRDERTSFSEF NQLEERVSVIENQNMEMKREE KFREKRVKRNESQLQEIWDM* KQDMRSTS
11599	41967	A	11670	843	2004	NNQCREVLKGVGDGAESQGSRT REERRSLSRCDQLEERVSVIED QNMENMKREGKFREKRIKNEQ SLQEIWYVYKRPNRLIGVPES DGENGTKLENTLQDIQENFPN LTRQANIQIEIQRTPQRYSSRR ATPRHVVRFKTVEMKEKMLR AAREKGRVTHKGKPIRLTADLS AGTLQARREWGPINFILKEKNF PPRISYPAKLSFISEGEIKYFTDK QMLTIVHLKTLDIYMYNIRRPK GGEKKADQEVNSEPRNNIVLET KGDGRGPQAPSPGGPPRRVRR SASGSRAGITFHPVHYL TRRPFA HRFHYQSHGYGVGSVQSALR HKTNSAARAALRDGGVDCRGR ERGSACQKRSDDEAGGLVLS LPRVMGSGWEVRR
11600	41968	B	11671	1	3221	

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11601	41969	A	11672	82	160	
11602	41970	A	11673	1	551	AAAMADSGTAGGAALAAPAP GPGSGGPGPRVYFQSPPGAAGE GPGGADDEGFPVRRQKGVTVS YDRKELRKRL\NL\EDWIL*Q\LN GAFYDCQ\EEEEPELEIDVDELL D\MESDDARAA\RVKELLVDC YKPTEAFISGLLDKIRGMQKLS TPPEEVRVPDPGRITVAPTQGSL PPDLVATAITGGT
11603	41971	A	11674	362	650	
11604	41972	A	11675	1	651	
11605	41973	A	11676	1	3101	
11606	41974	B	11677	1	2838	
11607	41975	A	11678	1326	1980	TSEASRQSERVDSAALSLSLS RSSKCRPWGTARVARAGGCLT PLLSRRFLETRPFTGPWDPGLG VTCWCCPPKRLKSTPRPKFSV CVLGDQQHCDEAKAVDATFEV CLGDQVLSNANGFLSLSAKKY DAFLASESLIKQPRILGPGLNK AGKFPSSLREEGQAICYSTNLT *SSLPSQVLC\LA\AVGHVKMT DDELVYNH\LA\VNFLVSLLK
11608	41976	A	11679	11	720	EAMSSKVS\RD\TYE\AVREVLH GTQRKRRKF\UETVELQISLKNY DPQ\KDKR\FSGTVRLKSHSPAL SFSVCVLGD\RQH\CD\EAKA\V DIPPHGPSEAAEKTSTKNKKLV QKSWPKKV*MPFLA\SESSDQA RFPRIPRAPGLNKAG\FP\SLLT HNGKHGGPKV\DEVKVPQSRFQ MKKVLCLAV\AVGHVKMT\DE LVFNH\LA\VNFLV\SLLK\KNW QKCSGALYYQEAPMGQSPKRL
11609	41977	A	11680	34	507	
11610	41978	A	11681	407	806	LRVGM\LRQSKANGPDDHLLG ASCTCGPSTGSPSPRLPSLPQRP QKGLLHQ\RATRMKPGNIAKGL WKRLSKGTVMKLWLLTAVPRL SGLLVCP\LVHQL\LA\FAFKLRF PIFLWFR\AANRRHARFSILFKLS RP
11611	41979	A	11682	1	1551	

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11612	41980	A	11683	1	751	MAGYSSETKLPEERSDSSIRGSR KSTVLQTLILLIPRQTGIKKLTQN RSTTWKLNLLNDYVWHNE MKAIEKMFETNENKDTTYQN LWD/YIQSSV*REIYSTKCPQEK AGKIQNDILTSQKKELEKEQEQ THSKASRRQEI TKRAEPEKIQT QKTLQKINESRSLFFKRINKIDR PLARLIKKKREKNQIDAINKVEK GISPPPIQNYKLPSSENTNTSMQ IN*KI*KKWINSWTHTPSQE*TR KKLNL
11613	41981	A	11684	49	551	VRATYFHHAPNCTEFVPRQL VSRAENLPQATSLPTEKASRAF RVLLIPRQTRSGVDLQQTPTDL QLRVLI VRRKTNKQKGHPHQN PICTSP LRRSNFFELKEEVRTHG KDAKNLEKRLDKWLTRISSVE KSLNDLMELRTMA*ELCDECTS FSS*FNQLEERSVSI
11614	41982	A	11685	1	1566	MNSLLTGQIPESQIHRDSSAAT WWKKIYRQKMGNDIEKSEVRG GLTPHTAGYSSETKLPEKRSQS SICGSPISAVLPPLIPRQTGS VDLQQTPTDLKRLVLT VRRKS NKQKGHPHQPICTSP LSKTKD RSTRQKVNDIQDLNSALHQA DLIDIYRTLHPKSTEYTFPSAPH HTCSKIDHIVGSKALL/EQM*KN RNYQKLSLRPQCNCQLELRIKKL TQNHSTTWKLNLLNDYWM QKRPLKIQQCFMLKTLNKL GID GTYLKIIRAIYDKPTANIILNGQ KLEAFLLKTGTRQGCPLSPLLL NVVLEVLARAI RQEKEIKGIQL GKEEVKLSLFADDMIVYLENPI VSAQNLPKLISNFSKVSGYKIN VQKSQTFLYTNNRQTESQIMSE LPFTIASRKIKYLGQLTRDVKD LFKENYKPLLKEIKEDTNKWK NIPCSWVGRINIVKMAILPKVIY RFNAIPIKLPMTFFTELEKTTLK FIWNQKRACIAKSILSQKNKAG GITLPEFRLYTRLQ
11615	41983	A	11686	1	4962	
11616	41984	B	11687	101	3772	
11617	41985	B	11688	1	1047	
11618	41986	A	11689	21	287	

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11619	41987	A	11690	131	723	LLEGKLTNRKDIHTKNPSVRH/ RSSKTKERVVSAMEDEINEMKRE EKFREKRVKRNEQSLQEWDYL KRPNRLIGVPESDGENGTLE NTLQDIHQENFPNLRQANIQIQ EIQRMPQRYSLRRATPRHIIVRF TKVEMKEKMLRAAREKGRVT HKGKPIRLT/ADLSAETLQARRR WGPIFNILKEKNFQPRISYPACKL
11620	41988	A	11691	1	1257	
11621	41989	A	11692	1	759	
11622	41990	B	11693	107	511	
11623	41991	A	11694	170	726	LLEGKLTNRKDIHTETPSVCHH HQRPKDIIHQENFPNLRQANIQIQ QEIQRTPOQYSSRRATPRHIIVR FTK/VEMKEKMLRAAREKGRV THKVKPIRLTADLLAETLQARR EWGLIFNILKEKNFQPRISYPACK LSFISEGEIKYFTDKQMLRDFVT TRPALKELLKETLNVERNRYQ PLQKHAKL
11624	41992	A	11695	1	569	MAGYSSETKLPEERSGSNICCSP ISAVLQPLLIPIRQTGSGVDLW QTPTDLQLRVLTVRRKINKQKG HPHQNPICSTSPSSKTKGQIRAE KEIETQKALQKINESRNWVFEK INKIDRPPARLIKKKREKNQIDA IKNDRGDIITDPTIEQTTIREYYK HLYANKLENLEERDKFLNTYTL PRLNQEEVESLNRPI TGSEIEAII NSLPTKKS PGPDGFTDAFYQRY KEDLVFLLKLFQSIEKDRILSN SFYEASIFLIPKLRDRTTKKEN* QTERSTTPKPHLYITIEDQRPD QSRTEGNRDTKSPSKNQ*IQEL/ WFLKRSTKLIASTKTNKEEKRE ESNRNCNK**RGYHHRSHRNT NYHQIRL*TPLCCK*TRKSGRKG* IPQHIIHSPKTKPGRS
11625	41993	A	11696	3	1039	
11626	41994	C	11697	1	1251	
11627	41995	A	11698	1	807	

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11628	41996	A	11699	1	713	MNSLLTGQIPESQIHRDSSAAT WWKKIYRQKMGNDIEKSEVRG GLTPHTAGYSSETKLPEKRS SICGSPISAVLQPPLLIPRQTGSG VDLQQTPTDLKLRVLTVRKRS NKQKGHPHQPKICTSPLSKTKD RSTRQKVNKDIQDLNSALHQA DLIDIYRTLHPKSTEYTFSSAPH HTCSKIDHIVGSKALL/QQM*K NRNYQKLSLRPQCNCQTRTQD*E THSKPLNYMETEQPAPE
11629	41997	A	11700	1	1768	MNLSRHLNEVKGELLWSLEWR DPDGGSSIRMEVGLGGWTQRLE EEKKGNVCSHGNLEKDFPYIPH LFLGLQKKMDLKGVFKSCFKI YCSSKHLKLTGFISEAVLCYGE GGEGDTVLTMKERWPHCEICVLI QCNKGRLLTPHTARYSSETKLPE ERSGSSICGSPISAVLQPPLLIPR QTGSGVDLQQTPTNLQLRVLT VRRKTNKQKGHPHQPKICMSPS SKTKDFKPTKIKRDKEGHYIMV KGSIQEELTILNIYAPNTEAPR FIKQVLSDLQRDLDSHIIIMGDF NTPISTLDRSMRQKVNKDIQEL KSALQQAADIDIYRTLHPKSTE YTFSSAPHHTYSKIDHIVGSKAL LSKCKRMEIITNCLSDHSAIKLE LRICKLTQNRSTTWKLNNVLLN DYVWHNMKMAEIKMFFETNG NKDDTYQNLWDYIQRSV*REI YSTKCPQEKAGRI*N*HPNIQL KELEKQEQTSHKVSRRQEITKIR AELKEIETQKTLQKINESRSWFF EKFNKIDRRRLARLIKKEKNQ IDAIKNDK/GISPLIPQYKLPSE NTINTSTQIN*KI*KKWINSSTHT
11630	41998	A	11701	535	666	KGRNIQLNGLVIGTLSN*LKCL KMFFTMLPGYINGGSSDFFLH
11631	41999	A	11702	20	262	
11632	42000	B	11703	1	1254	
11633	42001	A	11704	1	1032	
11634	42002	A	11705	481	1491	
11635	42003	A	11706	2	717	

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11636	42004	A	11707	348	1976	SRVRPVVHLRRAPMVCQGHHT PPVCGSLAGPDCVHYVSPAG YSSETKLPEERSGSNICSPISAV LQPQLLIPRRTGSGVDLQQTPT DLQLRVLTVRRKTNKQKGHPH QKPCMSPPSKTKGSNSHITLTL NVNGLNAPIKRHRLANWIKSQ DPSVCCIQETHLTRCDTHRIKIK GWREIQANGKQKKAGVAILV SDKTDFKPTKIKRDKEGHYMM VKGSIQEEELTLNYPNTGAP RFIKQVLRDLQRDLDSHTLMIG DFNTPLSTLDRSTRQKVNKDIQ DLNSALHQVDLIDIRTLHPKS TEYTFFSALHHIYSKIDHIVGSK ALLSKYKTEIITNCLSDHSAIK LELRKKLTQNRSTTWKLNLL LNDYVWHNMKAINTLFETN ENKDDTTYQNLWD/YIQSSV*REI HSTKCPQEKAGKIN*HPNIQL KELEKQEQTSHKASRRQEITKIR AKLKEIETQKILQKINESRSWFF EKINKIDRPLARPIKKKREKNQI DAIKNEKGISPLIPQKYKLPSN TINTSMQIN*KI*KKWINSSTHT PSQD*TRKKLLNL*INTSMQIN
11637	42005	A	11708	1124	1717	LLEGKLTNRKDIHTKNPSVRHH HQRPKVDKTTKMGKQSRKTG NSKNQASAPPPKERSSPATEQN WTENDFDELREEGFRRSNYSEL KEEVRTNAKEVKNFEKLDLDEW ITRITNAEKSLLDLMEKTTAR ELRDECTSPSSQCINQLEERISAM EDKMNMKREEKFREKRIKRR EYQLQEIWDYVVKRPNLCILGVP
11638	42006	A	11709	1	3549	
11639	42007	B	11710	209	403	
11640	42008	A	11711	3	248	
11641	42009	A	11712	61	594	IQPLVSVLDEKPSNGVLVHVMK LLIKTFLDGIFFDLMEENVLNT DEIHLIGKCLKFVVSNAENLVD DITETAQTAGKIFREHLWNSKK QLSSVHGSEHEDKALTCHWVG HPGFPEKLKERKKFCGIMVVGL FGFTTDSGKAGADIHGRFLQGN FCNDAVTKAHVEKDFIAFKSST

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11642	42010	A	11713	1	430	FSAVREDGGCYLWQIYPIKERM DRIRLVLIIENKFDHLPPIRNGA DFAIMEMKKLLEDLGYSVVDVE ENLTAR/HNVSQGETGKGLPIF ITQLIACFQRYSWRCHLAEVFW KVQQAFFESPEATVQMPTIERVS MTRYFYLFPGN
11643	42011	A	11714	3	1195	
11644	42012	A	11715	35	1288	
11645	42013	A	11716	1	1641	
11646	42014	A	11717	1	2933	MVCSAAPLLLLATTLPLLGSPV AQASQPLWPMAGKQTMWAQT STLTLTEELGQSQAGGESGG QLLDQENGAGESALVSVYVHL DFPDKTWPPELSRTLPLAASA SSSPRPLLTGLRLTTECNVNHK GNFYCACLSGYQWNTSICLHYP PCQSLHNHQPCGCLVFSHPEPG YCQLLPPVPGILNLSQLQMPG DTLSLTLHLSQEATNLSWFLRH PGSPILLQPGTQVSVTSSHGQ AALSVSNMSHHWAGE
11647	42015	A	11718	1	357	
11648	42016	A	11719	73	1494	KSSHCIKMGPIFHKTSELFLPA TSCPSCPDQNEEDVSQTQYKEC CGGGWCSSHIFAVWHFI*RPDA T*FG*SSAYGFVADQCP*GSS* LYHLWYSYSGSENKQCG*RAA LGAGFSDKTPAHTVTMACISAN QAMTTGVGLIASGQCDVIVAG GVELMSDVPIRHSRKMRLML DLNKAAXMGQRLSLISKFRNF LAPELPAVSEFSTSETMGHSAD RLAAAFVSRLEQDEYALRSHS LAKKAQDEGLLSDVVPFKVPG KDTVTKDNIGRPSSEQMAKLLK PAFIKPYGTVTAANSS/LLTDG ASAMLIMAEKALAMGYKPKA YL/RRDFMYVSQDPKD/HLLG PTYATPKVLEKAGLATMNDIDA FEFHEAFSGQILANFKAMDSD WFAE/NYMG*KKPRFGLPPLWR RFNNWG/GSLSGHPFGATGCR LVMTAANRLREEGRASMA*V AVACAAGGGGHA/MIV/EAYPK
11649	42017	A	11720	1	642	

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11650	42018	A	11721	17	960	KSGARSLQPQLRAPEDGGPLS LPNAAMARGPKKHLNRVAAIP KHWM LDKLTGGCA/PRHSPVP HKL/RECLPLIIFLRNRLKYALT GDEVKKICMQRFKIDGKVVRT *YNPTPAGFHGMSSAFDKTGEE NFPS*SIDTKGSAFA/VHPYLTTL EEGQSTSLVPKVKKRSFVGHHK GIPSSWVTS*WPATIR*PRSPSSK VN*YHFRDLETDWQRLDFV/KF \DTGNL\CMGDWGGANLGRN WVLITN\RERHPSFDPWFHVVK DANGN\SFATRLSNIFVIGKGNK PWISLPRGKGIRLTIAERDKRL AAKQSSG
11651	42019	A	11722	1	460	
11652	42020	A	11723	1	243	
11653	42021	A	11724	94	311	
11654	42022	A	11725	400	792	
11655	42023	B	11726	473	596	
11656	42024	A	11727	1	1707	
11657	42025	A	11728	3	484	
11658	42026	A	11729	122	253	
11659	42027	A	11730	1	803	RGGRGGAGAAGELAGPLPSP APFESPGFTPPGPWGSICPAFA HALHSGTVPARSGRTMARGAA LALLLFGLLGVLVAAPDGGFDL SDALPDNENKKPTAIPKPSAG DDFDLGDVVDGENDDPFPN PPKMPNPNPNHPSSSGSFS\DA DLADGVSGGEGKGGSDGGGSH RKEGEEADAPGVIPGIVGAVV VAVAGAISFIA/YQKK\KLCFK\ ENAEQGEVDMESHRAQRQK PAVQRTLLKIEDCEPKQPAF GSRVRTAA
11660	42028	A	11731	335	476	
11661	42029	A	11732	2	169	
11662	42030	A	11733	49	289	VPVVQVPAAPGPLPGPATGSCS ASAAPRPDPPPGHPEGHGHS P/GVLGFEVGFISYCEQPKQCV TIKIFESPPIRRRL
11663	42031	A	11734	22	412	ARVGFLLGQEGKAGARASGPA DDVC/GKGASAIRSHMRASRSP PSPRRCHHHHEATGTASGSAAG GPGAGCVWLCRLALTPSAQDG RNSTFQTYKKEVCLPRHSHPCW MHAAGTTAGGSVAMSACCPSS SR

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11664	42032	A	11735	250	571	KGPRVTQGATVPKRQAPSAGL D/GSPISQFPWSY/DV*AIAILCG QGVV*PLPVSPGGPAPPESSVAL AEWVCSGSRRLPSNSGIARRPIG VIQPLDFLQNWPKPVLRC
11665	42033	B	11736	1	1593	
11666	42034	A	11737	2	1175	
11667	42035	B	11738	206	354	
11668	42036	B	11739	850	1461	
11669	42037	A	11740	2	663	VLLDERSAALDGA KR DGT LAL AAGALCREARAAQVFFLKGGY EAFSASCPCLCSKQ/INVSANCP NHFEHGYQYSILCGMTTHKA DISSWFNEAIDFIDSINKAGGRV FVHCQAGISRSATICLAYLMRT NRVKLDEAFEFVKQRRSIISPNF SFMGQLLQLESQVLAPHCSAEA GSPAMAVLDRGTSTTTVFNFV SIPDHSTNSALSYLSLITSSHC
11670	42038	A	11741	1	474	
11671	42039	A	11742	3	1354	WAVCATRVGGAVGGTAKKPR SPEPRVTLTSSKSGFWFGAER PGGLAFPRKAPPCWPREQTKS TAGPITLGALRPAMVMEVGTL DAGGLRALLGERAAQCLLLDC RSFFAFNAGHIA GSVNVRFSTIV RRRAKGAMGLEHIVPNAELRG RLLAGAYHAVVLLDERSAALD GAKRDGT LALAAGALCREARA AQVFFLKGGYEA FSA SACPCLCS KQSTPMGLSLPLSTSVPD SAES GCSSCSTPLYDQGGPVEILPFLY LGSAYHASRKDMLDALGITALI NVSANCPNHFEHGYQYSIPVE DNHKADISSWFNEAIDFIDSINK AGGRVVFVHCQAGISRSATICLA YLMRTNRVKLDEAFEFVKQRR SIISPNFSFMGQLLQF*VPQD/VL VPHCSAEGWEAPDMAVLDRG TSTTTVFNFVFIPIVHSTNSAL SLPFRGPINGPFPAG
11672	42040	A	11743	196	1260	
11673	42041	A	11744	5	447	
11674	42042	A	11745	1	328	
11675	42043	A	11746	3	364	
11676	42044	A	11747	1	816	
11677	42045	A	11748	1	1377	

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11678	42046	A	11749	1	989	EGRTVLGGGLGSAAAMASRL LNGAKMPILGLGTWKSPPGQ VTEAVKVAIDVGYRHIDCAHV YQNEVEVGVAIQEKLREQVVK REELFIVSKLWCTYHEKGLVKG ACQKTLSDLKLDYLDLYLIHWP TGFKPGKEFFPLDESGNVVPSD TNILDTWAAMEELVDEGLVKA IGISNFNHLQVEMILNKPGLKY KPAVNQIECHPYLTQEKLQYC QSKGIVVTAAYSPGSPDRPWAK PEDPSLLEDPRKAIKAKHNKT TAQVLIRFPMQRNLVVIPKSVT PERIAENFKVDFELSSQDMTT LLSYNNRNRVRCALLSCTSHKD
11679	42047	A	11750	1	855	
11680	42048	A	11751	2	367	
11681	42049	A	11752	2	376	QTYSLRRATPRHIIVGFTKVM KEKVLRAA/NKPIRLTVDSLAE LQARKEGGPIFNILKEKNFPQRI SYPAKLSFISEGEIKSFDTKQML KDFVTRPALQELLKEALNME RNNQYQPLQKHAKW
11682	42050	A	11753	1	1536	
11683	42051	A	11754	1	2541	
11684	42052	A	11755	1	1788	
11685	42053	B	11756	1	1014	
11686	42054	A	11757	1	777	
11687	42055	A	11758	1	1029	
11688	42056	A	11759	1	2052	
11689	42057	A	11760	1	1392	
11690	42058	A	11761	1	993	
11691	42059	A	11762	1	1240	PTDPAAEGFCLLDAKTNKRKGP STPILPFCSPFIRGPKVDSTHGA WGQKQHR*TGIF*RSRAPSPPA KEHGSSPATEQSWMENDFDEL REEGFRRIWYSELKEEARTHGK EVINLEKK\LDEWITRITNAEKC LKVELMELETKAARELREECRS LRSRRNQLEERVSAMEDEMNE MK\QEEKFREKKKKK*TKAL KELWDYVVKP/NLRLIGIPESDE ENGTKLENTLQDIIQENFPNIAR QANWQIRGNYRERQRLPPRG RATPRTHIIVRFTKVGNGREKM FKGQPGGKGRVTLKGKPIITLT ADLSAETSTSQTKEWGPINFIL GKEFSNPEISYLSQT*AFISGEE LNSFYRTSQMLRDFCHHQASRL P*KSTRPALKELLKEALKHKG GNNPVPSHLQKFIA

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11692	42060	A	11763	1	1917	
11693	42061	A	11764	268	307	AHHTHLCLLTSPPEGR*VCWG CGLGWGVVLSLVCPP
11694	42062	A	11765	2	349	
11695	42063	B	11766	1	1734	
11696	42064	A	11767	1	603	
11697	42065	A	11768	1	420	
11698	42066	A	11769	115	796	EWSSVRRSLVEKRALRRPHQC LCFRMKTILSNQTVDIPENVDI TLKGRTVIVKGP/REGTLRRDFQ SPSMENFTFLERKKRLRVDK W/WGNRKE/LATVRTICSHVQN MIKGVTLGFRYKMRSVYAHFP HQPLLSRGNGSLV/E/RNFFG*K NISARVRMRP/GVA/CSV/SQAQ KGEF/ISLEGNDNELVSN/ALI QQATT/VVKNKDIFKLDGIYVFE KGTVQQADE
11699	42067	A	11770	1	295	ASTAGVSYYVAQAGLKLGLS LSKCRDYRCEPPCP*MSLYKY MAMARKAMSLYIYFFLDEFM YFAGTW/MKLETILSKSQGQK TKHRMFSLVGGN
11700	42068	A	11771	3	342	
11701	42069	A	11772	1	182	
11702	42070	A	11773	1	439	
11703	42071	A	11774	1	325	
11704	42072	A	11775	2	91	
11705	42073	A	11776	167	861	IWAILADPRMAQGKLRMEIGTK LRCLIWTVHKGVHVWTFWWV ERSQTGNLEVRRLWGLLTHL HSGVNSLFTRARIWNPSMIDW/I KKMWHIYTMYYAAIKKNQF MSFAGTWMKLSAPAAPTVLFL ASFTNHYNLRASLLVESCLAPS YTSVEPRFSIPQSLTPARGSSDG HTCFSHQSHDLSL/CADSTHFW LSAHIWQANAPPVPRAPSEL KTRLKCSQPLNLRPP
11706	42074	A	11777	1	660	
11707	42075	B	11778	1	2633	
11708	42076	A	11779	1	2985	
11709	42077	A	11780	398	605	
11710	42078	A	11781	204	585	VTMCDRKAVIKNADMSEEMH QDSVECATQALEKYNIEKDIAA HIKKEFDKKYNPTW/HCI/VGEG TFGSLC*HIETKH/HLTSYLGAK WAISFCFKFWFKRHGTVAHPV IPFQKQGIALLNFQLPED
11711	42079	A	11782	1	810	
11712	42080	A	11783	188	534	

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11713	42081	A	11784	1	1188	
11714	42082	A	11785	1	1137	
11715	42083	A	11786	19	428	ERRNSGNMALRVERSVRAVLC SLHVVLAPAAPCLSRPWQLGM GAVWVYCNLPEVGTGLNKQDE FGALERVKAASELYSPLSGEVT EINEALAEENPGLVNKSRVEDG WLJKMTLSNPS*LDELMSSEEAY EKYKISIEE
11716	42084	A	11787	66	631	RRDPRTPANMALRVVRSVRAL LCTLRVPLPAAPCPRPWQLG VGAVRTLRTGPAALLSVRKFT KHIEWVTTEGIGTVGNSFAQA EALGDVVYCSLPEVGTGKI*TKP SWSLVLESVKAASELYSPLSG AEVTEINAEALAEENPGTCKTNFC YEDGWLIKMTLSNPSE/LDELMS SEEAYEKYKISIEE
11717	42085	B	11788	46	743	
11718	42086	A	11789	209	401	MKPPVRSLSLTPPRSIIHGSSATEI EELNTTFKYLTGEQTEKMWQ RLKGMEIKLKN*G
11719	42087	A	11790	135	313	
11720	42088	A	11791	1	624	
11721	42089	C	11792	81	299	
11722	42090	A	11793	5	166	SPVMMSSFFLVCLLTT*RSPPSS SSSSSSSSSSSSSSSSSPSSSFS GSVV
11723	42091	A	11794	3	173	
11724	42092	A	11795	169	291	SCNSSLFSLSLVADPQIATYR /S*CSRLGHKGTLPGS
11725	42093	C	11796	1	429	
11726	42094	A	11797	1	279	
11727	42095	A	11798	3	376	
11728	42096	B	11799	1	736	
11729	42097	A	11800	753	2455	
11730	42098	A	11801	1	312	
11731	42099	A	11802	48	397	
11732	42100	A	11803	51	286	
11733	42101	A	11804	1	420	
11734	42102	A	11805	11	537	PDRPTRPCRQCARSFRRKLKAA VGVEGPSLSSGELGTRVPAAPS PTTRPRAMAFCLPSFACIY/SALI LHDDEVT/VTEDEKINALIKSSR V*MLSPFWPLGFAKALANVN MGSICNVGAGGPPCPASWVL QPAGRSLLPPLAASSLREKKV EAKKEGFRGSFD*LTWGFGSF
11735	42103	A	11806	114	399	

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11736	42104	A	11807	3	599	AIRRLRISAREEERENQPRLLPL SLGAGGGVGGFVQWPRFKAR DLRGKKKEELVKQLVDLKVVE LVPSARRQKQGGAAASKLSKI RIVVRKSLAPCSPLFTQTQKEN LRKFYKGGKKYKPLADLRPKKTR AMRRRLNKHENLRITKKQQR KERLYPLRKYAVKALGGALSIK HKENLTKKQQRKERLYPLRK YAVKA
11737	42105	A	11808	226	370	AGSP*FPQFSEA*RRGALGSGA DQDLSHPRITETLTSCSLQTSS PR
11738	42106	A	11809	3	7964	RSGSSSKFEPRSRSASVLPASAL GPPNTSPRQLVAHCALPATRMP VTEKDLAEDAPWKKIQQNTFT RWCNEHLKCVNKRIGNLQTDL SDGLRLIALLEVLSQKRMRYKY HQRPTFRQMQLENVSVALEFL DRESIKLVSIDSKAIVDGNLKL LGLVWTLILHYSISMPVWEDEG DDDAKKQTPKQRLGWQNKI PYLPITNFNQNWQDGKALGAL VDSCAPGLCPDWESWDPQKPV DNAREAMQQADDWLGVP
11739	42107	A	11810	1	636	
11740	42108	A	11811	3	261	OKKPLKQPKQA*EMDEVRA AEALAGAGALGRPELNTCLCS PEDKAFKQKQKEEQKKLEIK AKAAGKGPLATGGIKKSGKK
11741	42109	A	11812	1	621	
11742	42110	A	11813	1	1024	
11743	42111	A	11814	174	332	SHCLANAPGDVKVRNDPESPRE L*HL*R*RYNTRWKRSI*EEWC QGHSWRG
11744	42112	A	11815	1	1323	
11745	42113	A	11816	1	2322	
11746	42114	A	11817	1	336	
11747	42115	A	11818	22	391	PPPPAAKTRRKKVLATKVLGTV KWFNVNRNGYGFNRNDTKEDV FVHQTAIKKNNPRK\YLRVSGD GETVEFDVVEGEKGAEAAVNT GPDGVPV/EKGSRYAADRRRY RRCY\YDR\RRGPPEYV
11748	42116	A	11819	433	866	PPPPAAIDAEEKVLATKVLGTV KWFNVNRNGYGFNRNDTKEDV FVHQTAIKKNNPRK\YLRVSGD GETVEFDVVEGEKGAEAAVNT GPDGVPV/EKGSRYAADRRRYR IGYYGKARWPPFANYAGGRR RKGAAQVEGFLPPLPLD

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11749	42117	A	11820	63	484	
11750	42118	A	11821	1	819	
11751	42119	A	11822	150	463	
11752	42120	A	11823	63	594	FAKLNPNGKGGGEATRYMFSR PF*ENHGVVPLGHNN*RFYK GDIVDIQGEWGTLFQKGNCPH KVVTHGQNLGVLPMVTPAML VGHLL*TNQF*GKVSFKRINVR IEPIKHSKRSDFLKRVKEND QKKKEAKEKGTWVQLKRQPA\ PPREAHFVRTNGKEPELLEPIPY
11753	42121	A	11824	2	1376	
11754	42122	C	11825	132	341	
11755	42123	A	11826	155	245	
11756	42124	A	11827	3	293	
11757	42125	A	11828	204	467	LRAPHVACSRNQGPGMCNCL NTDQHTQTQRQG*EEKSSSK/ PISSLMEYYKRSQCYSVKARS VF*KLRAQAQLQETKKPVFR L
11758	42126	A	11829	1	768	
11759	42127	A	11830	348	568	REISYKERIGM*MPPSVILNSYV KSMLETYPHPLRLRGVVAPGLK KGFLTESLLALPDPSFSGRMTSF KITPV
11760	42128	A	11831	1	840	
11761	42129	A	11832	2	216	
11762	42130	A	11833	1	726	
11763	42131	A	11834	3	3231	PGGWLRRALPGRERLQSPVHA VPPQHGTSRLLVTPWAGAGR DQDFSSPPLLLGETDHLHDL PLSPPLTSDELFLPGICDPYVKL SLYVADENRELALVQTKTIKKT LNPKNWEEFYFRVNPNSHRLLF EVFDENRLTRDDFLGQVDVPLS HLPTEDPTMERPYTFKDFLLRP RSHKSRVKGFLRLKMA YMPKN GGQDEENSQDRDDMEHGWEV VDSNDSASQHQEELPPPLPPG WEEKVDNLGRITYYVNNH
11764	42132	A	11835	1	624	
11765	42133	A	11836	2	361	
11766	42134	A	11837	3	432	NSRVDDFVAAQDAKGGKVAP APAVVKKQEAKKVNNPLFEKR PKNFGGQQLRLARA EKAAG KGDVPTKRPPVLRAGVNTVTT LVENKKAQLVIAHDVDPDELV VFLPALCRKMGVPYCIKGGAR LGRLVHRKTCTTVAFT
11767	42135	A	11838	1	684	

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11768	42136	A	11839	9	247	AVTSDEPKGKKAKAKKVAPAP AVVKNQEAKKVVDPLEKRRHK N\FGGQDIQPKRASPRLCLEPR\ YIRLQRQRAILYKRLKGPFCDY PGFTRALDRQTV*SSLKLAAHK YRPETKQEKK\QRLFARAREEG VLAKGDVFNEDPPV\LRARSL TPFHHPWVEKQEKQLV\VNWH TDVADPNELVLLALPLCREKW GVPIYCNRYREKARLWDRLV QERPCTTCPPTQGELRKTKGG FWLKLGWKILRTQFTIDQILMR SRRHWG\GNVLG\PKSVGS*SP KLEK\AKAKELAH*TG
11769	42137	A	11840	1	273	
11770	42138	A	11841	1	218	
11771	42139	A	11842	1	1522	
11772	42140	A	11843	136	441	
11773	42141	A	11844	24	274	SRQAWHEAASASARRRGTRSP ALSPARAPAGPIWTNARRSARA NSVSPAAAPPPRRPVSLSDPGE SCTRDPRAPDCGPFRC
11774	42142	A	11845	194	365	
11775	42143	A	11846	1	782	LLVVGTTVVVYPNFRGKFEFM SRHVHLMCYRICVRALTAIITY HDRENRPNGGICVANHTSPID VILASDGYIAMVGOVHGGLM GVIQAMVACPHVWFERSEV KDRHLVVKRLTEHVQDKSKLP ILIFPEGTCINNTSVMFMKKGFS EIGATVYPVAIKYDPOGFDAFW NSSKYGMVTYLLRMMTSWAIV CSVWYLPPIID*ERQIEDAVQFA NRVKSATARQGGVLDLLWDGG LKREKVKDTFKEEQQLYSKM
11776	42144	A	11847	3	916	
11777	42145	A	11848	13	473	DPPTDSLSPDGGSEIEFLA PFSMPSLLGAPPYSLGGVGD YAPLMVLMCRVLCLEDKPIKLP CCKKAVCEECLKVYLSAQIQCP TCQFVWC*CAGCAWKTSPSSPC LAARRPCARSASKST/SSAQIQ PTCQFVWCFCCHSPWHEGVNC KEYKKGDLLRHWAIEIEHQQ RNAQKCPCKIHIQRTGCDH MT
11778	42146	A	11849	92	1103	
11779	42147	A	11850	1	516	
11780	42148	A	11851	1	642	
11781	42149	B	11852	200	608	

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11782	42150	A	11853	1	1856	MEETGMCEGHGASPGMEASSG EREKRGTEASPGDREKRGTE ASSGEREKRRTEASSGDREKR GTGKASSGEREKRGTEASYG EREKRGTAAGGQESCAHCGG WLMPRAKPSTHIRETNPRGTEA TAMAMDHVGGQADTTDSTDG SQWDPSEHSPNCGIREVGAGDP DTQQTGRHHCYYPACKETNEKT NTNRNSNTFIEQLLHAKQQRGN SGVPFKPGHMRALTTNALSW AKLYPDPWCLRMGGTGNEVFE NEIKTGSCWIKQEQPRPQSP RSQVRPEADPGPSPLTKMSAEN EYRPPSPKLAERDKPSRLRP RGVPWRRESRVRAGRECALLR VAAEGARPPPAGMSYDRAITVF SPDGLHFQVEYAQEAVKRGST AVGVGRDIVVLGVKKSVAK LQDHRPVRKICTLHDN\VCMA FAGL/TPADARIVIQTGPGVEFQ SHRA*TVEGPRVTVEYITPLTF ASLKASVYTQSKWGAPFG/IS GPHRGFSTFDGTP*LYQTDPSG TYHAWKA\NSIGRGAKSSARS SWEKNYTDKAIETDDL\TIKLV IKALLEVVQSGGKNIE\LAVMR RDQSLK\NLNPEEIEKYVA\IEIK EKEEN\EKKKQKKAS
11783	42151	A	11854	12	432	

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11784	42152	A	11855	1	1775	MSYPADDYSEAAAYDPYAYPS DYDMHTGDPKQDLAYERQYE QQTYQVIVEIKNFIQYFHKTVS DLIDQKVYELQASRVSSDVIDQ KVVEIQDIYENSWTKLTERFFK NTPWPEAAEAIAPQVGNDVFLI LYKELYRRIYAKVSGGPSLEQ RFESYNYCNLFNYILNADGPA PLELPNQWLWDIIEFIYQFQSF SQYRCKTAKKSEEEIDFLRSNP KIWNVHSLNVLHSLVDKSNIN RQLEVYTSGGDPESVAGEYGR HSLYKMLGYFSLVGLRLHSL GDYYQAIKVENIELNKKSMYS RVPRVPRSPTYYYVGFAYLMM RRYQDAIRVFANILLYIQRKTS MFQRTTYKYEMINKQNEQMH ALLAIAL/TMYPMRIDESIHLQL REKYGDKMLRM/QKGDPPQVY EELFSYSCPKFL/SPVVPNYDNI HPN/YHKE/PFLQ/QLK/VFSDDEV Q/QQAQLSTIRSLKLLHPCLV AKPGLASDLTEQEFRIQLLVF KHKMKNLRVDSA/VSQALDGEF QSASEVDFY/DKDM/IHADTK VARRYGDFFIRQ/NHKF/EELNPN P*RRMG/QRPWMIFTTHSGNLV
11785	42153	B	11856	1	537	
11786	42154	A	11857	98	334	WATERWKGRKNHEISWKCFFG KAIS*MRSSQMKPNFRCSSIT VLSVRGMVLF/LTACPRFKMSS RTDFRFGNPQVT
11787	42155	A	11858	4	422	
11788	42156	B	11859	1	2567	
11789	42157	A	11860	2	364	
11790	42158	A	11861	1	501	
11791	42159	A	11862	1	402	
11792	42160	C	11863	30	673	
11793	42161	C	11864	195	1263	
11794	42162	A	11865	3	648	
11795	42163	A	11866	200	420	ILPSALRPPNPNWNVG/YVQTQ LVSKPLSLPTGIPCSTTSNLIKPV ITKDARLHRVIVHGWG/KGTIPI AKIAIS

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11796	42164	A	11867	1	502	MQLPGRGHFSVCKANAGSTQA RQGASAGVAGCRGWLNYAAS EQIVLRVPHMRCEIPHKCVRRK SRIRPHSPFRLRNCWKGRSVRA FSLRLQAKGGCAARLSWVT PGFSQSRRCCTTASAKLACLQV RAQSEDISTVPIHYAYNMTRVG RMQMLGKYNPQSAKLVREAIL PTKATLDLSNQNNEDFSAFQLG LAQALHIKVIHMTREVMSDEL TKLLEGNLKPADMMVEFTT GSLPENAVDVLNTALGDRKSF VALMALMEYSRYLVAEDKSAF VTPLYVEADGVTNGPINAMML MTGGFLTPDWIRNIAKGG*FQ YTTFNRNSRSQCFFHIFQETSCK FFSMCF*SSLLTKHCHSSRDVW VFSTSFQHIRHTLIDGISNRTNQ LTCNTTSTRITIDGNSQVRVLSNTT
11797	42165	C	11868	1	3831	
11798	42166	A	11869	1	5370	
11799	42167	A	11870	1	3999	
11800	42168	B	11871	1	12036	
11801	42169	B	11872	1	16395	
11802	42170	A	11873	1	19997	
11803	42171	A	11874	1	70	
11804	42172	A	11875	44	613	AGTHLRPFSPSLAAMALRYPM AVGLNKGHKVTKNVSKPRHSR RRIGRLTKHTKFVRDMIREVCG FAPYERRAMELLKVSKDKRAL KFIKKRVGTHIRAKRKREELSN VLAAMRKAAAKKDLGPSPCPL PEIKDKLDRSPGSPAVRGWVW VCRGPAVPCLVPALSHTLSGCC LVVNQKPWPAHPSRGRSR
11805	42173	A	11876	1	150	FRGRCCVQRYRGCTLASA/CLL VGEAEAPSPVDPLERSRPYAVL RGQNLE
11806	42174	A	11877	447	725	
11807	42175	A	11878	2	206	RPVAYLLLQGWGRCCVQRYRG CTLASA/CLLVGEAEAPSPVDPL ERSRPYAVLRGQNLDQTLH*ST HQA
11808	42176	A	11879	1	413	
11809	42177	A	11880	122	268	
11810	42178	A	11881	1	555	

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11811	42179	A	11882	221	419	LQTLQGYSNQNSMVLVLPKQR YRPMQNRNALRNNAAYLQKSP *ADKQLQQ/ECQDTKSMCKNH KHSYTPITDKQRAKSRVNSHSQ LLQRE*NT*ESNLQGA*RTSSRR TTNHCSMK*KRIQTNGRTFHAH G
11812	42180	A	11883	1	2464	MDEFNLNTYTLPLRLNQEEVESLN RPITGSEIVAIINSLPRKKSPPGD GFTAIFYQRYKEELVPFLKLKLF QSIEKEGILPNSFYEAHILIPKPG RDTTIKENFRPISLMNIDAKILN KILANRIQQHIKKLIHHDQVGF PGMQGWFNIRKSINVIQHINRT KDKNHMIISTDAEKAADKIQQP FMLKTLKKGIDGTYLKIRIKYL GIQLTRDVKDLFKENYKPLLNE IKEDTKKWNIPCSWVGGRINIM
11813	42181	A	11884	2104	2637	MFQRGHISQWVVVVGALTFTFT SVLDTDPMRDNKRSGSEILPFC REHGTSFTYNHAHSPSCSPSCL FSGALALFSPENNSGFLCMTLPAS FTAGNRLFSSAGQPWWIQQGF KAHAKARRLILLAFHHYCCRP LAVELKPSPVSTPTFLFA*LLPP CSVPGAILHESFGAITWLDLAE
11814	42182	A	11885	69	417	QTHSQHYTEWGWKVESIPPENW NNTRMPIFTISIQHIIRSSSESQNT RERNQGHPNG*RGSQTVAF* YDRIPRKP*RLIQKTPRTASAAD TQANRVWSGPPASSNRPAEAGP DC
11815	42183	A	11886	376	597	ENKIPRNPTYKGCCEGLQGELO TAAQGNKRGHKHMEKHSRLM DRKNQYPSAADTQANRVWSGP PANSNRPAEAGPD*PGQNFQYH VE
11816	42184	A	11887	5	292	LTVSCPCSRMLFLTDTDLPLM FIKKLGANVASPSSKKPLFVIRL VITLTLPLACGLPTSSVSRTTFF RTMLPQAVEFAPPSTGTESHYY CCIW
11817	42185	A	11888	320	596	YPGKQGLEWTSSKQLQQTCKRY RERHKDTP/TRRATPR/RHNCQV HQS*NEGKNVKGSRERSGYS QREAHQTNRSRLGRNSTSQKRV GASIQRS
11818	42186	A	11889	3	239	EASRGRIQQHLPFCNICCSAAS TGDTQANRVWSGPPANSNRPA AEGLDK*KEN*QTERSTPKPD LYTHIKDQSL

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11819	42187	A	11890	3	278	EASRGRIQQHLPFCNICCSAAS TGDQTANRVWSGPPANSNRPA AEGLDG*KEN*QTERSTTPKPD LYITIHKDQRLPIGLFSPWISARI
11820	42188	B	11891	394	1213	
11821	42189	A	11892	856	1217	VDRSRLQKVSNNKLVAQKGGC SNPLQGS*KLDNPKDANS/RQQ PERTWKWIFPQPHR*GAFGPRH C*ESHL YQFGLDLLNSAGSGIG KNEVQEQKRAEVGARAAPKE LPEALSWFLKVLW
11822	42190	B	11893	1	894	
11823	42191	B	11894	93	938	
11824	42192	A	11895	149	508	LLEGKLTNKKDIIHKTPSVRHH HQRPKPKISL**ATSASQDTK SMCKNHKHSYTTITDKQRAINH E*TPIHNCFKESKIPRNPYKRC *G/RSSRTANHC SRK*KRTQTN GRTFHTHG
11825	42193	C	11896	1	1257	
11826	42194	A	11897	183	1065	YWRCNGFLS*YAEAAEEIVDCI TESLSILKTPLPKKMNEEMLCQ EFGFGLASVKIMWPRTEER ARERNCGFVAFMNRDAERAL KNLNATAFRPALSHFPLPMDT TSQIPKHPVTVSSTNKLILIKTH FQAQSSLNQNIHPMDPSHGQY SAFSPSTPNPSHPALP*PLAIQVH HAVCDGFHVGRLNELQQYC DEWQRDKLEEILRGLTPRKNDI GDAMVFCNLNAAEAAEEIVDCIT ESLSILKTPLPKKMNEEMLCQE FGRFGLASVKIMWPRTEERA RERNCGFVAFMNRDAERALK NLNATAFRPALSHFPLPMDTT SQIPKHSRQFNKQAHSDHQD SLSGPVQSESKYPSHGSIPWDSI LSLLTLNTQPIPPSLALTHMEME SGLHFHCFTASPPSAVPPPELE KTTLKFIWNQKRARIANSILSQ KNKAGGITLPDFKLYYKATVT KTAWTGSPTAIRQARTTRQEKE MKGIQIGKEEVKLSLFTDDVNL QVRENK
11827	42195	C	11898	138	644	

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11828	42196	A	11899	2	3088	ADKTPGGSKASSKTRSSDVHS SGSSDAHMDASGPSDSDMPST RPKSPRKHNRYNESARESLCDS PHQNLRLPLENKLKAFSIGKM STAKRTLKKEQEELKKKEDEK AAAEIYEELAAFEPSDGNKVK TFVRGGVVNAKEEHETDEKR GKIYKPSSRFADQKNPPNQSSN ERPPSLVIETKKPPLKKGEKEK KKSNELEFKEELKQIQEERDER HKTKGRLSRFEPQSDSDGQRR SMDAPSRNRSSG
11829	42197	C	11900	413	823	
11830	42198	A	11901	263	1246	NPGKQGLEWTSSTPADLQLR VLTVRRTNKKQGHPHQNPCT SPSSKTEVENLEKRLDKWLTR LTNVEKSLNDLMELKTMAREL HDEGTSFSSQFDLEERVVPM DQNMENKQEEKFREKRMKRN EQSLQEIRDYVKRPNRLIGVPE SDGEWKEPSWKTLCRILSRRTSP A*QGRPTFKFRKYRECHKDTPQ GEQLQDT*LSDSPKLK*RKKY* GQPERKKYRLPSANTKTSLRK* TRKSRRNG*ITGHIHPPKTPGR S*IPE*TNRL*N*GNN**PANQK KSRTRRIHSQILPEAQRGAGTIP SETIPINGKRGNNPKLIL
11831	42199	B	11902	67	2584	
11832	42200	A	11903	1	3793	MSDAEDERFLQFLRYRYVLT GDCRTVAGAGQWVQRTEREPKQ GEALPHPGSARGWGVPPRDD GWHLENRVPTLILRFSHSLSK QHTRRPYSAPGSEGTPTPCSL LAQQSEIKLQDGSEAGGGLLLI PRQTGSGVDLRQTPDMQLRV LTVRRKTNKQKGQPHQNPCTS PSSKTKAPHHTYSKTDHIVGSK ALLSKCKRSEITNCLSDHSAIK LELRKKRIQNRSTTWKLNLL LNDYCVHNEIKAEI
11833	42201	A	11904	1	441	

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11834	42202	A	11905	312	3705	FIMPAVASVPKELYLSSSLKDL NKKTEVKPEKISTKSYVHSALK IFKTAEECLDRDEERAYVLYM KYVTYVNLIKKRPDFKQQDDY FHSILGPGNIKKAVEEAERLSES LKLRYEEAEVRKKLEEKDRQE EAQRLQKKRQETGREDGGTLA KGSLENVLDSDKDTQKSNGEK NEKCETKEKGAITAKELYTMM TDKNISLIIMDARRMQDYQDSC ILHLSVPPEAISPGVTASWIEA IILPDDSKDTWKKRGNV
11835	42203	A	11906	1	609	
11836	42204	A	11907	3	755	LRVDNAPAHASGLFFCAGAAG TVLFAMAPSRNGMVLKPHFHK DWQRVRVATWFNQPARKIRRI RPRQAKARRIGAPRGGGPIRPI VRCPTGRVHNGSWRPGRGFQP GRSSRVAGHSRKPVPAPDPSGIS VDPKIRRETSSHGSPPLQAQAS GLKEVYRSQTQSSSRKPSAS/PL *GDSSAEELKLATQ/LTGPMVP VRNVYKKEKARVITEEVKNF KAFASLRMARINARLFGIRAK RAKEAAEQDVEKKK
11837	42205	A	11908	1	327	
11838	42206	A	11909	1	756	
11839	42207	A	11910	1	219	
11840	42208	A	11911	2	227	
11841	42209	A	11912	1	567	
11842	42210	B	11913	99	799	
11843	42211	A	11914	61	342	
11844	42212	B	11915	1	945	
11845	42213	A	11916	92	133	DPFSQKLKTLRKD*TNG*LQ*P MKRSP*MT*WS*KP*HENYVTH AQASVPDSINWKKGYQ*LKIK* MK*SKKRSLEKKE*KETNKASK KYGTM*KD
11846	42214	B	11917	1	368	
11847	42215	B	11918	1	106	
11848	42216	A	11919	1	705	
11849	42217	B	11920	1	834	
11850	42218	B	11921	1	1305	
11851	42219	A	11922	1	1187	
11852	42220	A	11923	228	619	

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11853	42221	A	11924	1499	2238	KGKKKVINQISLGQRMRLSQSS HGKVVQACQVPFHPNAPPAVQF QSRELQSGSRPRSCGEKATRCLE RQGPREVPLPKNAWA*QRKQE KKRSRKGS/GREPGLRRPPNAQ ARDSSRAPATHRKELKPEREH ISCSRSIRYQEWVSLRDTVHR NLVLDTKRHPALILVEYKERTS SPATEQSCMENDFDELREEGFR RSVITNFSELKEDVQTHHKEAK NLEKRLDKWLTRINSVEKSLND WMEKKTMA
11854	42222	A	11925	699	796	
11855	42223	A	11926	1029	1223	ERELPDPLRFPSEGNASALLSAS RTVRASTDLRPLSGTP*RDEPGT SDGNAEITRLRLRSQWEL
11856	42224	A	11927	186	1597	
11857	42225	A	11928	1	1200	
11858	42226	A	11929	1	600	
11859	42227	A	11930	1	663	
11860	42228	A	11931	908	1331	GDMRGREGGFGGLGRRTAMRC GCSPGIVREADNLVKLSRPSTV RVTRSSASVMVLTMLAPATFL RVNCWAG/RGR/*SQNETVSR TRCEEGR**KDYRVEEQRLRKN WDLARPGEELQAPSPEKRDPL RVKDQGRHPCVV
11861	42229	A	11932	1	1707	
11862	42230	A	11933	1	1012	MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQPDLDIYGLTHP KSTEYTFFSAPHHTYSKIDHILG SKALLSKCKRTEIHTSYLSDHSAI KLELRQNLQTNHSTTWKLNLL LLNDYWLHNEMKAEIKMFET NENKDTTYQNLWDAFK/RSV*R EIYSTKCPQEKAGKIQN*HPNID QQN**TTSKANKEKKREDSNRC NKK**RGYHHRSHRNANYVHR ILQ/YTSMQIN*KI*KKWINSSTH TLSQD*TRKKLNL*IDQ*QELKL WQ*SIAYQPKRVQDQMDSQPN STRVASKRIKYGLQLTRM*RTS SRRTTNHCSMK*KRIQTNGRTF HAHG
11863	42231	C	11934	1	1788	
11864	42232	A	11935	550	827	DVSWAGRSEDHRWIFLKEQRT GGPPK/ERSRSESRHQISCMCAA STWMERTAYGGSHRELLQL PQEHTRKTLPLQQTSAWYTRLF HTSCEI

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11865	42233	A	11936	584	1094	NWIPSLHLTKLLIQDGLKT*MLDLKP*KP*KKT*AIPFRT*AWAR TSLCKHQKQWQKPKLTNGI*L N*RVSA/PAKETTISMN/EATYR MGENFCNLI*QRANIQNLQ*T QTNLQEKNKQPHQKVGKGHEQ TLKKRHLCSQKTHEKMLIITG HQRNANQNHNEMPFHTS
11866	42234	A	11937	797	1044	EESIS*KWPVCPR*FVDSMPSPS SYR*VSSQNWKKLL*SSYGTQK EPTLPSQS*AKRTKLEASHYLTS NYTTRLQ*PKQHG
11867	42235	A	11938	176	374	LTNQKKSRTRWIHSQILSEVQR GADKQPNRE*TPHNCFKENKIP RNPTYKGCEGPLQGLQTTAQ
11868	42236	B	11939	1	1843	
11869	42237	A	11940	3227	3391	DPLPGQRQLLLQKQRRP*TAAG LLSFQPGQPHGSVPPTLSQPW LPGGWPELSG
11870	42238	B	11941	1	1479	
11871	42239	B	11942	1	2097	
11872	42240	A	11943	654	1341	KNRNYNKLRLRPQCNRTRTD *ESHKSLNMYMETEQPAPE*LL GT*RNENGRNKDVL*NQREQRH HIPESLGRIGSSV*REIYSTKCLQ E//MQERSKIDTLTSQLKELEKQ EQTHSKASRRQE/DN*NQSRTE GNRDTKNPSKNQ*IQELVF*KD QQN**TASKTNKEKKREESNRH NKK**RGYHHRSHRNTNYHQRI LQTPLRK*TRKSRRNGYIPRHH SPKTKTGRS
11873	42241	A	11944	471	611	
11874	42242	A	11945	1	585	
11875	42243	A	11946	3	1029	GRQHGGSQRMGGTASARASSG RLAPRGRGAFARRRCPSPRRW RLTCGPAAVEHSFCHNVGPGV RATADKYTCMFTYASQGGTNE QWQMSLGTSEDHQ/HFTCTI/W RPPRGKSYLYFTQKAEVAGR LRFYRHLGLTFKAA/SLKRES VPLENLRNFEVQNQSSGLTRPG GISKAELSKLIVGQGIRALSCD QQPLLRRGGTFSPPVKLGACVP ERAQHITGFLGTLKFSTWADV ALSRRGFGSWLKPWGREQRVQ GPPGSQQLFRPLPVKLFWTQD RRSRGTKRVGNMGMALGKAA MLPPTSSRASFMSLQNCFFMFT QGTSPQMNWEEKCFFIFK
11876	42244	A	11947	1	1206	

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11877	42245	A	11948	1	654	
11878	42246	A	11949	849	1089	SPEGKHYRCYL VHMPDTERSS L*MRPRAGRSSAEGPGCRQRSL ALDHMVQQAQRWCWRYQWWR RFSKEFNQWWRFSSEEL
11879	42247	A	11950	5	1376	
11880	42248	A	11951	2	278	VPQPDTRKGSVLK WISKRGKPL AVEIEESHCLCLPLRTECLGKIP VVHLFSCTRPVIWPSLELNVDV DSIAHMFVADLLMITLPSYDIP
11881	42249	A	11952	3	267	
11882	42250	A	11953	1152	1338	FKRGQYGRLLRFRFHGQILYA RRQGAIEPLAIQVHHAVCDGFH VGRMLNELQYQCDEWQGGGA
11883	42251	A	11954	394	615	ASDPLRGLLCGPSLLDERHPLL HGAQSHRPPKG*GVRANNAGL AGSSIYLQPRCGIHEVKPSGLLS REGQLQLQS
11884	42252	C	11955	114	362	
11885	42253	A	11956	1	211	
11886	42254	A	11957	395	547	
11887	42255	C	11958	412	641	
11888	42256	A	11959	3	905	SNNSPTSASRVAGITGVHRHCV NWWVLGLTDFKNEAVDPRAW TTKSKTPPQNKTKQENKNEDV GRDQVFEWLVTEEVSLSLKG EKLHWKEKEVQSTGKETDARS SMRNYLMLLGPEVQEKEPVKR RLARGKAFVELAEPTRAPGNSG FPVSGGVFTPSLGA LTWICKFR VKS WAILNSQLLDTMKKGIV YKNGDRIQGNRSADNRNNGVP LTGARDMQPAMPEPPTHSMGS CAARAFPMASASCFRAPSPIDH PKAEE\WGARRGTGGQ\PTCSP GAGIHWVKPAGLLSREGQLHL
11889	42257	C	11960	482	709	
11890	42258	A	11961	1	734	MRLESD/KHLVQFVPIHKSGL EYPIGPWLPFITNSRVQEAFYH DRHSFEAVLDNAAPESVDLAE AERLAEDRLLYVALTL SAFAP LVRRRGDKKGD TDVHQSA LGR LLQKGE PQDAAGLR TICIEALCD DDIAWQT AQTDGNQPWQVND VSTALNAKTLQRLPGDNWRV TSYSGLQQRGHGIAQDLMPRL DVDAAGVASVVEEPTLTHQF PAGASRGTFWHSLFEDLFTQ PVPDNWRL
11891	42259	A	11962	21	898	
11892	42260	A	11963	1	1962	

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11893	42261	A	11964	1	313	MRFYGGLEAEDPGQKAGETTR HTEDYISQLPLQRQGIPELALQK DLFINKIYGKEFNVCSTLEDPR VHVLCRDMDEAGNHSEQTIA RTENQTPHVLTHRRELNNENT WTQGGHEHTPEPVMGWG*RPR AAKSWGNNKAY*RLYFSAFA ETRDPRTPCPSERSFY*QDLWK/ MSSMSAGRL*RIPEFMSFVGW MKLETILSKLLQGQKTKHRMF SLIGGN
11894	42262	A	11965	47	178	QQLVHTAFVIRLIRGTTEGAWR NCKQMAR*QSISLECKFMPRT
11895	42263	A	11966	2	223	
11896	42264	A	11967	2	133	
11897	42265	B	11968	179	6003	
11898	42266	A	11969	1	1125	
11899	42267	A	11970	1	360	
11900	42268	A	11971	677	1238	
11901	42269	C	11972	193	471	
11902	42270	A	11973	17	280	
11903	42271	B	11974	1	654	
11904	42272	B	11975	526	597	
11905	42273	A	11976	1	1261	
11906	42274	A	11977	170	998	
11907	42275	A	11978	1	1130	
11908	42276	A	11979	1	369	
11909	42277	A	11980	1	300	
11910	42278	C	11981	207	451	
11911	42279	A	11982	1	348	
11912	42280	A	11983	2	469	RGIREGEEFVDVLAGMEVAVG GWGRGLWLHRHQAGIRGQSLG WRCRPWVGAGGVQAASERPD LAGSIMGPEVGALRRASPVIVIQ SQAGAFSSNTTCQQFRDPCFR GRYPASPHTLSPETAHL*LLL CLPAAGVLPHTWPLLDROGWH RGHAR

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11913	42281	A	11984	1	937	MAAPLVLVLVVAVTVRAALFR SSLAEFISERVEVVSPLSSWKRV VEGLSLDLGVSPYSGAVFHER QYIPVKMKSKAFWIFSWIYAM MYVGS/HSGNHLPLLLPSQLLG FHPRSL/VALYFLFQISLQTLVIF WYFFAEMFEHSLFFVCVFQIN VFFYTIPLAIKLEHPIFFMFIQI AVIAIFKSYPTVGDVALYMAFF PVWNHLYRFLRNIFVLTCIHVC SLLFPVLWHLWIYAGSANSNFF *GITLTFNVGQRPRLKAPRASS AARSDRGAASPAAGDAARPV SGRRPWDAPPHNYLNAVPPPSR
11914	42282	A	11985	1	521	
11915	42283	A	11986	1	207	
11916	42284	A	11987	1	867	
11917	42285	C	11991	1	225	
11918	42286	A	11992	72	425	
11919	42287	A	11993	1	354	
11920	42288	A	11994	460	752	
11921	42289	A	11995	93	401	PQKKYIHIFLDSLALLPRLECSG AISAHCKLHLLVSSDSPASASQ VAGITGARHHAWLIFVFLVEM GFHH/VGQAGLELLTSGDPPAL ASQRAGVSIFILFIF
11922	42290	A	11996	2	315	
11923	42291	A	11997	615	1180	
11924	42292	A	11998	3	151	
11925	42293	A	11999	2126	2241	
11926	42294	A	12000	1	765	
11927	42295	A	12001	924	995	
11928	42296	A	12002	1	789	
11929	42297	A	12003	2	132	FFFFLVEMGFHHVVGQAGLKL TSSDRPPWPVKVLGLQARAT
11930	42298	A	12004	504	755	

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11931	42299	A	12005	1	1322	MAILPKVIYRFNAIPIKLPVTFET ELGKTTLRFIWNQKRACIGKSV LSQKNKAGGITLPDFKLYYKAT VTKTAWYVYQNRDIDQWNRT ESSEIMLHIYNHLIFDKPDKNKK WGKDSL FNKWCWENWLAICR KLKLD PFLTSHTKINSRWIKDL NVRPKTIKTLEENLGNTIQAIG MGKDFMTKTPKAMATKAKID KWDLIKLSFCTAKETTIRLLG RPPALFTASSSVLKQLALEGILI LDSRALLGFLYEARHSHSNPN HDAQNATSKKNIRDGYDKIYR QEQLARMEKTLITAGGNVK WCSHFRKQIGGQWLTLETCTK TPQPFSSTSQISTDKDGLNPQL LKMDPGHMGWCPPGMGIPWQ LSSDDR VVWLAAGSGRHPGS GFKSL/PGLLHEGSYGH****S*I *GGNS*GSSGGPQCISGEERVFR
11932	42300	A	12006	12	143	
11933	42301	A	12007	1	534	
11934	42302	A	12008	1	591	
11935	42303	A	12009	2	353	
11936	42304	A	12010	1	1923	
11937	42305	A	12011	1	465	
11938	42306	A	12012	1	784	PGWEKMRSSSVVNTQALPT AAIPRDAKGRVYYFNHITNASQ WERPSGNSSSGGKNGQGEPA/R VRCSHLLVKHSQSRPSSWRQ EKITRTKEEALELINGYIQIKQS GEEDFVESLASQFSDCKHQPKA RG/DLGAFAQQKVR LQKPF*RT RFALADGGR*AGPCFTD/SGIHII LPHLSEG WGAQAWPRGRAGRL GRPAPPCPPASGRTPHSLPPSHSI YCSHNGWEGALPDWGPFTGG PGVPHLSVPSWGC DLQTLH
11939	42307	A	12013	1	319	PRERAPRGSVGAGGEICHTSVC CCQPSWTRL.LLLITWMLL/YYS ECKPFHCSREPDNHILLK1*EF GPPSTQGGHAAPLSRSRYS CCP DRYL.LRKL.GICQEHQL.L
11940	42308	A	12014	1	1058	
11941	42309	A	12015	1	861	

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11942	42310	A	12016	1	431	IVLGGVATTVCQLNEFIMTDNA VPADVLVLTKPLGTQVAVAVH QWLDIPEKWNKIKLVVTTQEDV ELAYQEAMMNMARLNRTGGL LICLPREQAARFCAEIKSPKYGE GHQAWIIGIVEKGNRTARIIDKP RIMEVAHKWPLKM
11943	42311	A	12017	1	1020	
11944	42312	A	12018	247	1436	GERGPRMTMSTRESFNPESYELD KSFRLTRFTELKGTGCKVPQDV LQKLLLESQENHFQDEQFLGA VMPRLGIGMDTCVPLRHGGLS LVQTTDYIPIVDDPYMMGRIA CANVLSLYAMGVTECDNML MLLGVSNNKMTDRERDKVMPLI IQGFKDAEEAAGTSVTGGQTVL NPWIVLGGVATTVCQPNFEMIP DNAVPGDVLVLTKPLGTQVAV AVHQWLDIPEKWNKIKLVVTTQ EDVELGLPGRRLMNMARLNRT AAGLMHTFNHAHAATDITGVFG ILGHAQNLGQASRRNDVSFVIF NLPGAWPRWLA VSKACGNMF GLMHVTCPETSGGLICLPRAE QAARFCAEIKSPKYGEHGHQAWI IGIVEKGNRTARIIDKPRIIEVA HKWPLKM
11945	42313	A	12019	219	380	RPLQIRSHSELLGVWVPTSEF*E DITTSVVTAGLLEVSWSGRVILC SKSFPALQS
11946	42314	A	12020	1	516	
11947	42315	A	12021	1	228	
11948	42316	B	12022	56	656	
11949	42317	A	12023	1	488	
11950	42318	A	12024	3	419	
11951	42319	A	12025	1	348	
11952	42320	A	12026	1	708	
11953	42321	A	12027	25	213	
11954	42322	A	12028	1	1165	
11955	42323	A	12029	1	411	
11956	42324	A	12030	1	996	
11957	42325	B	12031	1	744	
11958	42326	A	12032	1	444	
11959	42327	A	12033	1	555	
11960	42328	A	12034	1	2241	
11961	42329	A	12035	1	408	
11962	42330	B	12036	1	423	
11963	42331	B	12037	1	507	
11964	42332	A	12038	3	529	
11965	42333	A	12039	191	319	
11966	42334	A	12040	1	660	

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11967	42335	A	12041	1	579	
11968	42336	A	12042	1	2940	
11969	42337	A	12043	1	4280	MEYYAAIKKDEFMSFVGWTW MLEITILSKLSQGRKPKRRMLSL IGSQLLTNKGTSWMENEFDELT EVGFRRTLHPKSTTEYTFSSAPH CTYLLKIDHIIASKTLTKCKRTEI ITNGLSDHSVIKLELKIKKFTQN CITTTWKLKNLLNDYVWNNEI KAEIKMFFETSENEDTMYQNL WDTFKPLCRGKFIALNAHKRR QRRSKIDIQTAQLKELEKEQQT NSKASRRQEITKIRAEALKVTETR KTLQKINESRSW
11970	42338	A	12044	1	645	
11971	42339	A	12045	3	362	LDQLLDMSYE/QLMQLYSCAQ RRRLNPLGRKKQHSLKRLRK AKK/EAPPMEKPEVVKTHLRD MIILPEMVGSMGVYNGKTFN QPEMIGHYLGFEISITYKPVKH/G RPGIGATHSSRFILK
11972	42340	A	12046	1	519	
11973	42341	A	12047	2	599	PPRRSSEDPAKMAEVEHEEGSG PFRKFTLPAAVDL/DQLLDIVPT KQFDAAVQVAAQRRRLPEPGL RRKQ/HSPA*KRLRKAKKGGPA PWRKPEVVKT/HTLRDYDHSYP EMVG/SMGVYNGK/TFNQV GDQGVCGRPCLGWAGVA*CR RDQLTPSFALGLPQPEMIGHYL GEFSITYKPVKHGRPGIGATHSS RFILK
11974	42342	A	12048	8	224	RTASYPRRFPWDHLLICPCQQL LICFLSLWIRLVFTKVSCT*NNH NMFSCVWLLLLSMIFLRFTHIA CIRNI
11975	42343	C	12049	65	163	
11976	42344	A	12050	3	187	
11977	42345	A	12051	3	689	HASDQKEIIIEPFQAVDEVERVP EDYYTGPPVYLTEVTTLQQRLLQ PDFQPVCAQLYPRHKHLLIKR SLRCRCKEHNLSKPEFNPTSIFK KIQLVAVNYIPEVRIMSIPNLR MKESQVLLTLNPNVNLTHVTL LECEEGDPDDINSTAKVVVPPK ELVLAKGDAAAEYDELAEPQD FQDDPDIAFRKANKVGIFIKVT PQREEGEVTVCFKMKHDFKNL IAAPISP
11978	42346	A	12052	1	882	
11979	42347	C	12053	152	404	

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11980	42348	A	12054	3	398	LRKIKIDLKGFSDNPDGYIDVLQ GLRQSFDLTWDRIMLLDQSLT PNEKSAAKTAAREFGDLWV/V/S FQN*SCKTNRSSNGAPDAVHD *D/PTADPWTGPLAHALMLMTL KAPLTRKSQLHDPYYAPIQEEA V
11981	42349	A	12055	2	286	
11982	42350	C	12056	261	482	
11983	42351	B	12057	1	1133	
11984	42352	A	12058	438	575	NKTRMPSLTITPLQHSTESPSQSS QTREGNKGYPNW*RGSHTVTV C
11985	42353	B	12059	50	309	
11986	42354	A	12060	1	870	
11987	42355	A	12061	148	368	ELSSCSLMSHRAIHPSEERATT T/NQQSEPGSW*GWVGANRWC HKMSSGSLGTEPCGSLACSA WTVTVQAQ
11988	42356	A	12062	405	707	RLSLQTAGCSDVPVFPSPAGPP SPA*AP*SGSAASPWPFPAPSA HVAMPAPPRHWQQLSKMPPW PPDSPVPPGCLA*AEAPPHCPV HLPASRSALS
11989	42357	A	12063	90	470	KSVHSLPPSFSSLLPWTCNRTLS KPPALPSPSRQPECRRLHCSG SRHSSCPSSSSPSFSSSPSSSS SASASPPPPSPSPAPP*LWLQPL FCSQ*QLCHCQELVHLESRLTY PYHSSNQPF
11990	42358	B	12064	1	474	
11991	42359	A	12065	1	383	MEYYAAMKNDEFMSFVGTWM KLETHLSKLSQGQKPNACSHS WMDPQRRGKRQSLSISEAGAN QFPKSVFRFFGLGDSKVGSKWS ATCACEPIHTSEYCGDRVICKTT SSLRGASFAWCSSGNGE*WFP SSMSLQRT
11992	42360	A	12066	1	384	MIITGLEDYEMGLRMEGTLEIP GHYQKDKFLAQSTPDLLLPKTS LTNPFISNQLAERQIVTFTVYP DTERDRETRNLADLKQIKIDL KFSDNPDGYIDILRGLRQSFDLT WRDIMLLLNQTLAPN
11993	42361	A	12067	152	238	
11994	42362	A	12068	89	544	
11995	42363	A	12069	62	199	SWKPSFSANYHKDRKPNTACS HS*DPAFLAPSPVP*SRPLRPPQ D

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11996	42364	A	12070	1	655	SVSGLVEKVTFEQRLKGGEGDS TVGSSGNEIFRQWPCWELSNCG SLQGDAGCSCLVVHVTFPAGSL SGDGLPTAQWLQSLVLGGR RVNSTQGHRCCHWGSVAEPCV LVKRHHAAQEGLCFSQKTPRS QVPFHLFWDPGHHTLLCSYCPS GVAGTQPAVQAVSTAV*TAAE GEPLPMSENMRCLVFCPCDSLL RMMVSSSFRVPTKDMNSSFFM
11997	42365	A	12071	1	987	MLVLGYNRKNTGQTQKQGT NASDFHFLSQLEQVVSQKSK EAQCCVLRHLGCESSAPGIPP NLGIQLLTWAVMWDPFPTTLA RAPSLALELMTQYFNNWNWV YNNITDQGESKMSKLGKERR QREGERRERKREKREKRESQR KERKREKKGKREKREKDRSDL KQIKIDLKGFSDTPDGYIDVLQ GLGQPYLTLWRDIMLLDQTL TPNERSAITA VREFGDL WYLS QVNDRKITEEREQFPTGQAVP SVDPHWDTESEHGDWCHRYLL TDVLEGLRKTRKKPM*SMISTI TQKKEENPTAFLERLREALRKH
11998	42366	A	12072	1153	1379	CLASWKEKSLHCPQRKQRLR GEELEKLLKKWKETATQIKRSYC WI*PSKSPHYLTS*KR*WNY**L GNYSINIPAS
11999	42367	A	12073	1	864	
12000	42368	B	12074	8	441	
12001	42369	A	12075	62	332	TDSPHCTDPPSRPTVPASCLRK CCGSTMPTARPIMPTLMETR*M PISPRVS WAGPRPTSWPALISST LFPRMANHWRD*SRITWFQGG A
12002	42370	A	12076	34	409	TRAAGIRHEGKPEKTGLKRNFT N/DCRKS*TSG*RSTSSRSRSPS PAPRSRSCSR/RLPAPPPLSRSG DRPQTAPSCPMWRARLPSCPGS AIPIPRPA WTRSAACCGAASRLR PFGSSSTSPQWM
12003	42371	A	12077	1054	1368	
12004	42372	A	12078	298	514	PNWFKHDVSKSESFSNMWIA KILKA/ARPA L TQCV/RNSCFL QCRHLSSVSASDLT*DNVKRQF CVSPHTES
12005	42373	A	12079	2	1613	
12006	42374	A	12080	2	106	

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12007	42375	A	12081	42	305	YNTVLPAKCLGSLICWMN*SH SDQNMQVSVERSRLRVLYAC CGLLCTAYPQHFAHRYVDKIP GYPSRAGTLTGLHPMQVRCR
12008	42376	A	12082	206	6038	
12009	42377	A	12083	1	4316	MQWEEAEKDPGSCVFRPPV ALVFPLHSKWTLVNSPPSSGDP YVPGRPQASGQLSLSPAPPYVL PGPGKIKAGNPNLSLTSYRSEV FCAHRHLHPQLVCARGHIGSA HLSVDRGSLIWEVLESTVWART NEWSPVTRTVLISALASTHIPQP CESRPPVPPEYEVTVLRSGQTA QLPPWSSSTSWRLTDPSCPKHA AWLTDLASSKGPAAGGTGFSFS QPGTLTSTRTNPLKKEKSPEDL KQIKIDLGKFSND
12010	42378	A	12084	393	991	
12011	42379	A	12085	324	438	
12012	42380	B	12086	528	598	
12013	42381	A	12087	52	574	
12014	42382	A	12088	1235	1366	
12015	42383	A	12089	1	1800	
12016	42384	A	12090	1	513	
12017	42385	A	12091	3	77	
12018	42386	A	12092	1923	2171	GAFCPTLLHGYQVLQWPGSSL PHKEGPAPALEGGHVPYRWI*A SADSQSTEAGRIGPASTG*RQYP GGEEHACCLPALLHS
12019	42387	A	12093	1	360	
12020	42388	B	12094	21	3636	
12021	42389	A	12095	1	936	
12022	42390	A	12096	1	599	
12023	42391	A	12097	1	248	VGKSSIVCRFVQDHFHDNISPTI GASFMTKTVLCGN/ELHKFLIW DTAGQER/SRQIPPLDPHENGNN GTIKVEKPTMQASRRCC
12024	42392	A	12098	1426	1572	
12025	42393	A	12099	367	513	
12026	42394	A	12100	31	661	APALPGCEHMMMAIRELKVCLL GDTGVGKSSIVCRFVQDHFHDH NISPTIGASFMTKTVPCENDFT KFLIWDTAGQERFYSLAPMY RGSGAAVIVYDFTEAGFHPL KKWVKRLKELGPEINIVMAIA GNKCDLSDIREVPLKGC*RNTA ESIGAIIVVETSAKNAUNIE/LFQ GNSRPDPHPWTPHENGNGNTIK VEKPTMQASRRCC

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12027	42395	A	12101	1	487	MDKFLDITYTLPRLNQEEVESLN RPITGAEIVAIINSLPTKKSPGPD GFTAEFYQRLISNFSKVSQYRIN VQESQAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGRIINIVKMAILPKNW KKLL
12028	42396	A	12102	1	1563	
12029	42397	A	12103	1	1449	
12030	42398	A	12104	3	1606	
12031	42399	A	12105	2	402	
12032	42400	A	12106	172	329	
12033	42401	A	12107	1	720	
12034	42402	A	12108	97	206	
12035	42403	B	12109	1	1248	
12036	42404	A	12110	1	1419	
12037	42405	A	12111	1	1387	MDKFLDITYTLPRLNQEEVESLN RSITGSEIVAIINSLPTKKSPGPD GFTAEFYQRYKEELVLLLLKLF QSIEKEATLPSNFYEASIIIPKP GRDITTKENFRPISLMNDAKIL SKILANQIQHKKFVHDEVG FIPRMQGWFNHHSKNVIQYIN RTKDKNYMIIISIDAEKAFDKIQ QLFMLKTLKSLGIDGTYLKIIRA IYDKPTVKIILNGQKLEEFPLKT GTRQGCPSPLLFNIVLEVLR AIRQEKEIKGILLGKEEVKLSLF ADDMIVYLENPIVSAQNLLKLI SNVS*V*GYKINVQKSQAFLY TTNRQTESQIMSELPFTIASKRI KYLGIQFTRDVKDLFKENYKPL LNEIKEDTNKWKIPCSWVGRI NIVKMAILPKPPLLIPRQTGSGV DLQQTPTDLQLSVLTVRRKINK QKGHPHOYLIWTSPPSKTKGRQ LLASNRKLDGE
12038	42406	B	12112	1	711	
12039	42407	A	12113	1694	4489	IYRFNAIPIKLPMTIFFTELEKTTL KFIWNQKRARIKAIRSQKNKS GGITLPDFKLYYKATVIKTAW YWYQNRDIDQWNRTEPSEITPH IYNYLIFDKPEKNEQWKGDSLF NKWCWENWLAICRKLKLDPFL TPYTKINSRWIKDLIVRPKTIKT LEENLGITIQDIGMGKDFMSKT PKAMATKAKIDKWDLIKLSF CTAKETTIRVNRQPTKWEKTFA TYSSDKGLISRIYNELKQIYKKK TNNPIKKWAKDM

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12040	42408	A	12114	1	115	
12041	42409	A	12115	58	414	
12042	42410	A	12116	6	389	VMTTGTNSRVEPRVRGRVYKK KMDKKRQEKITEAKSKDKSQM DEEKTD/DEKPKLQVELEQEQYQ DKFKRLPLEILEFVQEAAMGKGI SEDSNHGSAPI.SLSSDPGKVN KTPSSEELGGDIPGKEFDTP
12043	42411	B	12117	50	5137	
12044	42412	A	12118	1	1194	
12045	42413	A	12119	1	2559	
12046	42414	A	12120	3	406	
12047	42415	A	12121	119	423	TSSCSSEKFVITHLLKPTSVNSS KSFSLQCSIG/VQGAAIL.WRRR GSLVFRIFSFALVSPHLCGFIYL WSLTMVTYFSLNGGRSPCQA AAPQVNLGLLC
12048	42416	A	12122	3	597	ISASADNVFMSVSSPSCSCFF TLRYLWKSEKPLYYSFVDPK VAYKKREMVVNQKQKHTG RVQSSNLEKKAPSSQFNWT EEDTDRTCFHGSHLQGVLLKEK GQSLLTKNLSLYWLSLTKQF*RCY GHHVPPYEEISYFLSNRNLNLF SFLLRIKTSFL/HEEVSLVEKVL FEEKIQCKERNQDPRKVRTTL
12049	42417	A	12123	1	883	
12050	42418	A	12124	23	362	FAFNMPPEPKIVPAP*KGSKKA VTKAQNKGDEKRLSRKESYS VYVYKVLKQVHPDGTGSSKG MGIMNSFVDDILERIAGEAFL AHYNKRSTITSREIQTAVRLLLT REMYK
12051	42419	A	12125	2	405	
12052	42420	A	12126	1	398	LHSAMPEPAKSAPAPKKGSKK AVTKAQKDKGKKRKRSRKESY SIYVYKVLKQVHPDGTGSSKAM GIMNSFVNDIFERIAGEASRLAH YNNKRSTITLPREIQTAVRLLLP GELAKHAVSEGTKAVIKYTS A
12053	42421	A	12127	1	401	
12054	42422	B	12128	48	424	
12055	42423	A	12129	3	462	DAWVSGRLTELPSSCFFPIFRQ LLPVMPEPSKSAPAPKKGSKKA VTKAQKDKGKKRKRSRKESYS VYVYKVLKQVHPDGTGSSKAM GIMNSFVNDIFERIAGEASRLA HYNNKRSTITSREIQTAVRLLLP ELAKHAVSEGTKAVIKYTSK

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12056	42424	A	12130	74	504	FAFNMPEPAKSAPAPK/KGS/KK AVTKAQKQKDGKKRK/RSRQGR AYSVVYVKVLKQVHPDTWHL LLRPWGMELLSFNDIFRNGIAG LRVSLGRl*QQGVSTIHLPGEl HDGPLRLACLPGGVWPSKAVF RGAPRPFNQVNTSV
12057	42425	A	12131	53	471	
12058	42426	A	12132	1	241	FKDTCRMTFIAALFTIAKTWNQ PKCPTMWHIYTMEEYAAIK/SD EFMSFVGTWMKLETITLSKL*Q GQKTKHRMFSLIGGT
12059	42427	A	12133	1	244	
12060	42428	B	12134	1	2142	
12061	42429	A	12135	1	1962	
12062	42430	A	12136	3	393	IWMKLETILSKLSQG*KTKHR MFSLTGGNLTMRITLGHRLPSL PHRLRPCARLHLRCPWPWPPSR RRCARSTTPATPPSTATSRWSS TPPTCTCLWPSTSTGTTWPWRT SSATSCACRTTKWSMPRS
12063	42431	A	12137	2	87	
12064	42432	A	12138	1	270	
12065	42433	C	12139	1	214	
12066	42434	A	12140	1	684	
12067	42435	C	12141	1	333	
12068	42436	A	12142	1	189	
12069	42437	A	12143	215	310	
12070	42438	A	12144	2	91	
12071	42439	C	12145	1	229	
12072	42440	A	12146	1	268	
12073	42441	A	12147	1	278	
12074	42442	A	12148	2	274	WMKLETILSKLSQRQKTIHHLF SLIALFTIAKKWKPPRYLSVDK WIKKLWY/HTYTMEEYSAFKK EAILPIAIWMLKDIMLSEISQ TWP
12075	42443	A	12149	2	136	
12076	42444	A	12150	2	95	
12077	42445	A	12151	1	233	
12078	42446	A	12152	377	484	
12079	42447	A	12153	2	91	
12080	42448	A	12154	1	891	
12081	42449	A	12155	1	1194	
12082	42450	A	12156	785	892	
12083	42451	A	12157	191	317	
12084	42452	A	12158	410	520	
12085	42453	A	12159	683	796	
12086	42454	A	12160	830	927	

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12087	42455	A	12161	18	539	PTDP*LGIVQKEVYKSCYKIDIC T/RVCVPAALFTIANTWNQPKC TSMIDWVKKMWHIYTMEEYVA AIKTDEFMSFAGTWMKLETHL RKLSQGQKTKHRMYSLIGGNL TMRTFGHSAGSHHTPGPIMRCG AGGGIALGEIPNVNDELMTGTAN QHGTCPMQQNCTLCTCTLKLK V
12088	42456	A	12162	1	108	ASTAGVSYYVAQAGLKLGLS LSKCRDYRCEPPCPE*MSLYKV MAMARKAMSLYIYFFLDEFM YFAGTWMKLETHLSKLSQGQK TKHRMFSL*GVSYYVAQAGLK LLGLSLSKCRDYRCEPPCPE
12089	42457	A	12163	1	701	
12090	42458	A	12164	274	435	
12091	42459	A	12165	1	3658	
12092	42460	A	12166	749	856	
12093	42461	A	12167	1	598	
12094	42462	A	12168	538	664	
12095	42463	C	12169	1	873	
12096	42464	B	12170	177	325	
12097	42465	B	12171	1	1245	
12098	42466	A	12172	1	3313	
12099	42467	A	12173	1940	2060	
12100	42468	A	12174	1	1213	
12101	42469	B	12175	155	559	
12102	42470	A	12176	2	321	PAPRGGAYRGRQTSLSGGLHP V*ASWLLCLPKQAWAM/VGRP PQASLLPCSLISDCCASNQRDSV GVGPSEPCAGYNLLLCRFLSQS EKHSIRVGAVDCSCSYLAIL
12103	42471	A	12177	1	519	
12104	42472	A	12178	1	477	
12105	42473	A	12179	119	375	KRTQT*AIAGAPPPASLPPCSLIS DCCASNE*GSVGIGPSKPGAGY NLLCHLISPSISPTSSPKSDTCPI ADFSNKS PDRSSAGDILLAMQS LGSMAIFLILILPTREHGKFFHLF VSSFISLSSGL
12106	42474	B	12180	1	363	

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12107	42475	A	12181	1	1309	MAEGEEGTSYMAAGERVVAIA LIDGFRPLTLESTFFNSGSCSKL EQHSTYLGDFAFDGTTIKQDFR LLGQTSVDRLLQLSQGQAVPEP KQHIGPKQKYRSTGPNRALR NNAAYLQFLIFGNLEKTKPWG KDSLLIKVFEEAVLWIECFAFIF YDARGVLIVVQVDSCKLEQHS TLSRALLIYKGFRCFRNHHQTG FSPAGANQRGPLAATLSGPGGE GQSAVARLTGEKKNHPGAQYA NRLSPRVGRFINAAGTTGFTG KRAVSATQLMDFADFGTTIKQ DFRLLGQTSVDRI.LQLSQGQA VKGNNQLLPVSLVKRKTTLAPNT QTASPRALADSLMQLARQVSR LESGHLISDCCASNQPDVSGVG PSEPGAGYNLVVRHFLSPSEKH SIRVGVTRFSRCRPSPLPLTQKG NSLTPCASQLRQCLALLRLR*R AISCPCSHW*KEKPPWRPIRKP LPARWPIH*CSWHD RFPD/CESG HLISDCCASNQPDVSGVGPSEP GAGYNLVVRHFLSPSEKHSIRV GVTRFSRCRPSPLPLTQKGNSLT PCASQLRQCLALLRLRH
12108	42476	B	12182	1	1335	
12109	42477	A	12183	1	1675	
12110	42478	B	12184	57	1530	
12111	42479	A	12185	1	1419	
12112	42480	A	12186	1	574	RVDDFVRQTRPSAQAAAEKM AANQPPPLMMKHSQTDLVSR KTRKILGVGGEDDDGEV/HRSP ISQALGTEIKFTIREPLGLTVWQ FVSAVLFSGIAIMALAFPDQLY DAVFDGAQVTSKTPIRLYGGAL LSISLIMWNALYTAEKVIIRWTL LTEACYFGVQFLVVTATLAETG LMSLGIRLTRSSRRGR
12113	42481	B	12187	79	387	
12114	42482	A	12188	1	908	
12115	42483	A	12189	2	70	
12116	42484	A	12190	1	1158	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
12117	42485	A	12191	2	611	FVSVPSVLLGLQFWRSERD/TA RLQ SARWRVERGR LKELLSRQ RPRRREEVVVGREVCRTMEV RASLQKIVSNGDEQLEKAMEEI LRDFEKRPSLLVDCQSSSEISD HSFGDIPASQTNKPSLQLILDPS NTEISTPRPSSPGLPEEDSVLF NKLTYLGC MKVSSPRNEVEAL RAMATMKSSSQYPPFVTL YVP
12118	42486	A	12192	3	497	
12119	42487	A	12193	1	804	
12120	42488	A	12194	1	1243	MAPVEHVADAGAFRLHAAL QDIGKNYITIREVVTEIRDKATR RRLAVLPYELRFKEPLPEYVRL VTEFSKKTGDYPSLSATDIQVL ALTYQLEAEFVGVSHLKQEPQ KVKVSSSIQHPETPLHISGFHLP YKPKPPQETEKGHSACEPENLE FSSFMFWRNPLPNIDHELQELLI DRGEDVPSEEEEEENG FEDRK DDSDDDGGGWITPSNIQIQQE LEQFDVPEDVRVWLA*PPDFA MQNVLLQMGLHVLAVNCMLI REARSYILRCHGCFKTTSDMSR VFCSHCGNKLKKVSVTVSD GTLHMHFSRNPVKVLPNPRGLRY SLPTPKGGKYAINPHLTEDQRF PQLRLSQKARQKTNVFAPDYIA GVSPFVENDISSRSATLQVRDS TLGAGRRRLNPNACRKKFVKK
12121	42489	C	12195	164	350	
12122	42490	A	12196	1	378	
12123	42491	B	12197	265	1539	
12124	42492	A	12198	1	2511	
12125	42493	A	12199	1	1077	
12126	42494	B	12200	38	1451	
12127	42495	A	12201	1	207	
12128	42496	A	12202	1	197	
12129	42497	A	12203	1	216	
12130	42498	A	12204	1	335	
12131	42499	A	12205	1	174	
12132	42500	A	12206	1	1309	
12133	42501	A	12207	1	1266	

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12134	42502	A	12208	1	590	IDRFDA PCGLEELEDHEDEFNE EDERAIE MYRRRLAEWKATK LKNKFGEVLEISGKDYVQEVTK AGEGLWVILHL YKQGIPLCALI NQNL SGLARKFPDV KFIKAISTT CIPNY PDRNLPATILVYPG DGIN G/QFIGPLSVGGMNL TRDELEW KLSGSAIMTDLEENPKKPIEDV LLSSVRRSGPHEEGQRFGR
12135	42503	A	12209	291	416	SHYLKIHAEKLESEYDQISPPNSQ PDKENPVLST**SIQRRHMTLFLK MNLKILKYRKPEA*SQR LVSK R*KHSIRGSGINLSFVPTGFQIVP FHLFETSLWL
12136	42504	A	12210	437	773	DYTTIGELKTAIQRSKINFCPIH SHSSHNAKSFVITVTL LHRHLL *KVSYNKVQSLFIQC GFSEAGA GVYNYCPPRQRQPGDKPRW RWRGRGNRCSANSHGLQLYA
12137	42505	A	12211	1	1183	
12138	42506	A	12212	1	459	
12139	42507	A	12213	1	513	
12140	42508	A	12214	91	1168	
12141	42509	A	12215	323	429	
12142	42510	A	12216	870	1305	SPGLPHCWQPCRARSRTD VV NVLVSGSGSGAYKEPAILVGPE NLTLTVHQTAVLECVATGNPRP IYVSWRLGWPPNP TKAQEQRRA KTESQRKQPRDKARENQPKAA RPKRAAPKSHEAARKTNPTTAS TKRQAAPTNTPKESS
12143	42511	A	12217	1	2695	
12144	42512	A	12218	1	258	
12145	42513	A	12219	1	624	
12146	42514	A	12220	247	425	
12147	42515	A	12221	31	858	LLEIVNSSIQPEKQAGWLSQAV HGAPDGNRPM LHPETSPGRG HLLAVLLALLGTTWAEVWPPQ LQEQA PMAGALNRKESFLLLSL HNRLRSWVQPPAADMRRLDW SDSLAQLAQARAALCGIPTPSL ASGLWRTLQVGNWMLLPAG LASFVEVVS LWF AEGRYRHA AGE*ARNATCTHYMQLVWATS SQLCGGRHLCSAGQAAIEAFVC AYS PRGNWEVNGKTI VPKKG AWGSLCTASVSSLLKAWDHAR GLLGGPRETLGKEPTEPW TALK
12148	42516	A	12222	1	1519	
12149	42517	A	12223	1	789	

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12150	42518	A	12224	1	505	ATEDPGVAMGRPARCYRYCK NKYPKSRFCRGVPDAKIRIFDL GRKKAKVDEPFLCGHMSVDEY EQLSSEALEAARICANKYMKVS CGKDGFIHVRRLHPFHVIRINK MLSCAGAD/RIHISKKWGFTKF NADEFEDMVAEKRLLIPDGC GV KYIPSRGPLDKWRALHS
12151	42519	A	12225	135	828	RFWVSPHGPAAPARCYRYCKN KPLPKVLRFCRGVPDAKIRIFD PGAERKQKVE*VFRFCGHMVS DEYNQLSS*ALEVAARNLCPIS TMVKS\CGKDGFIHVRRLHPF HVIPHQTRCCSCAGADRLQTG MRGAFGKFPQGTVARVHIGQVI MSIRTKLQNKHEV\DALRRAK YFKFPGRQ/KIHISKKWGFTKFN ADEFEDMVAEKRLLIPDGC GV YIPSRGPLDKWRALHS
12152	42520	A	12226	2	367	
12153	42521	A	12227	2	376	QTYSLRRAIPRHIIIVGFTKVEM KEKVLRAA/NKPIRLTVDSLAFET LQARKEGGPIFNILKEKNFQPRI SYPAKLSFISEGEIKSFDTKQML KDFVTTRPALQELLKEALNME RNNQYQPLQKHAKW
12154	42522	A	12228	1	714	
12155	42523	A	12229	122	939	YPGKQGLEWTSNKIQQTCS*GS SLLLEGKLTNRKDIHTKTPSVRH/ RSSKAKERVSVIEDQMNKRE EMFREKRVRKNEQSLQEIWEY VKRPNRLIGVPESDGDNGTKL ENTLQDIIQQYFPNLAQANIQI QEIQRMPPQRCSRRAPRHIIVR FTKAEKMKMLRAARGKRV THKGKPIRLKVDVLAETLQARR EWGPIFNILKEKNFQPRISPAK LSFISKGEIKSFDTKEMLRDFVT TRPALQELLKEALNMERNRY QPQQKHAKL

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12156	42524	A	12230	1	1043	MGDFLHSTDNRNYLIKFWAKLS AKKTPANSSSPLGDHQHPCITK NLQIPEKWLIGLLLPLKADLLK EDAGTHCKEAKNLDERLDEWL TRINSVEKFLNDLMELKTMAQE LHYACTSFSSQFDQLEERSVIE NQMSEMKREEKFRKRVKRNE QSLQKIWDYVVKRPNLRLTGVP SDWENGTKLENSLDIIEQENFP NLARQANIHIQEIQRMPQRYSS RRATPRHLIVRFTKFEMTEKMN RAAREKGQVTHKGKPIRITADI SAETLQARREWGPIFNILKEKN FQPRISYPAKLSFISEGEIKSFTD KQMLRDFVTTPTLQELLKEAL /NMERNNQYQLQKHAKL
12157	42525	B	12231	1	1275	
12158	42526	A	12232	1	1584	
12159	42527	B	12233	1	1023	
12160	42528	A	12234	1	2052	
12161	42529	A	12235	5160	6183	VSKHPQASAGDTQTNRVWSGP PANSRPAEAGPDC*KEN*QTE RTS/WQNPICMSPSSKTKEAKNL DKRLDEWLTRINSIEKTLNDLM ELNTMARKLRDACSFSQFDQ VEERSVIEDQMNMCKREEKF REKRIKRNKQSLQEIWDCKVRP NLRLIGVPESDGENGTLENTL QDIIQENFPNLARQVNIQIEIQ RTFQRYSSRRGTPRHIVRFTKV EIKEKILRAAREKGRVTHKGKPI RLTAVLLAETLQARREWGPIFN ILKEKNFQPRVSYPAKLSFISEG EVKSFTDKQMLRDFVTTTPAL QELLKEALNMERNRNYQLLQK HATLSRPSMLG
12162	42530	A	12236	1	975	
12163	42531	A	12237	3	1186	
12164	42532	A	12238	1	906	
12165	42533	A	12239	1	1882	
12166	42534	A	12240	1	1394	

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12167	42535	A	12241	1	4935	MGPGRARLALLAVLALGTGDP ERAAARGDTFSALTSVARALAP ERRLLGLLRRYLRGEEARLRDL TRCNDETTITYLLDKRLTLVLTAA NIPYSSPENGAKRRRQDAFPPIH YNTQDALLQYLSGVGWGAPPA AQAHRDAPFVDSIAQVLLRTSG GSAEASGWSLRSRWAVGGATG SWVLSKGDRAASLGERVVTGWA TLNVGRSFAYCLTTCVQPPLDV GPRKEHAPRPPSLPTSTRQRGQ SEKSDANGRRRKQKT
12168	42536	B	12242	88	1014	
12169	42537	A	12243	686	1920	IKPQRWGKKQNRKTGNSKKQS ASPPPKERSSSPATEQSWTENDF DELREGEFRSSVITNFSLEKEHV VTHRKEAKNLEKKILDEWITRI TNAEKSLKDLMEKLTQAQLR NECTNLSNRCDQLEETVSAME DQINEMNEMKQEGKFREKRIK RNEQSFQEIIGDYVVKRPNLHLI GVPESDGGQNGTKLENTLQDIH ENFPNLAQANIQIEIQRTPO RYSLRRAATPRHIVRFTKVEMK EKVMLSAAAREKGRVTHKGKPIR LTTADLSAETLQAQKTEWGPIF NILAKEKNFQPRISYPAKLSFIS EGEIKYFTDKQMLRDFCHHQG LPLKELLKEEALKHWKGTTRY QPLAKTLPKYRSTRQKVNKDT QELNSALHQADLIDYRTLHTK STEYTFQHHHTPIPKLTT
12170	42538	A	12244	1	633	
12171	42539	A	12245	3	109	
12172	42540	A	12246	2	575	
12173	42541	A	12247	1	237	
12174	42542	A	12248	1	1065	
12175	42543	A	12249	2	338	
12176	42544	A	12250	1	1319	
12177	42545	A	12251	1	744	MQKALCAAPDLGTFVTVLTPPP GAQIGSRRRERSKVPYIVRQCVE EIERRGMEEVGIYHVSGRVAA DIQALKAADFVN/NRTMHSSWE ESDELLKARDDPHSGQHSRDG ALAKAGMADKKDMSVMMSET DMNAIAGTLKLYFRELEPEPLFT DEFYPSFAEGIDRLERVAEKEA VNKMSLHNLATVFGPTLLRPSE KESKLPANSPQITMTDSRSLV MSQVEVLLYFLRLEAIPALDSK RQSILFSTDV

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12178	42546	A	12252	1	507	
12179	42547	A	12253	1378	4280	STPMAVAGPLGRPWSTSPTRAS TSGASWKGRRARARSCAARAPL SRRSALPGPAGTPPPGVLRIEA AIPRTAAPMRTSPPARRTSPLAS PAACPQAPPTACSGTKAALPR RTRNSPSTAAVPPRRSAISGTGT ARLSCPRPPSWASARPGRSOPT MTRAPSMETQMARSEHLDTA ALQTGQRSSAGTKMGCPPLMT RPPHRTPTSAARAGAAGMRWSR EP*SPLK/RSELDLEKGLMRK WVLSGILASEETYL
12180	42548	A	12254	1	1109	MRTPYKTSPPMRMLYMTSLMTP TRHANEDAVDDIAYKDTVQDI TSEDAVYDIANEDVYDIANED ALQDIANEVAYDIANEDIVYD IANEDALYDITNEDAVYNIANE DAVYGIANEDAVYEFANKHAV YDIANEDTVQDICKEDAANK CYPPGFFPIRCRHEHLPVCIIDVI CSLIKCRHEHLPSSLIQDRLGA QASRRERSKVPIVIRQCVEIER RGMEEVGIYRMSGVAADIQAL KAAFNVSERCPAQDGMVWVA VVSAMRSQSAPRPHVTSFSVS FLHLSGSSRRPLHFRALSNNKD VSVMMSEMDVNAIAGSLKLYF RELPEPLFTDEFYPNFAEGIGEH WRPWPHGRRLLHVHCCPQRL
12181	42549	A	12255	1351	4308	WKGRRARARSCAARAPLSRRSA LPGPAGTPPPGVLRIEAAPRT AAPMRTSPPARRTSPLASPAAC PQAPPTACSGTKAALPRTRN SPSTAAVPPRRSAISGTGTARLS CPRPPSWASARPGRSOPTMARA PSMETQMARSEHLDTAALQT GQRSSAGTKMGCPPLMTRPPH RPTSAARAGAAGMRWSREPWS PLK/RSELDLEKGLMRK WVLS GILASEETYL SHLEALLPMKPL KAAATTSQPVLTQS
12182	42550	B	12256	1	1017	
12183	42551	A	12257	2310	2834	EEKYNNMQTLRRAEDVFPFVIG VAAHKGGVYKTSVSVHLAQDL ALKGLRVLLVEGNDPQGTASM YHGWWPDLHIHAEDTLFPYL MLRLAIETVAHDYDVIVIDSAP NLGIGTINVVCAADVLIPTPAE LFDYTSALQFFDMLRDLKKNV DLKGFEPDVRILLTKYSSNSNGW

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12184	42552	A	12258	106	108	NFLFVLRRLQWVVGGLCW*AAE LNKVCL
12185	42553	A	12259	1	901	
12186	42554	A	12260	23	482	KPRELGPISPVWLPPDRLPERPQ RRRPSGVDPGWSWLGSGCGSTG CSALMSCSCGSTPLLSLALKVT PGGVVLGAPSGSEDGS*PNRKAC GSEMEICLTTRGVWGPEVALG VGGGLQQSCRAPCGGLPKLLRS WSQSSLSNPSGRGASSGEAA
12187	42555	A	12261	1	1938	
12188	42556	A	12262	1	2235	
12189	42557	A	12263	43	1827	THVRLAGARASPRAPRLRPKP RPQGLPCLPGLRRARLEGGARG RADEMFLPLPAAGR VVVRRL AVVRSGRSLSLADMTKGLVL GIYSKEKEDDVPQFTSAGENFD KLLAGKLRETLNISGPPLKAGK TRTFYGLHQDFPSVVLVGLGK KAAGIDEQENWHEGKENIRAA VAAQCRIQDLELSSVEVDPG DAQAAAEAGAVLGLYEYDDLK QKKKMAVS AKLYGSGDQEA W QKGVL FASGQNLARQLMETPA NEMTPTRF AEIIEKNLSASSKT EVHIRPKSWIEEQAMGSFLSVA KGSDEPPVFLEIHYKGSPNANE PPLVFGKGITFDSGGISIKASA NMDLMRADMGGAATICS AIVS AAKLNL PINIIGLAPL CENMPSG KANKPGDVVR AKNGKTIQVDN TDAIEGRLLADALCYAHTFNP KVLNAAATLGAMDVALGSGA TGVFTNSSWLWNKLFASMET GDRV*RMPLFDHYTRQVVD C QLADIVNNIGKYRSAGACTAA AFVKEFVTHRKWAHLDIAGVM TNKDEVPQSTGKA*LGPRTRL IEFLLRFSQDNCLVQILKNVFH SVLNWTVELKKVFE
12190	42558	A	12264	1	405	GIRSAEVGKHLAHILLSRQQGR RPVTLIGFSLGARVIYFCLQEM AQEKDCQGIIDVILLGAPVEGE AKHWASLSGRVVSGRINGYCR GDWLLSFVYRTSSVQLRVAGL QPVLQDRRVENVDLTSVVS G
12191	42559	A	12265	1	1072	
12192	42560	A	12266	105	514	

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12193	42561	A	12267	44	872	NARPWWVRLGLLIEFRRRGLSCRE RAREMEMGRRRIHLELRNRTSPD VKELVLDNSRSNEGKLEGLTDE FEELEFLSTINVGLTSLANLPKL NKLKLELSDNRVSGGLEVL EKCPNLPHLI*GGNKIKDLSTIE PLEKLENLKSLLDFNCEVTNLN DYRENVFKLLPQLTYLDGYDR DDKEAPDSDAEGYVEGLDDEE EDEDEEEYDEDAQVVEDEEDE DEEEEEEEDVSGEEEEEDEKGY NDGEVDDEEDEELGEEERGQ KRRKREPDEGEDDD
12194	42562	A	12268	1	388	KRGAAMDGRVQLIKALLALPIR PATRRWRNPFPFETFDGDTDR LPEFIEQTGSYMFDVENTFSSDA LKTALPQSLPSIASHRQTAAPS DLDSPRRYLGWQSLDSDSDS WPPPKGSVTFSETYFLPTP
12195	42563	A	12269	1	127	
12196	42564	A	12270	5	434	ISRLYLDGLAGPHTASAAEAS DRSEDLRWTVCAQLIQUALLAL PIRPATRRWRNPFPFETFDGDT DRLPEFIVQTCSYMFDVENTFS SDALKVTFLITRLTGPAQWVI PYIKKESPLLNDYRGFLAEMKR VFGWEDDED
12197	42565	A	12271	515	1137	
12198	42566	A	12272	1	762	
12199	42567	A	12273	1	468	
12200	42568	A	12274	2716	3411	KREEETKKKSKREMEVVKKKQ CTYSFKSQGKFLSTHARQFSIGS QPISASQTVEEIMKSILTLQSQV NSLAAVTLQNR*GLDLLTAEGK GLCTFLGEECCFYTNQSGIA*D ATQRLQEKASEIRRLSNSYTNL WSWATWLLPFLGPVAAILLLL AFGPRIFNLLVKFVWSRIEAIKL QMVLQIEPQMSSNNFYRGPLD *PAGTSPGLESSLKDDTTAKPL LRPYAGSS
12201	42569	A	12275	8312	9221	
12202	42570	A	12276	74	471	
12203	42571	A	12277	4043	4159	LFCQSGFHSLLTPSTATCSTIR* VATSRRLRPVFTCRRS
12204	42572	A	12278	1	1332	
12205	42573	B	12279	29	1316	
12206	42574	A	12280	1	580	
12207	42575	A	12281	2	710	
12208	42576	A	12282	1	1559	
12209	42577	A	12283	1179	1490	

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12210	42578	A	12284	2	313	
12211	42579	A	12285	599	743	GALART*PPQQRWVSCPR/GVP/ GAL*REFTMFLSLQAENSIDFVS RELCAHSIRKLQAHVLLIK*VFI K
12212	42580	A	12286	208	398	
12213	42581	A	12287	716	1069	
12214	42582	C	12288	326	577	
12215	42583	A	12289	188	590	
12216	42584	A	12290	860	1121	VPFLTSWVNVGFKSSALHSSAL LQFWLTLWE*LPAWARCCCL PNGSFWGPRSSRLDVAWERPV APGWREVSPLLSELWTAASGP YG
12217	42585	B	12291	1	1614	
12218	42586	B	12292	1	1080	
12219	42587	A	12293	3	219	
12220	42588	A	12294	890	1094	VESGTHLGQYKIYFGFLYQKKF SLQSHGYILFGCPQYW/ITSDC PSIPCMWYSRTL*VTWSKKQVT SE
12221	42589	C	12295	1	3912	
12222	42590	A	12296	881	1151	
12223	42591	A	12297	1	1323	
12224	42592	A	12298	1817	2284	VWDGSILYQKLGAIDLGLSS*VI PLASSLSQYPLPSSFIQRILNT YSVKGLRSWTVNEDRVDAVSS GGIWLQVEASLVLY*MLYFSIIT LLIILGLVHVNFKILDSSSELITD KLCGGLGFTLYTYSKLI*SDVTF PRAFASTQTSMLTKYTVE
12225	42593	A	12299	1	1109	
12226	42594	A	12300	1	367	
12227	42595	A	12301	1	531	
12228	42596	C	12302	1371	1746	
12229	42597	A	12303	1	645	
12230	42598	C	12304	387	680	
12231	42599	A	12305	655	2498	
12232	42600	A	12306	1	528	ENLGNTQDTGMGKDFMTETP KAMTTKAKIDKRDILKLSFCT AKETTIRVNRQPTWEWEIFAVY PSDKGPISRIYKQLKQIYKKKSN NPIKKWAKNNRHRFSKEDIYV AKKHMEKSSSLVIRKMHIKTT VGYHLMPPVRMAIHKSGNNRC WRGCGE/C*WEGQLVQPLWKT VWQ
12233	42601	A	12307	1	1359	

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12234	42602	A	12308	1968	2648	TQTNLQEQKNKQLHQKVGKGYE QTLKRRHLCSQQTHMQPTDT WKNAAHQLAIREMQIKTMTMY HLTPLRMAIHKSGNNSCWRGC GEIGTLLHCWWDCCLVQPLWK TVWRFLKDLESEIPFDLAIPLLCI YPKDYTSFCYKDTCTCMFIAAL FTIAKTWN*PKCSSVIDWIKKM WHIY/TTMEYYGAIKRNKIMSF AGTWMKLDAILSKLTQKQKT KLRMFLLSIRS
12235	42603	A	12309	1	403	
12236	42604	A	12310	3	264	FFYAHIMFIAALFTIAKTWNQS KCTSMIDWIKK/MWHIHTMEY YAAIKR/RGFMFSFTRTWKLEA IILSKLTQEQTKAHHMFSLIRGS
12237	42605	A	12311	79	432	
12238	42606	A	12312	1	933	
12239	42607	A	12313	70	675	
12240	42608	A	12314	1	339	
12241	42609	A	12315	3	422	
12242	42610	A	12316	1	471	
12243	42611	A	12317	1	963	
12244	42612	A	12318	375	542	ENDKARRSDTPSML*WVEGMK *SVKAPHTLHLASDYVLEPWG GESATFIPASWDC
12245	42613	C	12319	1	2148	
12246	42614	A	12320	1	1881	
12247	42615	B	12321	1	1074	
12248	42616	C	12322	143	439	
12249	42617	C	12323	123	362	
12250	42618	A	12324	474	603	NHKNPRRKPRQYHSGHRHGQG LHV*NTKNNGNKSQNGQMGSN
12251	42619	A	12325	5169	5756	CPSLPPPHGKPAACPRSPPGGC CTPRSARTVPRGLSENSQTKCH SADLPPEGPRVFWTPPGTGAAP APPAPAPGPARCGPRRCHAWPP QRSSGAGRSPPPRHFAEFLKM VAFLRILILRAVSLRLSLDLLEIS* G*RP*GPSWGGPPQSTPSAASA ASKTSSPRRWSTPAWAFSLARA HPRWVAPSTAAQCTAAP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, \possible nucleotide insertion)
12252	42620	A	12326	21	98	ESWLVLGRRKAGRLIGACGFEP PHFLTLDLEMHDRDSCPLDCKVY VGNLGNNGNKTELEAFGYYG PLRSVWVARNPPGFAFVEFEDP RDAADA VRELDGRTL\CG\CRV RVVELVRMGEK\RSRNRGPPPS\ WGRPRD\DYRR\RSPPPR\RRSP R\RRSFS\RSRSRSL*ERVGWC WAGGKREDSSSERVDSRRIF
12253	42621	A	12327	919	1043	
12254	42622	A	12328	460	657	CFSPGMWQKTHSRKHSFGAICP INPVGEC\VRKIKQLD*ITWINA I*LPLRDGLFYFLNFPFCCRG
12255	42623	A	12329	1	2235	
12256	42624	A	12330	1	255	
12257	42625	A	12331	2	429	CRADLNSRIDDFVPNPSVAVSG ASYAVA AVMTHYKAADSKR EQFRKYFEKSGVLDLTKVVLV ALYEEPE\KLNSALDFLKHHLG AATPENPEIELLRLEAEMKEK YEAIVEENKKLAKLAQYEP QEEKRAELGFFSV
12258	42626	A	12332	670	860	
12259	42627	A	12333	2	450	VNKAGGLIYQLDSYAP\RAEAE KTFYSYPLDLLKLHDERVLVAF GQRDGI RVGHAVLAINGMDVN GRYTADGKEVLEYLGNPANY VSIRFGPR\LTNEKMLASMF HS\KFVVLADP\RQAGIDSLLRK IYEIYSDFA\KNPFYSLEMP
12260	42628	A	12334	1	2034	
12261	42629	A	12335	1	324	
12262	42630	A	12336	2	694	FGTRGKAAMAIFSVYVVKAG GLIYQLDSYAPRAEAEKTFYSP LDLLKLHDERVLVAFGQRDGI RVGHAVLAINGMDVNGRYTA DGKEVLEYLGNPANYPVSRFG RPR\LTNEKMLASMFHSLFAI GSQLSP\EQSSGIEMLETDTFK LHCYQTLTGK\VV\ADPR\Q AGIDSLLRKIYEIYSDFA\KNPF YYSLEMP\IRCELFDQNLKLALEV AEKAGTFGPGS
12263	42631	A	12337	2	1658	

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12264	42632	A	12338	3	997	VQKPNRQWRLVQDLRIINEAV VPLYQAVRNPYTLSSQIPEETG WFTVLDLKDALFCIAVHPDSQF LLAFEDPLNPISQLTWTVLPQG FRDSPHLFGQALADLSQFSYL DTLVLRVYVDDLLAAPSETLCH QATQVLLNFLATCGYKVSCLK AQICSQQVKYLGLKLSKGTRAL SEERIQLAYPHPKTRKQLRGL LGITGFCQIWIPRYSEIARPLHTL IKKTQKANTHLVRWTPEAEAA FQVLKKALTQAPVLSLPTGQDF VSLYVTEKTGIALGVLTQHYGE ERNs*LPTEYLSNIRKPLGDYV WLYRNLKRQSYTARVIRKER
12265	42633	A	12339	3	421	
12266	42634	A	12340	3	4804	KRLNIEQKTEVAFSEAVWMQ PSVLLDDLADIAGLPAVPEHE HSPDAVQSQRALAHNDMIKE FISMGSVALIATSQSQQSLHPL LVSAQGVHIFQCVQHQPNNQE QRCEILCNVINKLDCDINKFT DLDLQHVAKETGGFVARDFTV LVDRAHSRLSRQSISTREKLVL TTLDLQKALRGFLPASLRSVNL HKPRDLGWDKIGGLHEVRQIL MDTIQLPAKYPELFANLPIRQRT GILLYGPPGTGKTL
12267	42635	A	12341	1	2223	
12268	42636	A	12342	1	3864	MQWEEAEKDPSGSCVFQRPPV ALVFPLHSKWTLVNSPPSSGDP YVGRPAQSGQLSLSPAPPYVL PGPGKIKQAGNPNLSIYRSEV FCAHRHLHPQLVCARGHIGSA HLSVDRGSLIWEVLESTVWART NEWSPVTRTVLISALASTHIPQP CESRPPVPPEYEVTVLRSQGT QLPPWSSSTSWRLTDPSCPKHA AWLTDLASSKGPAAGGTGSFS QPGTLTSTRINPLKKEKSPEDL KQIKIDLGKFSND

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12269	42637	A	12343	204	963	DCACTFHCRSATKIVKDLKAQ GLVKPCNSPCSTPILGVQKPNG QWRLVQDLRIIDEVVVVYVDDL LLAARSKTLCHQATQALLNFLI TCDYKVKPKAQLCSQKVVKYL GLKLSKGTRVLSEERIQQIPAYP HPKTPKQLRGFLGITGFCRIWIP RYSEIARPLYTLIKKTQKADTH LVEWTPAEVAFQALKEALTQ APVLSLPMGQDVPLYVTEKTI ALGVLGVLTVQVRG/LSLQPMAY LSKEMDVVAKGWPH
12270	42638	A	12344	1	1178	MPESPTLLGRDILAKAGAIHIL NIGEGTPVCCPLLKEGINPEVW ATEGQYGRAKNAHPVQVKLK DSASFYQRYPLRPEAQQLGQ KIVKDLKVQGLVKTCNSPCDTP ILGVQKPNGQWRLVQDLRIIDE AIVPLYPAPNPYTLLSQIPEEA ELFTVLDLKDAFFCIPVHPESQF LFAFEDPSIPMSQLTWTVLPQG FRDSPHLFHHTLAQDLSQFSYL DTLVLCPLRNQOECHQATQV LLNVLATCGYKVKSKQAQLCS QQVKYLGVLKSKGTRAL/QQ*R TDRT*LSSTNSCNLRHSRGPSSRG SLD*SQPOLVY*WKFFCRKRTS KRGVCSGQ**WNT*KKSPHSRN *CSAGGTNSPPSGTRIRRRKGL IRIYMLPLILSAPYDHLH
12271	42639	A	12345	1	841	
12272	42640	A	12346	3	1428	
12273	42641	A	12347	2	268	
12274	42642	A	12348	1	897	
12275	42643	B	12349	1	1650	
12276	42644	A	12350	232	1002	TPGSTVHAPEADQGLQKIVKDL KAQGLVKPCNSPCSTPILGVQK PNGQWRLVQDLRIIDEVVVVYV DDLLLAARSKTLCHQATQALL NFLITCDYKVKPKAQLCSQKV KYLGLKLSKGTRVLSEERIQQIP AYPHKTPKQLRGFLGITGFCRI WIPRYSEIARPLYTLIKKTQKAD THLVEWTPAEVAFQALKEAL TQAPVLSLPMGQDVPLYVTEK TGIALGVLGVLTVQVRG/LSLQ MAYLSKEMDVVAKGWPH
12277	42645	A	12351	1	2217	

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12278	42646	A	12352	1	6530	MWGSDDLRLAGAGGGGAAVTVA FTNARDCLHLPRRLVAQLHLL QNQAIEVVWSHQPAFLSWVEG RHFSQDQGENVAEINRQVGKQL GLSNGGQELHAVSLEQHLLDQI RIVFPKAIFFVWVDQQTIFYFIQI VALIPAASYGRLETDTKLLIQPK TRRAKENTFSKADAIEYKKLHS YGRDQKGGMMKELQTKQLQSN TVGITESNENESEIPVDSSSVAS LWTMIGSHFSQSEKKQETSWG LTEINAFKNMQSKVVPL
12279	42647	A	12353	1734	4349	MPNRACFQCGLQGHEKDKCPS RKPVQCLTIESQEVNCLLDAGA AFSVLLSCPGQLSSRSVTIRGVL GQPVTRYFFQPLSCDWGALPFS HAFLIMPESLTPLLEIEILVKAG AIIHLNIGEGTPICRLLFEEGISPE VWATEGQYQGAKNHAFVQVK LKDSTSPYQRYPLRPEAQQR LQKIVKDLKAQGLVKPYSSPCN TPH.GVQKPKRQWRLVQDLRII NEAVFPLYPAPSPYTLSSQPEE AEWFTVLDLKDAFFCIPVHPDS QFLFAFEDPSNPTSQLTWTVL QGFRDSPHLFGQALAQDLSQFS YLDTPVLQCMDLLLAARSET LCHQATQALLNFLTTCGYKVS KPKAQLCSQVVKCLGLKLSKV TRALSEERIQPIIAYPYPKTLKQ LRGLGITGFCRIWIPRYGKIAR PLYTLIKETQKANTHLVRWTP AEAFAHALKKALMQAPVLSLL TGQDFSSYVTNKQTKKKK/T* IALRVLALV*GTSLOPVAYL/SK EIDVVAKGQPHCLRVVVAVAV LVSEAVKIIQGRNLTWVTS NGILTAKGDLWLSNHLKYQ ALLLEGPMLRLCTCAALNLDTF LPHNEEKIEHNCQQVIAQTYAT RGDHLVPLTDPNPNLYTDGRS FVEKGLQKVGAVVSDNGILES NPLTPGTSACLAKLTRALELGE GKRVNIIYTDSKYAYLVLHAHA
12280	42648	A	12354	5	138	
12281	42649	A	12355	1	909	
12282	42650	A	12356	3	245	
12283	42651	A	12357	1	1080	

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12284	42652	A	12358	3	955	VPRKSVHSGDAEYHKVLEKEA SDSRENKVGTTWLQILSGSFAS RVTEHTQPLQESVSLWISSEQN IPPKFMGRLNKLKATYKRKYS AAKSKVEKKKKEKVFAVTTKP VGGDKNGGTRVVQTRIKLPR YHPTEDVPRKIVEPPQKNLFSQ HVRKTAKTALPPGTILILTG/RH RGKRVVFLKQLASGLVITAP LVLNRVPLRRTHQKFVIATSTKI DISNVKIPKKKDKTPLLTDAYL \KKKKLRKPR/HPRKGEIFDTVK RGNMRITEQRTIDQKAVDSQIL PKIKAIQA/LQGYLRILCLL*RN GIYPHKLVF
12285	42653	A	12359	1	555	
12286	42654	A	12360	1	300	
12287	42655	A	12361	1	588	
12288	42656	A	12362	1	264	
12289	42657	A	12363	1	870	
12290	42658	C	12364	239	400	
12291	42659	A	12365	9	98	SWKPSFSAN*HRNRKPNTTCSH SQVGVDL
12292	42660	A	12366	9	81	
12293	42661	A	12367	3	169	
12294	42662	A	12368	134	481	GCCGGTIKNSFSFPLPNWPRFV MFPSLCVLIVETCETWICTLIVQ LPLMSENMRCLIFCSCVSLLRM MVSSFVHVHDHKVKSHPSP/G NLRKSKEASPSPKTSKVGKLTQV PSVCG
12295	42663	A	12369	41	388	SYGQMMKCPQTFPPSPGYGAG VFSSDKIGQMTFMERT*RMSCK EAAQDHTAREKEKVELKFPSLP FRRKELL*PCTWLGSPISLVTL D FPWPQSGRLSMPVLWTCLPG SLEIG
12296	42664	B	12370	1	909	
12297	42665	C	12371	295	2025	
12298	42666	A	12372	14	260	
12299	42667	A	12373	1	142	TCTCVFIAALFTIAKTWN*SKCP SMRDWIKKNVAHTHHGILCSH KKE
12300	42668	A	12374	1	395	

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12301	42669	A	12375	2	976	REHLAEGMAVGTASADLNISA CWLRRQQISQHSARALLRDRL PPQENSSWHPAGAPLGRNFQFK EQAAIFAVLQPPLVIPRKIGSGV DLEQTPADLQKRGLTVTRKTN KQKAIASSTERTPTQKPPFKSH QHQRPNVDKSAKMRKNQSKK AENSKNQNTSSPPKDHNSPAR EQNWMEFDELTEVGFRRW VITNSSELKKHVLTCCKEAKNL EKRDMDDEAGNHHSQQTNTGTE NQTPHVLTHKWELNNENTRTRI YKKHGAAICLASGIYHSVDLPF WGLDLPFWDEDSGSTILSGSG QWPSSHSSTRQCTSVDSVWGL
12302	42670	B	12376	1	111	
12303	42671	A	12377	34	346	
12304	42672	A	12378	1	585	
12305	42673	A	12379	3	14703	
12306	42674	A	12380	1	636	
12307	42675	A	12381	1	1626	
12308	42676	A	12382	1	3246	
12309	42677	C	12383	62	202	
12310	42678	A	12384	1	286	
12311	42679	A	12386	1	1176	
12312	42680	C	12387	1	942	
12313	42681	A	12388	785	892	
12314	42682	A	12389	2	91	
12315	42683	A	12390	1	708	
12316	42684	A	12391	3	96	TWMKLETIILSKL*QRQKTKHR MFLIGGN
12317	42685	B	12392	1	1954	
12318	42686	A	12393	1550	1830	DTISHQLEWQSLKSQETTALLTI AKTWNQPKCPSMIGWIKMMW HIYTMEEYAAIK/SDEFMCFAW TWMKLETIILSKLSQEHKTKHH MFSLTSGS
12319	42687	A	12394	3	553	
12320	42688	A	12395	1	1428	
12321	42689	A	12396	642	753	
12322	42690	B	12397	1	759	
12323	42691	B	12398	1	900	
12324	42692	A	12399	623	775	
12325	42693	A	12400	992	1156	
12326	42694	A	12401	86	349	

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12327	42695	A	12402	1	2521	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIQMGQWFRNRSI NIVQHINRTNDKNHMIISDAEK AFDKIQQRFMLKTLNKLIGDGT YLKIIIRAIYDKSTANIVLNGQKL EAFPLKTGTROGCLSPLLFNIV LEVLAIRQEKEIKGIQLRKEE IKLSLFADDMIVHLENPIVSAQN LLKLIDNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIA SERIKYLGQLTRDVKDLFKEN YKPLLNDIKEDTNKWNTPRS WVGRINIMKMAILPKVIYRFNA IPIKLPMTFFTELEKTTLKFIWN QKGARIAKSILYRFNAQELEKT TLKFIWNQKGARIAKSILSQKN KAGGITLPDFKLYYKATVIKTA WYWYQNRDIDQWNRTEPSEIM PHIYNHLIFDKPKDKKKWGNDS LFNKWCWENWLAICRKLKLDLP FLIPYTKINSRWIKDLNVRPKTI KTLEENLGNITQDIAMGKDFMS KTPKAMATKAKIDKWLINLK SFCTAKETTIRVNRQPIEWEIF AIYSSDKGRISRIYNELKQIYKK KTNNPIKKWAKDMNRHFSKED IYAARKHMKKCSSSLAIREMHI KTTMRHHLTSVRMAHKKLGN DWCWRGCGEIGRLLHCWWDG KLWQPLWKSVMRFLRDLELET FPDPASPLLGIIYQKE\YKSCYYK DICT/RVCVPAALFTIANTWNPQ
12328	42696	B	12403	80	5612	
12329	42697	B	12404	68	505	
12330	42698	A	12405	1	471	
12331	42699	A	12406	194	430	IAIMRLLQISIILSSCLREVKSM QAYRKALRKLKADVKRYQKS LVVQKRS*ER*SLVLILILPARTF QSYLAPIC
12332	42700	A	12407	1	546	
12333	42701	A	12408	2	418	
12334	42702	A	12409	302	746	ETSHQVMDRSNPVKPALDYFS NRLVNYQISVKCSNQFKLEVCL LNAENKVVDNQAGTQGQLKV LGNLWPPYLMHEHPAYLYS WEDGDCFTPKALDPLPACDLC DQLHLRSRQGGVCGGDPCEQ LLLLVAVSLQAPAIASAAAGRPV
12335	42703	A	12410	83	552	
12336	42704	A	12411	1	459	
12337	42705	A	12412	34	588	

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12338	42706	A	12413	1	466	
12339	42707	A	12414	950	1230	CSWHDRFPDWKAGRILPISEPPS NRIFACWGKPAWTACCN/FSQG QAVKGNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQ VSRLESGQDFADFGTTIKQDFR LLGQTSVDRLQLSQGQAVKG NQLLPVSLVKRKTTLAPNTQTA SPRALADSLMQLARQVSRLESG QDFADFGTTIKQDFRLLGQTSV DRLLQLSQGQAVKGNQLLPVS LVKRKTTLAPNTQTASPRALAD SLMQLARQVSRLESGQDFADF GTTIKQDFRLLGQTSVDRLQL SQGQAVKGNQLLPVSLVKRKT TLAPNTQTASPRALADSLMQLA RQVSRLESGQ
12340	42708	A	12415	497	847	
12341	42709	A	12416	1	337	MGVVPEELFLEELNLSGLKWD FADFGTTIKQDFRLLGQTSVDR LLQLSQGQAVKGNQLLPVSLV KRKTTLAPNTQTASPRALADS LMQLARQVSRLESGQHPEFAPP SHGD
12342	42710	A	12417	716	961	
12343	42711	A	12418	1	1218	
12344	42712	A	12419	1	1104	
12345	42713	A	12420	548	1078	
12346	42714	B	12421	83	345	
12347	42715	A	12422	1	681	
12348	42716	A	12423	1	1431	
12349	42717	A	12424	566	871	
12350	42718	A	12425	145	980	
12351	42719	A	12426	2	702	
12352	42720	B	12427	1	1156	
12353	42721	A	12428	188	584	
12354	42722	A	12429	1	1194	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
12355	42723	A	12430	170	1855	LLEGKLTNRKDIPHQNICTSPS SKTKGILPISEPPSNRIFACWGK PAWTACCN/FSQQQAVKGNQL LPVSLVKKRKTTLAPNTQTASPR ALADSLMQLARQVSRLESQGD FADFGTTIKQDFRLLGQTSVDR LLQLSQGQAVKGNQLLPVSLV KKRKTTLAPNTQTASPRALADSL MQLARQVSRLESQGINHTPNSF HIGAGGSWCLSESPPVVLNYK YPLVCGYTDGNAEVSKFGNFFL DLSRTRCLAEGNYTSGDNHTLR DPHYVEDKGHKYLVFEANTGT ENGYQGEESLFNKAYYGGGTN FFRKESQKLQSQAKKRDAELA NGALGIIELNNDYTLKKVMKPL ITSNTVTDEIERANVFKMNGKW YLFDTSRGSKMTIDGINSNDIY MLGYVNSLTGPYKPLNKTGL VLQMGDLDPNDVTFTYSHFAPV QAKGNVNVITSYMTNRRGFED KKATFAPSFLMNIKGNKTSVVK NSIRREGFCFRNHHQTGFSPA GANQRGPLAATLSGPGGEGQS AVARLTGEKKNHPGAQYANRL SPRVGRFINAAGITGFPTGKRA GFCFRNHHQTGFSPAGANQR GPLAATLSGPGGEGQSAVARLT GEKKNHPGAQYANRLSPRVGR FINAAGITGFPTGKRAV
12356	42724	A	12431	851	2237	
12357	42725	A	12432	2	2346	
12358	42726	B	12433	329	479	
12359	42727	B	12434	656	2404	
12360	42728	B	12435	486	834	
12361	42729	A	12436	1	693	
12362	42730	A	12437	1	114	
12363	42731	A	12438	152	391	AGGWALPSLGLPSWTSRCPWR RGSAGLLLEASVPVQQ*PKLLD RLSRRWPGEHPRPARVRSCM ALGPRRLGVLCOEPS
12364	42732	A	12439	1	1707	
12365	42733	A	12440	1	897	
12366	42734	A	12441	36	420	
12367	42735	A	12442	2	217	
12368	42736	A	12443	1	903	
12369	42737	A	12444	1	1626	
12370	42738	B	12445	107	757	

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12371	42739	A	12446	1	1655	MGTVPRSAQGETWVWLCEHIIIGG ERSFTEYSLSCHRIESSTSSIKLEL GGNNVEPLESSRVFDSIVQNEE ADAVSTGEEGVTHEGTQGGKV IPQMHHMGSGLQPKSFSQNRSQV NNDMIVTDNNGAVKFPQLCKF CDVRFSTCDNQKSCMSNCISITSI CEKQPQEVCAVACWMSEIECTN VMYSPLPCKFLHLSPIEVLPIRS PVNQSGRCKIRHIGSNRLQRS TCQNTGWESAHVMKTPGFREY NTSNPDLLLIVFQVTGISLLPPL GVAISVIIIIFYCYRVNRQQLSS TWTGKTRKLMFSEHCAIILE DDRSDISSTCANNINHNTELLPI ELDTLVGKGRFAEVYKAKLKQ NTSEQ*DSGQFKILFPIEYAS WKTEKDIFSDINLKHENILQFLT AEERKTELKGQYWLITAFHAK GNLQEYLTRHIVISWEDLRKLGS SLARGIAHLHSDHTPCGRPKMP IVHRDLKSSNILVKNDLTCCCL DFGLSLRLDPTLSVDDLANSQG CYEVCSSGRFLVTIFKGNRLRE RTEKNTRITPRDWVYEWLW
12372	42740	A	12447	1555	3277	RAAGSAMGRGLRGLWPLHIV LWTRIASTIPPHVQKSVNNDMI VTDNNGAVKFPQLCKFCDVRF STCDNQKSCMSNCISITSEKQP EVCVAVVRKNNDENITLETVCH DPKLPYHDFILEDAAAPKCIK EKKKPGETTFMCSSEDCNDN IIFSEEYNTSNPDLLLIVFQVTGI SLLPPLGVAISVIIIIFYCYRVNRQ QKLSSTWETGKTRKLMFSEH CAIILEDDRSDISSTCANNINHN TELLPIELDTLVGKGRFAEVYK AKLKQNTSEQFETVAVKIFPYE EYASWKTEKDIFSDINLKHENIL QFLTAEERKTELKGQYWLITAF HAKGNLQEYLTRHIVISWEDLR KLGSLSARGIAHLHSDHTPCGR PKMPVIVHRDLNSSLNVLKNDLT CCLCDFGLSLRLDPTLSVDDL NSGQVGTARYMAPEVLESRMN LENAESFKHTDVYSMALVLEW MTSRCNALGEVKDYEPPFGSK VREHPCVESMKDNVLRDRGRP EIPSWLNLHQGIQMVCELTTEC CDHDPYARLTAQCVAERFSELE HLDRLSGRSCSEKIPEDGSLNT

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12373	42741	A	12448	3	1354	
12374	42742	A	12449	1	168	
12375	42743	A	12450	2	147	
12376	42744	A	12451	3	523	LQFFRSEVVKMKNHLLFWGVL AVFIKAVHVKAQEDERIVLVN KCKCARITSRIIRSEDPNEDIVE RNIRIVPLNNRENISDPTSPLR TRFVYVHLSDLCKK\CDPTEVEL DNQIVTATQSNICGWMTVPQS TCYTLSTGKNKCYTAVVPLVYG GETKMYETALTPDACYPD
12377	42745	A	12452	3	274	
12378	42746	A	12453	1	120	
12379	42747	A	12454	119	461	PVPQDLQA AVLGRITLALFKIAY KTGTLQVCKRLLLSFVCL/CPA PRGRQASLSCGGLHPVRASWLL CLPKQAWAMAGAPPPAWLPCC SLISDCCASNQRDSVGVPRSEPG VGYSLV
12380	42748	A	12455	2	370	
12381	42749	A	12456	1	3135	
12382	42750	A	12457	1	942	
12383	42751	A	12458	1	462	
12384	42752	A	12459	1	297	
12385	42753	A	12460	935	1338	CTDGLFVWMSFLVFSFPLPPCS LISDCSASNERDSVGVPSEPG AGYNLVVRRFLSPSEKRSIRV* VTRFSRCRPSPLSLTRKGNSLTP CASQVRQCLALFRLAHGVRTH SPAPT VWHSLPKVGPFLNSVP
12386	42754	A	12461	1	268	
12387	42755	A	12462	3	479	
12388	42756	A	12463	1	262	
12389	42757	A	12464	1	304	MAGAPAPASLPPCSLISDCCAS NQRD SMGVGPSEPGAGYNLVP V\EKRSIRVGVTGFSRCCPSPLSL TRKGNSLTPWASQVRQCLALL QLAHGRGSPNPRP
12390	42758	A	12465	1	512	
12391	42759	B	12466	1	1257	
12392	42760	A	12467	1	705	
12393	42761	A	12468	1	3039	
12394	42762	B	12469	66	467	
12395	42763	C	12470	360	747	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
12396	42764	A	12471	3771	4703	SFOQFCVSFSPSLWFYLLLVFDD GDVQMRFRGCGPCFCLLVLLTD RTLSCRSVGIPIRCVRCQCA/LLG GASQLGCSGVKGSRDPLEEAV CPFS/DLQLRAGGNTALFKAVR QGHLSQLRLLSFVCLCPAPRG GAYRGGQASLSCGGLHPV*AS/ RLCLCPKQAWAMAGAPPPASL LAPC/LISDCCASNQSDSVGVGP S/ERPGVGYSLVVRFLSRSEKR NIRGGVTRFSRCRPSPLSLTRK GNSLTPCASQSEGNAGPAGF AHGARTHWALRPVTVHWSLCE MNPVPQMEMQKSPVFCVAHA GGCRPEL
12397	42765	A	12472	1	1038	
12398	42766	A	12473	27	428	LADRSAIPGFAFAVTFLLALVG AVLYLYPWTLKPC*SHY*GIN LVVAV*VKTT*GKNCMKMV*L IL*RVTLPS*RFGLRLEKAF*M GHLIKT*LGKNNMKMPCSNWS LF*GTS*KNEKEGTSVNIFSLTP
12399	42767	A	12474	107	362	NKPCFEFYLAALIYLLYHGRK KADTKIPP*ISRFLLIYPSHELTI FIVIIMCDLGCTWAICFLTISE EVQKKLYEENQVFG
12400	42768	A	12475	193	637	TSSEVVKKQIAQVHNFVIMQL ARENILSS/EDLLVIKVPVLY*GV NENMLTEVPFSFFYDVP*NRL QLHEGIFILFFPSHFVK*PI*KAF SNLRPNCAMILLEANDFLIIFKC TTHYHLNRLHSTKTKHMLAEG HVLGLVWVGEPFI
12401	42769	A	12476	1	1930	
12402	42770	A	12477	1	362	
12403	42771	A	12478	58	160	GVSLQSTSEEGRMQRQE*TERE IKVTCRSHYRLA
12404	42772	A	12479	3	410	
12405	42773	A	12480	1	807	
12406	42774	A	12481	154	375	
12407	42775	A	12482	2	512	
12408	42776	C	12483	29	455	
12409	42777	A	12484	209	433	
12410	42778	A	12485	1	1546	
12411	42779	A	12486	3	931	
12412	42780	A	12487	1	363	
12413	42781	A	12488	1	351	
12414	42782	B	12489	82	263	
12415	42783	A	12490	1	1878	
12416	42784	A	12491	24	242	
12417	42785	A	12492	1	3558	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
12418	42786	A	12493	2	478	HNSLKSNDKENSFSADHVTTA VEKSKESQVTADDEEEKAKA ELIMDDDRVTVDPLLSKSQSILIS TSATASSKKTIEDRNKIKKKSTN NRASSASARLMTSEFLKKSSSK RRTPSTTTSSHYLGLTKVLDQK PFTEEA*EPDRADNIRGSCLFR
12419	42787	A	12494	1	1047	
12420	42788	A	12495	1	1055	
12421	42789	A	12496	212	611	
12422	42790	A	12497	2	195	YVMGRNDGGYLMIDSKTAEIK FVKNNMRDSTFVNKTITAEVL AIDRYSGKNCLLSISWYICG
12423	42791	A	12498	1	429	
12424	42792	A	12499	1	503	
12425	42793	A	12500	3	825	GTTKWQTVRRQKREWIKFAAA CREGEDNSKRNPAAK*SDLQNS LLPALY*KHURSDCESNQKITY RISGVGIDRPPYGVFTINPRTGEI NITSVVDREITPLFLIYCRALNS RGEDLERPLELRVKVMDINDN APVFSQSVYTASIEENSADNTL VVKLCATDADEENHLNSKIAY KIVSQEPGAPMFILNRYTGEV CTMSSFLDREQHSMYNLVVRG SDRDGAADGLSSECDRIKVL VNDNFPT/FRENFQNSSRFSNS LLSSFDQWRKL
12426	42794	A	12501	986	4030	KQRLTWTFSPGKSETMMGLFP RTTGALAIFFVVILVHGLRIET KGQYDEEEMTMQQAQRQKR EWWKFAKPCREGEDNSKRNPAA KITSQYQATQKITYRISGVGIDQ PPFGIFVVDKNTGDINITAIVDR EETPSFLITCRALNAQGLDVEKP LILTVKILDINDNPPVFSQQIFM GEIEENSASNSLVMLNATDAD EPNHLNSKIAFKIVSQEPAGTGM FLLSRNTGEVRLTNSLDRQA SSYRLVVSGA
12427	42795	B	12502	1	3572	
12428	42796	A	12503	1	594	
12429	42797	A	12504	1	612	
12430	42798	B	12505	200	532	
12431	42799	A	12506	2	735	
12432	42800	A	12507	5	400	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in UNSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
12433	42801	A	12508	2	1260	GQAASPASPASPAMAWAA LLGLLVALLLLLLSRRTRRP GEPPLDLGSIPWLGALDFGKD AASFLLTRMKEKHGDIITLVGG RYVTVLLDPHSYDAVWVEPT RLDFHAYAIFLMERIFDVQLPH YSPSDEKARMKLTLLHRELQAL TEAMYTNLHAVLLGDATAGS GWHMGLLD/CLQLPAQSRPL DSLRN*GAATHP*KPGPGPRPLS *CLPHLSPARPAAPQTGPWLPV SGGQGPVHVCQKSPVEAIPSQ AGQAGPPEQMAGELPAAPGGD GCVRGDAGTGPAAA VGHTGE YGSRCLLAPALPSQES*SPGCCP RRAREYPLASGAACLDHDSPT EGSRQHTC/DLIAC*VRASGLQL PPSSPARL/GGPGHAHGRERIQ PATW*PPPPLPPEPPERPRNLH RPRGI
12434	42802	A	12509	3	466	
12435	42803	A	12510	1	1134	
12436	42804	A	12511	2	1211	
12437	42805	A	12512	2	405	HEMLLASEIKHLPRLLIGQERE TQTSELKIKRRGNEEAPS/PPPSS AYERGTRPDDRYDTPTSKKK VRIKDRNKLSTEERRKLFEQEV AQREAOQKQQQMQLNGMTSP LPYDSLGYNAPHHFAGYPPGY PMQA
12438	42806	A	12513	191	898	
12439	42807	A	12514	1	270	
12440	42808	A	12515	2	1328	
12441	42809	A	12516	1	2868	
12442	42810	A	12517	1	1254	
12443	42811	A	12518	1	576	

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12444	42812	A	12519	1919	3044	HQGPSTPPSWAMSGPPTPLSRE DWHQGPSTPPSWAMSEPT/SSI QGLASGAVHTJLLGDVRATYTS IQGVTSQVSVQSRRAAQMAVPSS RILQLSKPKAPATLLEWDPVP KPKPHVSDHNRLHLAKVPRK EGSGKKVGAFFPEIKGPEAFRDK ARAMESQSNMDMPFDELLALYG YEASDPISDRESEGGVDVDPNLP DMTLDKQIAKDLLSGEEEEET QSSADDLTFSVTSHEASDLFPN RSGCLLAGAEASSRGLLPRAQP VPRGAGLADNSRGALLRAHGT VRVGTATVVKPADAPPESPRDR RSRNDSHRPTGPSESERQPQSN QPTLLLRGHGTIRVRTTATVVKP ADAPAESPRDRSRNDSHGQSS
12445	42813	A	12520	413	1412	
12446	42814	A	12521	293	412	NHLSVAGNGSSPCGL*AGALGL LLWLLASSGHRVLSGMI
12447	42815	A	12522	2	181	
12448	42816	A	12523	1	277	
12449	42817	A	12524	1	739	
12450	42818	A	12525	1	326	
12451	42819	A	12526	3	566	
12452	42820	A	12527	1	465	
12453	42821	A	12528	1	1167	
12454	42822	A	12529	260	395	EVATATPTLSNHYPDQSAAIN/D QG*PLHQKQDHLKQAQMNISIF
12455	42823	A	12530	209	958	FRCVLISFWSHKLHLWYHEGRI VPSDRIVPPHGI/VSSHGVALPQR ILMRQFTLLEGLNKDGRFLIQLS GTAPWSSYFNSVAKFGVIHRIH SFFLSHNGHKAVALDLLSNVG GSCLCGDASSFTTPSRITMTSK SWLARSVAEMSYR/WTALVNH VADDQRGHQKNVIALDWVINR NVQLVNRNHLPRFCSCFLDHL AHRGTNDHAFQVTHSEHAQ LAISDGNHSMMAENQSFPCPSVS LSCFHENAA
12456	42824	A	12531	1	1965	
12457	42825	C	12532	520	684	

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12458	42826	A	12533	701	1307	GRHLTTNHTAAVVFPPFRPLCS SFFRYSGRFVAGATASGRGQG PAG*DNCQRAWRGAFYKFQAT LSAGAGTRAEEGSDGDGEAAE PGAGTAREPARLRGVSRRFVL DGRRCCLCYFKNPHDPLPLGHL DIAEACFSYQRADEAAEQPAHF QVRSAGAATVLEVGTRALRGV HLIRAHRGIAQWSPVSFLQ AVLPAWLL
12459	42827	A	12534	1	1356	
12460	42828	B	12535	1	1449	
12461	42829	A	12536	3	2449	
12462	42830	A	12537	1	3327	
12463	42831	A	12538	1	1359	
12464	42832	A	12539	1	672	
12465	42833	A	12540	1	1281	
12466	42834	A	12541	1	399	
12467	42835	A	12542	1	399	
12468	42836	A	12543	171	426	PVSCATGEEEDNVLPFKGDDL R**PGKLWCEFHASSISQALGQ HPRRSVLDTQSHVPLVRRKTT CFSQRAMISPDPPSQEAGALS RNNLLAPYSALTFMENGNCLL QLFQLGKLLVQASHLHGQLLV FVQKIIISM
12469	42837	A	12544	1	988	
12470	42838	A	12545	3	129	LFHPCQDSQHH*CVCCRLTGH GAA*VHGPGCAVQTYRASH
12471	42839	C	12546	532	1101	
12472	42840	A	12547	197	355	
12473	42841	A	12548	1	1275	
12474	42842	A	12549	3	131	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, /=possible nucleotide insertion)
12475	42843	A	12550	1746	3504	ESDPSNSTTSM DRTLL/MSSIVP RLPSACRILPTGTIPE*SCVHRT ASLIPLPPGSRKYSPLPLNSLI FLKN/SAYTAVPALQTDWATSP ISLHLRTSFNSPHLYPPEELIYFL DRSSKTS PDISHQQA AALLRTY LKNLSPIYNSTPIFGPLTTQTTI PVAAAPLCISWQRP TGIPLGNLSP SRCSFTLHLRSP TTNINETIGAF QLHITDKPSINTDKLKNISSNYC LGRHLPCISLHPWLS SPSSDSDP PRPSSCLLIPSPENNSERLLVDT RRFLIHHENRTFPSTQLPHQSPL QPLTAAALAGSLGVVWQDTPF STPSHLFTLHLQFCLAQGLFFLC GSSTYMCLPANWTGTCTLVFL TPKIQFANGTEELPVPLMTPTQ QKRVIPLIPLMVGLGLSASTVA LGTGIAGISTSM TFRSLSNDFS ASITDISQTL SVLQA QVDSLAA VVVLQGGRLGLDLLTAEKGGLCI FLNEECFFYLNQSGLVYDNIKK LKDRQAQLANQASNYAESPWA LSNWMSWVLPVPSLPIPIFLLLL FGPCIFRLVSQFIQNRQAITNHS IRQMFLLTSPQYHPLPQDLPSA
12476	42844	A	12551	2	394	
12477	42845	A	12552	1	882	
12478	42846	A	12553	45	409	
12479	42847	A	12554	1	1035	
12480	42848	A	12555	118	312	
12481	42849	A	12556	1	1083	
12482	42850	B	12557	1	1122	
12483	42851	A	12558	97	439	
12484	42852	A	12559	1	450	
12485	42853	A	12560	1	471	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=-possible nucleotide deletion, \=-possible nucleotide insertion)
12486	42854	A	12561	2	1407	WGKNRAEKLETLSRVPLLLQ RNAVPHQQWNKAGRRMTLS* EKKASDD/PNYSKLQEEIQTGK KEVKHFEKNLDECITRITNREK CLKELMELKAKARELREECRL RSQCDQLEERVSVMEIEQTTIRE YYKHL YENKLQNLEEMDKFLD TYTLRRLNQEEVESLNRPIGTSE IVAHINSLPTKKSPGPDGFTAKF YQRYKEELIPLLKLFQSEIEKEGI LPNSFYEA SIIIPKQGRDITTKK ENFRPIFLMNINAKILNKILANRI QQHIKKLIHHDQVGFIPGMQ WFNICKSRNVJHHNRTKDKNH MIISIDAEKAFDKIQPFMLKTL NKLGIDET YLKIIIRAIYDKPTAN IILNGQKLEAFPLKTGTQRGGCPL SPLLFNIVLEVLARAIRQEKEIK GIQLGKEEVKLSLFADDIMIVYL ENPIVSAQNLFELISNFSKVSGY KINVQISQAFLYTNYRQSAKS
12487	42855	A	12562	1	846	
12488	42856	A	12563	1	1281	
12489	42857	B	12564	1	274	
12490	42858	B	12565	1	2265	
12491	42859	A	12566	1	2742	
12492	42860	A	12567	1	1272	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, / =possible nucleotide insertion)
12493	42861	A	12568	222	2130	RKKNNKKK*TKPPRNMGLEKRT KMSDWCCT*K*GEWNQV/AK TLCRILSRRT/YPNLRQADIQIQ EIQRTPQRYSSRRATPKHIVRF TKVEMKEKMLRAAREKGRVT HKGKPIRLTADLSAETLQARRE WGQIFNII.KEKNFQPRISYPAKL SFISEGEIKPFTDKQMLRDFVTT RPALKELKKEVLNEMERNRKK LNRPTIGSEIVAIINSLPTKKSPG PDGFTAEFYQRYKEELVPFLLK LFQSKEKEGHIHPNSFDEASIIIP KAGRDTTCKDNFRPISLMNIDA KILNKILANQIQHIKLIHHDDQ VGFIQMGQGFNQCQINVIQHI NRTKDKNHVVISIDAEKAFDQIQ QRFMLKTLNKLIDRMYLKIIIR AIYDKPTANILNGQKLEAFPLK MGTTRQGCPLSPLFNIVLEVLA RAIRQEKIKHIQLGKKEVILSL FADDMIVYLENSIVSAQNLLKLI SNFSKVSQYKINQKSHALFHT NNRQTESQIMSELPFTIASKRIK YLGQILTKDVKDLFKENYKPLL NEIKEDTKKWKHIPCWSVWGRIN IVKMAILPKVIYRFNAIPIKLP TFFTELEKTTLKFIWNQKRAHT AKSILSQKNKAGGITLPDFQLY CKATVTKTAWY
12494	42862	A	12569	1	474	
12495	42863	A	12570	1	1197	
12496	42864	A	12571	1	1518	
12497	42865	A	12572	1	3189	
12498	42866	A	12573	1	2199	
12499	42867	A	12574	3	2820	ENKDTTYQNLWDAFKAVCRG KFIALNAHKKRQERSKIDTLTS QLKELEKQEQTHSKASRRQET KIRAEKKEIETQKSLQKINESRS WFFERINNDRPLARLIKKKKREK NQIDTIKNDKGDITDPTETQITTI REYYKHLVANKLKNLEEMDKF LDITYLPRLNQEEVESLNRPIITG SEIVTINSLPTKKSPGPDGFTAE FYQRYKEELVPFLLKLFQSIEKE GILPNSFYEASIIIPKGRDRTTK KENFR
12500	42868	B	12575	1	1593	

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12501	42869	A	12576	1	3549	MGDFNTPLSTLDRSRRQKVNK DTQELNSALHQVDLIDYRTLH HKSTEYTFPSAPHHTYKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRINKLTQNRSTTWKLN NLLNDYWHNKMKAIEIKMFF ETNKNKDDTTYQNLWDAFKAV CRGKFIALNAHKRKQERSKIDT LTSQLEKEKQEQTHSKASRRQ EVTKIRAEKKEIETQKTLQKINE SRSWFFERINKIDRMLARLIKK KREKNQIDTIKNDK
12502	42870	A	12577	1	2724	
12503	42871	A	12578	1	3567	
12504	42872	B	12579	709	2064	
12505	42873	A	12580	1	3370	
12506	42874	A	12581	1	2024	MGFYHVGQAGTELLTSNDPLT SASQASRITGKALQKPTVPVP YEKMLQDQSALIVQGLPEGVA FKHPENYDLATLKWILENTAGI SFIINSATIEPPAAQPMSTHMG HSLCVLVVETHAKPVA VQSSSF TRNPEVISLEVAAVTVKEESD PDYDYITFKDLPGLAIYETKAYV LWPQLSKICKNGDKNKAYRG QQCRLRQQNPLAALTGKISVSV YVSHPSLRVSIGWTRQVARQT MQKDRDGPLKNEGECNCAGSE KNTLTSQLEKEKQEQTHSKAS RRQEITKIRAEKKEIETQKTVEK INESRSWFFERINKIDRPLARLIK KKREKNQVDAIKNDKGDITDP TEIQTTHREYYKHLANKLENY EEMDKFLDITYTLPRLNQEEVES LNRPIITGSEIVAINSLPTKKSPG PDGFTAIFYQRYKEELVPFLK LFQSIKEGILPNSFYEASIIIAK PGRDITTKKENFRPISLMNIDAKI LNKILAKRIQQHIKKLIHHDQV GFIPGMQGWFNIRKSNVIQHIN RAKDKKHMIISIDAEKAFDKIQ QPFMLKSLNKL/DIGKNYFKVH MGPKKSPCRQVNPKEQSWR HHST*LTQILQGYSNQNSMVLV PKQRYRSMQNTALRN NATYL QLSDL*QT*EKQAMGKGFI**
12507	42875	A	12582	722	4214	

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12508	42876	A	12583	228	1152	KNRDYKNLSLRPQCNQTRTON *ESHKPLNYMETEQPAPE*LL DT*RMKAEIKMFFETNENKDT TYQNLWDAFKATASKTNKEKE KNQIDTIKNDKGDIITDPTIEQT TIREYYKHLIYANKLENLEEMD KFLDTYTLPRLNQEEVESLNRPI TGAIEVAIINSLPTKKSPGPDGF TAEFYQRYKEELIGWLRRESVSK ICLKFDHQVQVITGRLIIRFQIAF GTVVLCQLTRHIDVVFVGKRLA NARFAPSLGGAPDLFTLKPCFV AVETQGDLPQATTVDIDGCL GKPANVQVALDIDVKGFGQQW
12509	42877	A	12584	1	2028	
12510	42878	A	12585	2	2264	
12511	42879	A	12586	1	2130	
12512	42880	A	12587	1	2900	MENDFDELREEGFRQSNYSEL EDIQTKGKEVENFEKNLEECITR ITNTEKCLKELMELKTKAQELR EEWRSLSRSCDQLEERVSAME DEMNMKGEGKFKREKRIKRN QSLQEIWDYVKRPNLCLIGVPE RDGQNGTKLENTLQDVIQENFP NLARQANVQIQEIQRTPQRYSS RRATPRHIIVRFTKVEMKEKML RAAREKEIQTTISEYYKHLTYN KLENLEEMDKFLDTYTLPTLNQ EEVESLNRPIITGAE
12513	42881	A	12588	1	2745	
12514	42882	B	12589	1	3288	
12515	42883	A	12590	1090	2526	
12516	42884	A	12591	1	3242	
12517	42885	A	12592	3862	8976	RAKSPANIIMTGSNSHITILTN VNLNSPIKRRHLASWIKSQDP SVCCIQETHLMCRDTHRLKIKG WRKIYQANGKQKKAGVAILVS DKTDFKPTKIKRDKEGHYMMV KGSIQQEELTILNMYAPNTGAP RFIKQVLSDLQRDLDSHTLMG DFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDYRTLHPKST EYTFPSAPHHSYSKIDHILGSEA LLSKCKRTEIITNYLSHSAIKL ELRIKNLTQSR
12518	42886	A	12593	1	1000	

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12519	42887	A	12594	1	979	MNNAKENFLGRFQDGRIGTAP VYSPQHQRRRRRVISALPTEPPL VIPRQTGFQVDLQQTPTDLQLR VLTVRRKTTKQEGHSTKTPSVR YHHQRPKEDKTTKMGNRQSRK AENSKNESASSPPKECSSSPATE QSWMENDFDKYTEVGFRLQVI TNFSELKEDVQTHHKEAKNLE KRLDEWLTRINSIENTLIDLME KTMARELRDSCSFQRQDQVE ERVSVIEDQMNEMKREEKFRE KKMLEVLPRAIRQEKEIKGIQL GKEEVKLSLFADNMTVYLENPI IS/PKISLS**ATSASQDIKSMC KNHKHSYTPITDKQRAKS
12520	42888	A	12595	1140	2210	KPWHKFNFTHAQASADLIKW KKGYQ*LKIKLMK*SKKTRNTN YHQNTINISMQIN*KI*KKWRNS WTHTLQY*TRKLLNLIDQ*Q ALKL/QAIHYSLPTKNVQGMQD SQSNTRVWGILARAIRQEKEI KDIQLENEEVKLSLFADDMTVY LENSIVSAQNLLKLRILYGLIQL TTDVKDLFKENYKPLLNIKIED TNKWKNIPCSIRGINIMKMAI LPKLIYRFNAIPKLPMTFFTELE KATLKFIVNQKRAHIAKTILSK KNKAGGIMLPDFKLYYKATAT KAAWYWYQNRDIDKKLTQIYK KKTNNPIKKWAKDMNRHLSKE DIYGANRHMKKCSSSLVIREKQ IKTTMR
12521	42889	A	12596	520	697	GLCSVPLLCISVLVPVPCFCGYC SLVV*FEVR*SDASSFVLLA*DF LGNVSVFLVPYEL
12522	42890	A	12597	1	1410	
12523	42891	A	12598	1	1461	
12524	42892	A	12599	77	457	QALKLRQ*LIAYQPKRVQDQM DSQTSNARGTKRSWYHSF*NYS N/PTEKEGILLNSFYEAIGIIPKP GRDITTKKENFRPISLSINAKIL NKILANRILQHIKKLNIITKSASS LGCKAGSTYANQ

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12525	42893	A	12600	1	919	MGDFNTPLSTLDRSTRQKVNK DIQELNSALHQADLIDYRTLHP KSTEYTFPSAPHHTYSKIDHILG SKALLSKCKRTEIITNCLSDHSA IKLELRIKKLTQNCSTTWKLN MLLNDYWEHNKMKAEIKMFF ETNKNKDDTYQNLWDTLKAVC RGKFKALNAHKRKKERSQIDTL TSQLEKEKEQEQTSHKASRRQE ITKIRAELEKETETQKTLQRLMN PGAVLEVLAARIRQEKEIKGIQL GKEEVKLSLFADDMMIVYLENP MSQPKISLS**ATSAKSQDIKSIY KNHQHSYTPIRDQKRAKS
12526	42894	A	12601	1	1264	MDKFLDTYTLRLNQEEVESLN RPTGSEIEAINSLPTQKSSGPD GFTAIFYQRYKEELVPFLLKLF QSIEKEGILPNSFYEASIIIPKPG RYTHKKNNFRPISLMNIDAKIL NKILANRIQQHHKKLIHQDQVGI IPGMQSWFNHHSINVIQHINRT KDKNHMIIISIDAFAFDKIQPF MLKTLNKLKIPKNPTKYGCE GPLQGELEQITAQRNKGRRHKQM EEHPMLMDRKNEYHKNNGHTPK VIYRFNVIPKLPMTFFSELEKST LKFIWNQKRARIAKTILSQKNK AGGIMLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTEPSEM TPHIYNHLIFDKPDKNKQWGW DSLFNKWCWENWLAIGRQLKL DPFLTPYTKINSRWIKDLNVRP KTIKLEENLGNTIQDISMGKDF MSKTPKAMATKAKMDKWDLI KLKSFACTAKETTIRQSWPEMTK FTFSNTDVKNWKGKNNIGR HKTSVNTCKMDSGLVLERWM EWNPGFPLSIDAKCHKDLPRDI QFDSEKGVDFVLNYSKANMR WAGSMFL*FIESF*HEWLLNFV KGLFCIY*DNHVVVFVGSYYML
12527	42895	B	12602	1	1827	
12528	42896	B	12603	13	1377	
12529	42897	A	12604	557	664	KTPLSQPKISLS**ATTAKSQDT KSVYKNQQHSYT

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12530	42898	A	12605	77	1866	QAPKLRQ*LIAYQPKKVQDQTD SQPNSTRGTTKSWYHSF*NFSN/ PIEKEGIFPNLFYEANILIPKPGR DTTKENFRPISLMNVNAKILN KLLANQIQQHKKLIHHNVQGF PGMQGWFNICKSINVIQHINRT KDKNHRSSISIDAEKAFNKIQPF MLKTLNKLDDMIYVLENPIVSA KNLLKLISNFSKVSQYKINVQK SQAFLYTNNRQAESQIMSASF TIASKRIKYLGLQTRDVKDLFK ENYKPVNLNKIKEDTNKWKNI LWIGRVNIMKMAILPKVIYRFN APIKLPMTFFTELEKTTLKFIW NQKRAHIAKTILSKKNKAGGIT LPDFKLYYKATVTKTAWHWY QNRDIDQWNRTEPSEIHHPIYNH LIFDKLDKNKTLGKDYLFNKRC WENWLAICRKLKLDPLTRYT KINSRWIKDLNIRPKTIKLEEN LGDITQDIGMGKDFITKTPKAM ATKAKIDKWDLIKLSFCTAKE TTIRVNRQPTWENIFAIPYSDK GLISRIYKELKQIYKKSSNNPIK KWAKDMNRYFSKEDIYAANR HMKKCSSSLALREMQIKTTMR YHLIPVRMAIHKSGNNRCW
12531	42899	A	12606	67	243	GLCCVFLIYISVLVPVPCCFGYC SLVV*FEVR*HDASSFVLA*D* LGDVGSFLVPYEL
12532	42900	A	12607	1554	1692	
12533	42901	A	12608	640	816	GLCSVALVCISVLVPVPCCFGY CSLVV*FEVR*HDASSFVLA*D *LGNVDSLVPYEL
12534	42902	A	12609	1626	1739	

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12535	42903	A	12610	1	2014	MKREGSLEKKRIKRNEQSLQEI CDYVKRANRLRIGGPESDGENG TKLENTLQDMQEKFPNLAQA NIQIQEIQRTPQRYSSRA IPRHI IVRFTKVEMKEKMLRAAREKG QVTHKGKSIRLTADLSAETLQA RREWGPIFNILKEKNFQPRISYP GKLSFISEGEIKSFDTKQMLRDF VTTTPALKELLKEALNMEKNK QYQPPQKHAKLTREARANTFK PSRRREITKIRAELKEIETPKTAQ KINESRSWFSERINKIDRPLARL RKKKREKNQIDTIKNDGDDIT HPTIHTIIEYYKHLYANKLEN LEEMDKFLDTYTLPRPNQEEVE SLNGPIAGSEIQAIIINSLPTKSP GPDGFYQRYKEELVPFRLKLFQ SIEKEGILPNSFYEAIIILPKPGR DTTKKENFRPISLLNINAKILNKI LANRIQQHIKKLMHHDQVGFIP GMQGWFNIRKSNVQIHINRTK DKNHMIISDAEAKAFDKIQQPF MLKTLNKLGDGTYHKIIRANY DKPTANILNGQKLEAFPLKTGT RQGCPLSPLFNIVLEVLARAIR QEKETEGIQLGKEEVKLSLFAD DMIVYLENPM SQPKISLS**ATS AKSQDTKSMCKNHKYSYTPIT DKQRAKSSVNSPFTIA SKRIKYL GIQLTRYVKDLFKERSMK
12536	42904	A	12611	1	700	MDKFLDTYTLPRLNQEEVESLN RPITGSEIEAIINSLSTKKSPGPD GFIAQFYQRTKDKNHMIISDAE KAFDKIQQHFM LKTLNKLGDG TYLKIIRAVYDKPTASIIINGQK LEAFPLKTGT RQGCPLSPLFN VLEVLARAIRQEKEIKGIQLGKE EVKLSLFADDMIVYLENPM SQ PKISLS**ANSAKSQDIKSMCKN LKHSYTLITDKQRAKSSVNSHS QLLQRE
12537	42905	A	12613	1	1765	
12538	42906	A	12614	1	2310	

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12539	42907	A	12615	1	836	MENEFDELTEVHFRRWVITNSS ELKEHVLTCCEEAKNLARRNK LENLEEMDKFLATYTFPSLNQE EVESLNRPTSSIEAAINSLPTK KHGPGDGTAKFYQRYKEELHI NRAKDKNHMIIISDAEKAFDKI QHPVKLIKLNKLGIDGTLYKIIIR AIYDKPTANLILNGQKLEAFPL KTGTROGCPLSPLLFNIVLEVLA RAIRQEKEIKGIQLGKEEVKLSL FADDRLYI*GTPLSQPKISLS** ATSAKSQDTKSMYKNHSHSYT PTTDKQRAKS
12540	42908	A	12616	355	4502	QSARFRGRRTLRRPGVGYSLVV *FEVR*CDASSFVLLA*DCLGN AGSFLVPYEL
12541	42909	A	12617	248	362	
12542	42910	A	12618	529	680	YYTRCSKWWNCVLP*YIYNF HLPHGKLKNTDYIKKKLHDFFF KNSKHI
12543	42911	A	12619	1	641	
12544	42912	B	12620	36	48	
12545	42913	A	12621	1	326	
12546	42914	A	12622	1	444	PGSTHASAHACERLQTRTLRAF SSQRRFPATASRASLSSNMAKIS SPTETERCIESLIAVFQKYAGKD GYNYTLSTKTEFLSFMNTELA TKNQKDPGCP*PHDGRKLGQPT VDGQLDFSEFLNLIGQAMAC HDSFLKAVPSQKRT
12547	42915	A	12623	2	6008	
12548	42916	A	12624	530	856	

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12549	42917	A	12625	1	952	MAARGTGDKVKPGCEEAGAAF ELPPSVYAAALHESHQHQPCPA GGARAQRVPGGIVTEPLCTTP KDMVFLSDDGDDDDDDNDND GGGDDDDNDGNDNDGNDNDGND DDGDDDDNDGDDDDNDNDGND NDGNDNDNDGDDDDNDNDND GGDDDDGVDGDDNDSDGNDG DDDDSDDDGDSNGYDDGDD GNDDDGDDSDDDSDNDGDD NGDGGDDGGGGDDDDNGHDD DGDMMMMIVMMVMMVMMVV MMVMMVMMVVVVQLRKRAEA SVSEAKCSINVSDDNDGDDGN DGDGDDSDGDDDDGGDGGD SELTNQFPTNHSGMKASKLRK DSDHREW*W**WWWCN*GR EQRPVFLKQSAQLMSVMIMMM VMVMMVMMIVMMVMMTMV VVMVVIVNSPINSRLITQA
12550	42918	A	12626	3	380	
12551	42919	A	12627	5	765	RQWEVGRWSGTTFSCFKKTL YFTNPSPSSSLVTVILRREVT CGGAPEQRYQIIPVCVAARLPT RAQDVLDAHLSEVNAVRFGN SSLLATGGADRLIHLWNVVGSR LEANQTLEGAGGSITSVDGDP VRNSAPVAVDCALSDLHTGQG YQVLAATYNQAAQLWKVGEA QSKETLSGHKDKVTAAKFKLT RHQAVTGSRDRTVKEWDLGRA YSPKRQRPSTGHDDGGFVE KKRGKCGEKRDQIVTVSV
12552	42920	B	12628	1	2802	
12553	42921	A	12629	458	708	QNRHRHHGPFMSVAVSSQLLD TPAERLSLHTWKIAQRPGRGTP HFPDGA/VQAETLPQTGRPR GTPHFPDGAASSFGYCCLVA
12554	42922	A	12630	2300	6491	EGLEALIHQERLSYWANQVSED RPVCKAIQKQFEGLVDTGAD VSIHALNQWPKNWPKQKAVTG LVGIGTASEVYQSMEILHCLGP DNQESTVQPMITSIPLNLWGRD LLQQWGAETMPAPLYSPTSQK IMTKMGYIPGKGLGKNEDGIK VPVEAKINQEREGIGYPFLGAV TVEPPKPIPLTWKTEKPVVWNQ WLPKQKLEALHLLANEQLEK GHIEPSFSPWNSPVFVIQKSKGK WHTLTDLRAVNAV

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12555	42923	A	12631	1	434	MTVSKNKCHTKGGKKGTEKK VVASFSKIYWYNVKAPAMFSIR NIGKALVIGTHGTDFVSDGFKG GLIEIPDSIGKDEKACRSIYPLH DVFVRKVVKMLKKPKFELGKLM ELHGEGRSSGKATGNESGA/KV E*ADGYGSPAQKSF
12556	42924	A	12632	1	642	
12557	42925	A	12633	260	534	
12558	42926	A	12634	1	438	
12559	42927	C	12635	391	750	
12560	42928	A	12636	199	451	
12561	42929	A	12637	120	992	RDRIPGPVCKGKWKNERILIFS SRGINFRTRHLMQDLRMLMPH SKVHDTNMARSDNLSVINEGCE MNNWLRCIYFEAKKKQDLYM WLSNSPDGPSAKFLVQNIHTLA ELKMTGNCLKGSRPLLSFDPAF DELPHYALLKELLIQIFSTPRYH PKSQPFVDHVFTTILDNRIWFR NFQIIEEDAALVEIGPRFVLNLIK IFQGSFGGPTLYENPHYQSPNM HRRVIRSTAAKYREKQVQKDV QKLRKKPEPKTLLPHDPAADV VTPAEEKPIEQVVKPETKVDL KASV
12562	42930	A	12638	1	342	
12563	42931	A	12639	1	580	PGWEKMRSSS/GVNTQEALPT AAIPTDAKVRVYFNNHITNASQ WERPIGNSSSGGKNGQGEPARV RCSHLLVKHSQSRPSSWRQEK ITRTKEEVALELINGYIQIKSGE EDFESLASQFSDCSSAKA/RGD LGSFSRGQMOKPF*RTPRFAL RTGGDERGPCFTD/SCIHIILPHL SEGKPRPLGAGQGG
12564	42932	A	12640	3	116	
12565	42933	A	12641	2	253	
12566	42934	A	12642	3	512	EDYLERKQ/VPTQCQTHSKLG GPMTLKREVKP/KVDVSPSKKG PLQHIHTLLVCHVRIFYPGSIQ/ VRWFLNGRKKTAGVVSPLNLR NGDWT/FQILVMLEM/TPQQGD VYTCCQVHTSLDSPVTVEWKA QSDSARSKTLTGAGGFVLGLIIC GVGIFMHRSSKAFNEDLHKQG
12567	42935	A	12643	1	363	
12568	42936	B	12644	70	1229	
12569	42937	A	12645	1	430	
12570	42938	B	12646	1	1321	
12571	42939	A	12647	3	446	

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12572	42940	A	12648	1	417	
12573	42941	A	12649	269	452	TILRSFGYFFRRINIMLTEEKIKS DHRKISQLIFLQKLCQTLQSENV SQGGMLYRAKA*H*T*TLVVW *HVMSPYHKGLGLMLSLCSVK HSTLRDVFTL
12574	42942	A	12650	83	1385	
12575	42943	A	12651	1	974	MNPLECVDRSSQPWGNPTWTS SGMRSVTLVGVFKLTLFALAQT LNAAASLTGQELLAGFPFVGINI LPGYGPTAGAAIASHIGIDKIAF TGSTEKEAELHSWIKGLTCISIE PDFQKSLKDGIILCILMKNKLQPA SFPKINHSMQKWHQLENLSNFI KAVVSYDMNPMDLKFANNLFE SGNMRHMQVSLFALAGKVKT KRPQSGVDIGIKYSEKQEQNFS DAAMKAGQCIGLQMGNTNKC TSQLGMTVYGMGTNNCASQVS MTAPGTRQHICDTKLGTDKCG NSSMSLQMGYT/QGAANQPRV CEWQRGIRQQGLPPCLGPSQE
12576	42944	A	12652	1	1103	MNPLECVDRSSQPWGNPTWTS SGMRSVTLVGVFKLTLFALAQT LNAAASLTGQELLWNFPPLMF AWKIAPALCCGNTVVIKPAEQT PLSALYMGALIKEAGFPFVGINI LPGYGPTAGAAIASHIGIDKIAF TGSTEKEAELHSWIKGLTCISIE PDFQKSLKDGIILCILMKNKLQPA SFPKINHSMQKWHQLENLSNFI KAVVSYDMNPMDLKFANNLFE SGNMRHMQVSLFALAGKVKT KRPQSGVDIGIKYSEKQEQNFS DAAMKAGQCIGLQMGNTNKC TSQLGMTVYGMGTNNCASQVS MTAPGTRQHICDTKLGTDKCG NSSMSLQMGYT/QGAANQPRV CEWQRGIRQQGLPPCLGPSQE
12577	42945	A	12653	1	729	
12578	42946	A	12654	259	390	SFCSANFEVFRLLTAQQ*FVR*H ALSHIF*G*V*SFPKSTKRVNF
12579	42947	A	12655	68	735	
12580	42948	A	12656	1	825	
12581	42949	A	12657	3	470	
12582	42950	A	12658	1	1683	

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12583	42951	A	12659	1	1748	MNKPPIRNLSENAAPLDLEGIL KDAKIPVSGPFLVKIGYAFVDC PDEIWALKAEIALSGKIELHGK IEVEHSVPKRQRIKQLQIRNIPPH LQWEVLDS*LVQYGVVESCQ VNTDSETAVVNVYSSKDQAR QALDK/LLDKLNGFLENFTLK VAYIPDEMATQQNPFQPRGR GLGQRGSSRQSGSPGVSQKPC DLPLCLLVPTQFVGAIIGKAT IRNITKQTQSKIDVHRKENAGA AEKSITILSTPEGTSAAKCSILEI MRKETQDVKFTTEIPLKILAQN NFVGRILIGKEGRNLKKIEQD TKITISPLQELMQYNPEHTITAK GNVETCAKAEIEIMKKIRER*E NDITSMN/LQAHLIPGLNLNAL GLFPPTSQMPPTSGPPSAMTPP SPQSEQSESETVHLFIPALSVRA LISKQGGHIKQLSRFAGASSKIA PVEAPDAKVRMVMIAAGSPEAR FKAQGRIGYKIKKEENFVSPKEE VKLEAHIRVPSFAAGRVIGKGG KTVNELQNFSSAEVVPVRDQTP DENDQVVVKITGHFYACQVAQ RKIQEILTQVKQHQQKALQSG
12584	42952	A	12660	3	803	
12585	42953	B	12661	1	330	
12586	42954	C	12662	127	342	
12587	42955	A	12663	324	491	
12588	42956	A	12664	1	891	
12589	42957	B	12665	1	1869	
12590	42958	A	12666	2	136	
12591	42959	A	12667	108	355	
12592	42960	A	12668	2	811	FGMRGSRGGWAGEMAASGES GTSGGGSTEEAFMTFYSEVKQ IEKRDSVLTSKNQIERLTRPGSS YFNLNPFVQLQIDPEVTDIEIKK RFRQLSILVHPDKNQDDADRA\ QKAFEAVDKAYKLLDQEQKK RALDVIQAGKEYVEHTVKERK KQLKKEGKPTIVEEDDPFLFKQ AVYQTMKLFALIEIKRKERE AKEMHERKKRQREIEIAQEK KR/EEREWQKNFEESRDGRVD SWRNFQAQFRRKKEKKNRTE LRPESKNGSNVE
12593	42961	A	12669	731	850	
12594	42962	A	12670	201	377	LMTLPCKIPSPGSSWLKISPIEHL MTPTPASQRTTPDCNFPLPTQI L*NGPTPISLH

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12595	42963	A	12671	742	2982	KIPFPDASFLPCLHKFNLKGGK NSKGFKMAEFESLMNIHGFDL GSRVMDLKLPGCGGNGLVFSA VDNDCDKRVAIKKIVLTDPSV KHALREIKIRRLDHDNIVKVFE ILGPSGSQLTDDVGSLETNSV YIVQEYMETDLANVLEQGPLLE EHARLFMYQLRLGLKYIHSAN VLHRDLKPANLFINTEDVLKI GDFGLARJMDPHYSHKGHLSE GLVTKWYRSPRLLLSPNNYTK AIDMWAAGCIFAEMLTGKTLF AGAHELEQMQLILESIPVVHEE DRQELLSPVPIRNDMTEPHK PLTQLLPGISREALDFLEQLTFS PMDRLTAEALSHPYMSIYSFP MDEPISSHPFHIEDEVDDILLMD ETHSHIYNWERYHDCQFSEHD WPVHNNFDIDEVQLDPRALSD VTDEEEVQVDPKRYLDGDREK YLEDPAFDTNYSTPCWQYSD HHENKYCDLECSHTCNYKTRS SSYLDNLVWRESEVNHYEYEPK LIIDL SNWKEQSKEKSDKKGKS KCERNGLVKAQIALEEASQQLA GKERENQGFDFDSFIAGTJHLA SSQHEPTDVGDKLNDLNSSVS QLELKSLSKSVSQEKQEKGMMA NLAQLEALYQSSWDSQFVSGG EDCFFINQFCEVRKDEQVEKEN TYTSYLDKFFSRKEDTEMLETE PVEDGKLGERGHEEGFLNNSGE
12596	42964	A	12672	826	1041	WKITVKGGVFLWWAGVGDTK VLSGGAF*ARMSQEEDFHKVM SSVKARTGHLHFFCGGMSSVK AGQGPFVLL
12597	42965	A	12673	1	1482	
12598	42966	A	12674	3	488	
12599	42967	A	12675	2	114	

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12600	42968	A	12676	1	897	MSNRVVCREASHAGSWYTASG PQLNAQLEGWLSQVQSTKRPA RAIIAPHAGYTYCGSCAAHAYK QVDPSTIRRIIFILGPSHHVPLSRC ALSSVDIYRTPLYDLRIDQKIYG ELWKTGMFERMSLQTDDEHS IEMHLPYTAKAMESHKDEFTIIP VLVGALSESKEQEFGLFSKYL ADPSNLFVVSSDFCHWGQRFR Y\SYIDESQGEIY* SIEHLDKMG MSIIEQLDPVSFSNYLKKYHNNTI CGRHPIGVLLNAITELQKNGM NMSFS\FLNYAQSSQC\RNWQD SSVSYAAGALT ^{TVH}
12601	42969	A	12677	2	114	
12602	42970	A	12678	1	897	MSNRVVCREASHAGSWYTASG PQLNAQLEGWLSQVQSTKRPA RAIIAPHAGYTYCGSCAAHAYK QVDPSTIRRIIFILGPSHHVPLSRC ALSSVDIYRTPLYDLRIDQKIYG ELWKTGMFERMSLQTDDEHS IEMHLPYTAKAMESHKDEFTIIP VLVGALSESKEQEFGLFSKYL ADPSNLFVVSSDFCHWGQRFR Y\SYIDESQGEIY* SIEHLDKMG MSIIEQLDPVSFSNYLKKYHNNTI CGRHPIGVLLNAITELQKNGM NMSFS\FLNYAQSSQC\RNWQD SSVSYAAGALT ^{TVH}
12603	42971	A	12679	1	912	
12604	42972	A	12680	1	156	
12605	42973	A	12681	112	1120	
12606	42974	A	12682	33	415	NMNKPIPTSTYVRCLNVGLIRK LSDFDIDPQEGWKKLAVAIKKPS GDDRYNQFHIIDAVPKTANTLP SKEAITVQKQMPFCDKDRTL MTPVQNLEQSYMPDSSSPENK SLEVSDFRHSFSFYELKN
12607	42975	A	12683	3	311	
12608	42976	A	12684	1	1125	
12609	42977	A	12685	1	1365	
12610	42978	A	12686	3	141	VVSTVVPDS/AHKLFIGGLPNYL NDDQCHGLSKG\AFCEYVDIN VT ^V

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12611	42979	A	12687	1	1255	GTRSTSSLRRQMKNIHVHNYSEA EIKVREATSNDPWGPSSSLMSEI ADLTYNVVAFSEIMSIWKRL NDHGKNWRHVYKAMTLMLEYL IKTGSERVQQCKENMYAVQT LKDFQYVDRDGKDQGVNVRE KAKQLVALLRDEDLREERAH ALKTKKLAQTATASSAAGVS GPPPEAEQAWPQSSGEEELQLQ LALAMSKEEADQEEIRIRGDDL RARRWQSRARRGRLGARRSRPS WTLTSSRPQLLPRPQTPGGAQ HPWLLPSPRLPPRTPGAAPLSL QLLIPGEVQPPRRPLGTGGGLLP LQDPQLTLGVGPQLQLGRGPR LIHGEVPMVGSRSVGPQPPIGH RPRPSQIPGEGHLPSPAPMAQQ QPGDSTRSPTSSLTLTDSARHCR PPGAAQESWSCWQERCRPEAL
12612	42980	A	12688	116	1541	
12613	42981	A	12689	3	415	
12614	42982	A	12690	1	1440	
12615	42983	C	12691	117	314	
12616	42984	A	12692	3	120	
12617	42985	A	12693	1	729	
12618	42986	A	12694	79	870	EWSSVRRSLVEKRALRRPHPC LCFRMKTILSNQTCRPFPEINVD ITLKGRAVIV*GPAEGTLR\RDF \NHLQW*NLSLSWKEKKRGRS VDK\WWGNRKGNWPT\VRTYL VVHVQNMIKGVLPGLPVTKD EGLVYA\HFPHPTLVIPGRNGSS LLKSRNFLGVKNTSRRVSG*RP G\VACS\VSSSPRKDEFNPLKGN DIGACFQISAGFGFQQAPHTCL KTRDIQGNFWDGYPMVLWKK GTVSARAGWNKDLKEFTWATE RKMPG
12619	42987	A	12695	2	293	
12620	42988	A	12696	1	273	TRGPWCDSVLRGCSLEQRSFIS VRLLSYLSACRHPMEDSMDMD MSPLRPQNYLFG\SLGAGAKDE LHIVEAEAMNYEGSPKIVLAT LKMS
12621	42989	A	12697	1	1308	

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12622	42990	A	12698	124	1135	DKNSMGLPGVIPSAAVLSWSI HLSSSALSPTISACRHPMEDSM DMDMSPLRPQNYLFGCELKAD KDYHFKVDNDENEHQLSLRTV SLGAGAKDELHIVEAEAMNVE GSPKIVTLATLKMSVQPTVSLG GFEITPPVVLRLKCGSGPVHISG QHLVAVEEDAEESEEEEEVK\
						LLSISGKRSAPGGGSKVPQK\
						KLAADEDDDDDEEDDDDD
						DDDDDFDDEEAEEKAPVK\
						RDTPAKNAQKSNQNGKDSKPS
						STPRSKGQESFKKQEKTPKPK
						GPSSVEDIKAKMQASIA/EKGG
						LPKVEAKFINYVKNCFRMTDQ
						EATQDLWQWRKSL
12623	42991	A	12699	201	416	
12624	42992	A	12700	2	678	
12625	42993	A	12701	3	2149	
12626	42994	A	12702	1	219	
12627	42995	A	12704	267	437	
12628	42996	A	12705	507	845	
12629	42997	A	12706	426	704	SRRWGGVHSCPPSPPTAGHWT LLILCAKARRSEAAAMVLASRRR RPGPRPRRRRLPVLSRGGAG PARGRGPGSGWGPLRAAPSP
						SSTV
12630	42998	A	12707	195	892	
12631	42999	A	12708	1	893	
12632	43000	A	12709	1	777	
12633	43001	A	12710	1	439	KTQVAPSTDGIQIPSSNSRTDE REFFIASYNRKKEDEGEGNVWIA KSSAGAKGEGILISSEASELLDFI DNQAQVHVQKYLEHPLLEPG HRKFDIRSWVLVDHQYNIYLY REGVLRTASEPYHVDNFQDKT CHLTNHCQKKKKK
12634	43002	A	12711	1	394	SGTRPVFLVPHTIGIPHPAIVTP QVQKEHPHTDSDLMHVQKQHE QRKEQEPKRPKHPKPLNAFMLY MKEMRANVVAECTLKESAAIN QILGRRWHALSREEQAKYYEL ARKERQLHMQLYPGWSARDN
12635	43003	A	12712	1	789	
12636	43004	A	12713	1	870	
12637	43005	A	12714	1	729	
12638	43006	A	12715	1	828	
12639	43007	A	12716	1	213	
12640	43008	A	12717	1	664	
12641	43009	A	12718	1	695	
12642	43010	A	12719	96	269	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
12643	43011	A	12720	3	241	
12644	43012	A	12721	213	660	EGPARHRLSPVRSKMTKKR RNNGRAQKRAARHVRGPSPLK/ CFPSGLPPNCAICVPKDKAIK KFVVRNIVEAAAR/DISEASV FDAYL/LPKL/YVKLHV/CVSCAI HKQK*SGNRSS*SPAKTRTPPR FR/PGG*LPHGPPTKSP
12645	43013	A	12722	1	303	
12646	43014	A	12723	610	928	FLSLPTFLFV/IFSGEELLVLALV FLSLFFFFFFLRWFSFVVAQAV/ VQW/INLSSLPFGKQFSCLSLP SSWDYRCPPPRPANCFITRDG VSPCCPGWSRTSDLR
12647	43015	A	12724	1	2775	
12648	43016	A	12725	1	6039	
12649	43017	A	12726	2	3661	
12650	43018	A	12727	1	1173	
12651	43019	A	12728	1	1632	MPNPKNSKGGKRNKRANSSGD EQENGAGALAAAGAAAGAAAG GALAAAGCGAAAAGAPGAG GAAGAGGAGTGAANAAAAAG AAAAGDAKNEAPCATPLCSFG RPVDLEKDDYQKVVCNNEHC PCSTWMHLQCFYEWESSILVQF NCIGRARTWNEKQCRQNMWT KKGYDL/AFRCSCRCGQGNL KKDTDWYQVKRMQDEKKKKS GSEKNTGRPPGEAAEEAKCRP PNKPQKGPSHDLPRRHSMDRQ NSQEKA V GAAAYGARSPGGSP GQSPPTGYSILSPAHSFSGPRSSR YLGEFLKNAIHLEPHKKAMAG GHVFRNAHFDYSPAGLAVHRG GHFDTPVQFLRRDLSELLTHIP RHKLNTFHVVRMEDDAQVGGQ EDLRKFILAAALSASHRNVNCA LCHRALPVFEQFLVDGTLFLSP SRHDEIYDVPCHLQGRMLHL YAVCVDCLEGVHKIICICKSR WDGSHWQLGTMYYDILAASP CCQARLNCKHCGKPVIDVRIG MQYFSEYSNVQQCPHCGNLDY HFVKPFSSFKVLEAY
12652	43020	A	12729	1	1485	
12653	43021	A	12730	1	1074	
12654	43022	A	12731	2	3394	
12655	43023	A	12732	1	2190	
12656	43024	A	12733	1	1251	
12657	43025	A	12734	1	1710	
12658	43026	A	12735	3	679	

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12659	43027	A	12736	209	337	
12660	43028	A	12737	365	538	
12661	43029	A	12738	2	196	
12662	43030	A	12739	1	2639	
12663	43031	A	12740	3	173	
12664	43032	A	12741	1	1479	
12665	43033	A	12742	1	921	
12666	43034	A	12743	1	798	
12667	43035	A	12744	2	773	
12668	43036	B	12745	75	321	
12669	43037	A	12746	321	738	
12670	43038	A	12747	1	3190	
12671	43039	A	12748	287	1636	ACGAMERAPPDGPLNASGALA GDAAGGARGGSAAWTAVL AALMALIVATVIGNALVMLA FVADSSLRTQNNFFLLNLAISDF LVGAFCIPLYVPYVLTGRWTFG RGLCKLWLVVDYLLCTSSAFNI VLISYDRFLSVTRAVSYRAQQG DTRRAVRKMLLVVVLAFLLYG PAILSWEYLSGGSSIPEGHCHYAE FFYNWYFLITASTLEFFTPFLSV TFNLSIYLNIGRRTRLRLDGR EAAGPEPPPEAQSPPPPGCWG CWQKGHGEAMPLHRYGVGEA AVGAEAGEATLGGGGGGGVA SPTSSSGSSRGTERPRSLKRG KPSASSASLEKRMKMVSQSFTQ RFRLAIRDREKESLAVIVSIFG LCWAPYTLMIIRAACHGHCV DYWYETSFVLLWANSVNPV LYPLCHHSFRRAFTKLLCPQKL KIQPHSSLEHCWK
12672	43040	A	12749	1	2142	
12673	43041	A	12750	3	711	VWVNSDLMVINRSTTELPLTV SYDKVSLGRLRFVWHMQDAVY SLQQGFSEKDADEVKGFVDT NLYFLALTFVAAFHLLDFDLA FKNDISFVKKKSMIGMSTKA VLWRCFSTVVFLLDEQTSLL VLVPAGVW/AAIELWES*/RK/ VI*RWTFVWGLMPEFQFGTYS ESERKTEEYDTQAMKYLSYLL YPLCVGGAVYSLNLIKYSWY SWLNSFVNGVYAFGLFMLPQ
12674	43042	A	12751	1	2025	
12675	43043	A	12752	494	747	ATVKWITLCNRNRIKLPFIKKE GTGKAPKSRKSVLGLGP**VHT SPGDPAEGEGLPAGERPDGNLS QSPNSLRFYIKKKKAYK
12676	43044	A	12753	9	731	

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12677	43045	A	12754	143	641	RSWVLLGVGARGSTPRTYQVP SPSLAPSALC*VS*VPLESLSCH ADNWKQELTKFISPDQLPVEFG GTMTDPDGNPKCLTKINYGGE VPKSYYLCKQVRLQYEHTRSV GRGSSLQVENEILFPGCGCLRVL RFYNTYSLVHSKRISYTVLELL PDQTFMEKMEKF
12678	43046	A	12755	1	1506	
12679	43047	A	12756	2	526	CQPVRAA*RHGNTPLATV*PAS T/WWWSEKQKEEQEMQNW ESAS/VSGYPDILSCAMSONPR KRRKPRNVSAAPPVHQAQMNI SVEQMETSQTHQATPLTWGQM KRLAHVAEENLRSONKPLTTSN LMVAMMVVISLAVSLPVAGAD QNYIYWAIYIPFP
12680	43048	A	12757	1	1443	
12681	43049	A	12758	3	766	
12682	43050	A	12759	29	253	
12683	43051	A	12760	34	252	
12684	43052	A	12761	1362	1611	SSVLHPWDARLVQHTKSIHH HINRTNDKNHMIISIDAFAFD KIQQDFMLKTLNKLGDGTLYK IVRATYDKPTASILNG
12685	43053	B	12762	1	1755	
12686	43054	A	12763	1	2109	
12687	43055	B	12764	1	1497	
12688	43056	B	12765	1	1527	
12689	43057	B	12766	1	1746	
12690	43058	B	12767	1	2853	
12691	43059	B	12768	1	1479	
12692	43060	B	12769	1	1932	
12693	43061	A	12770	1269	1581	NTGKPNPAAHQKGYPPRSSGPH PWDARLVQHTKSIHHHINRT KDKNHMIISIDAFAFDKIQLPF MLKTLKSLGVSYNMFRTLTIPI AQVDTRGNQLPSYLI
12694	43062	B	12771	1	4404	
12695	43063	B	12772	56	2080	
12696	43064	B	12773	1	5445	
12697	43065	B	12774	295	2831	
12698	43066	A	12775	89	459	
12699	43067	A	12776	2	980	
12700	43068	A	12777	1	378	
12701	43069	A	12778	1	363	PGVALPGRRCRQAPADLLP*MR AYWPDVIYSFANRSRFBKHEW EKHGTCAAQVDALNSQNYFG TSLELYRELDLNSVLLKLGKPS INYYQVADFKDALARVYGVIP KIQCLPPSQDEDRQ

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12702	43070	A	12779	1	577	QRFKNDRCRDPRTGPIHGLWPD KSEG/CNRSW/PFNLEEIKDLCP EMRAYWPDVIHSFPNRSRFWK HEWEKHGTCAAQVDALNSQK KYFGRSLELYRELDL/NQVADF KDALARVYGVIPIQCLPPSQD EEVQTIGQIEICLT.KQDQQLQN CTEPGEQSPKQEVWLANGAA ESRGLRVCEDGPVFYPPPKKTK
12703	43071	A	12780	1	624	MRPAALRGALLGCLCLALLCL GGADKRLRASVSRPFSLEHPEP GHCLDLHLRAYPAR/WSS*PWP QDFWVR*PTWES/VSDLLPEMR AYWPDVIHSFPNRSRFWKHEW EKHGTCAAQVDALNSQKKYFG RSLELYRELDLNRGERVPTQFP RELVVNRSLAPPTPGFLSGHVI SVHTSSPLPSAMSGSFLRPLPEA ESGMLLGQPADP
12704	43072	A	12781	1	612	
12705	43073	A	12782	113	1149	RGAPRGPGRQGCCGHSRSPAR GPRDTGLGRPRAPGAPGGRCCS GGSAARAAGLGDVSPGSLPRAA GGKWEPERQLAAFSQVGTMR PAALRGALLGCLCLALLCLGG ADKRLRDNHEWKKLIMVQHW PETVCEKIQNDCRDPDPYWTIH GLWPKDSEGCNRSW/PFNLEE KDILLPEMRAYWPDVIHSFPNRS RFWKHE/WPKRHGTCAAQVD ALNSQKKYFGRSLELYRKLDL NSVL/LKLGKPSINYQVADFK DALARVYGVIPIQCLPTSQGE EVQTIGQ/IDLCLIKARTQLQN CTEPGEQSPKQEVWLANGAA AESRGLRVCEDGPVFYPPPKKT
12706	43074	A	12783	2	515	
12707	43075	B	12784	62	359	
12708	43076	B	12785	219	523	
12709	43077	A	12786	1010	1550	DTENIPSSRRRERSKVPYIVRQC VEEIERRGMEVGYHVSGR/V AADIQALKAAFNVSECRPAQD GMEVWAVVSAMRSQSA PRPRH VTSFSVSFLHLGSSRRPLHFRA LSNNKDVSVMMSEMDVNAIA GSLKLYFRELPEPLFTDEFYPNF AEGIGEHWRPWP HGRRLLVH CCPQRL

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12710	43078	A	12787	2	951	GSNLYCTLEGDSFGYFVNKAK TRVYRD/THADPNWNEEFIEL EGSQT/LRLCYEKCYNKTKIPKE DGESTDRLMGKGQVQLDPQAL QDRDWQRTVIAMNGIEVKLSV KFNSREFSLKRMPSRKQTGVFG VKIAVVTKRERSKV/PYI/VRQC VEIEPPKALEGGWASTACPAG VATDIQALKAADFNNKDVSV MMSEMDVNAIAGTLNLYFREL PEPLFT\DEFYPNFAEG/IRVAEK EAVNNM/SLIINLATVFGPTLLR PSEKESKLPANPS/QPITMTDSW SLEVMQVQVLLYFLQLEAIPA PDSKRQSILFSTEV
12711	43079	A	12788	3	644	
12712	43080	A	12789	168	378	
12713	43081	A	12790	1	486	
12714	43082	A	12792	83	536	
12715	43083	A	12793	1	662	
12716	43084	A	12794	3	357	
12717	43085	A	12795	2	421	
12718	43086	A	12796	2	908	
12719	43087	A	12797	1	846	
12720	43088	C	12798	87	413	
12721	43089	A	12799	1	508	MCQGDYAWGGHMCRRGHLR RGHSHERDTPRGPERPPRPAR DRESKDERRRPPPKDPPAVRT\N PDSPTATPPPPPPPPPPPPPPPP PAAPSAFAALRLRGPGRKWT RGQLPLPATAPPEARVRALPRGG YSSPGRATSARGAPWPLPSRT GKPPRPCSANTQEHC
12722	43090	A	12800	1	393	
12723	43091	A	12801	1	582	
12724	43092	A	12802	1	1422	
12725	43093	A	12803	1	1080	
12726	43094	A	12804	2	261	SCPFGGNCFYKHAYPDGREET QRQKVGTTSSRYAQRNRNHFWE LIEERENSNPFDNDEEVVTFEL GEMLLMLLAAGGDDDELNTS
12727	43095	B	12805	60	802	
12728	43096	A	12806	2	238	
12729	43097	A	12807	1	1017	
12730	43098	B	12808	1	939	
12731	43099	A	12809	1	708	

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12732	43100	A	12810	1	2653	MGDFNTPLSTLDRSMRQKVNK DIQELNSALHQADLIDYRNHLP ESTEYTFPSAPHHTYSKIDHILG SKAPLSKYRSEIKINCLSDHSA IKLELRIKKLTQNRSTTWKLN LLNDYVWHNEMKAEIKMFFE TNENKDDTYQNLWDTLKAVCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTHSKASRRQEI SKIRGELKEIETQKTLQKINESR GWFFEKINKIDRLARLIKRRK EKNQIHAIKNDKGMSTNHTIEI QTTIREYYKHLANKLENLKEI DKFLETYSPLNQEEVESLNR PITGSEIEAIIISLPNKRSPGPDG FTAKFYQRYKEELLISNFSKVS GYKINVQKSQAFLYTNNRQTES QIMSEL PFTIASKRMKYLGIQPT RDMKDLFKENYKPLLNEIKEDT NKWKNIPCSWVGRINIVKMAIL PKNWKKTTLKFTWQKRARIA KSILSQKNKAGGIMLPDFKLYY KATITKTAWYWYQNRDIDQW NRTEPSEIMPHIYNHLIFDKPDK NKKWKGKDSL FNKWCWENWLA ICRKLKLDPLFTPYTKINSRWIK DLNVRPKTIKLTLEENPGNTIQDI GMGEDFMSKTPEAMATKAKID KWDLIKLSFCTAKETTIRLNR PPTEWEKIFAIYSSDKGLISRIYN ELQQIYEKKTNNPIKKWAKDM NRHLSKEDIYAAKRHMKKCAS
12733	43101	B	12811	1	2748	
12734	43102	A	12812	1	1962	
12735	43103	B	12813	1	1833	
12736	43104	A	12814	176	421	QQPASPTRSVLLFPKTAHISGSP APPNVGLLNPSTGAQKKTMT SAGLGRLSL*K*LNLPCEVACA GETWVTSMMSGNQCN

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12737	43105	A	12815	1	1615	LISNFSKVSGYKINVQKSAFL YTNNRQTESQIMSELPFTIASKR MKYLGIQPTRDMKDLFKENYK PLLNEIKEDTNKWKNI PCSWVG RINIVKMAILPKNWKKTTLKF WNQKRARIAKSILSQKNKAGGI MLPDFKLYYKATITKTAWYWY QNRDIDQWNRTEPSEIMPHIYN HLIFDKPDKNKKWGDLSFNK WCWENWLAICRKLKLDPLTP YTKINSRWIKDLNVRPKTIKTL ENPGNTIQDIGMGEDFMSKTPE AMATKAKIDKWDLIKLSFCT AKETTIRLNRPPTEWEKIFAIYS SDKGLISRIYNELQYIEKKTNN PIKKWAKDMNRHLSKEDIYAA KRHMKKCASSLAIREIQIKTTM RYHLTPVRMAIKKSGNNRCW RGCGEIGTLLHCWWDCCLVQP LWKS VWRFLRDL EIPFDP AIP LLGIYPKDYKSCCYEDTCTHMF IVALFTIAKTWNQPKCPTMIDW IKKMWHIYTM EYYADIKKDEF MSFVRTRMKLETILSKISQIEK KTKHRMFSLIGGN
12738	43106	A	12816	1	996	
12739	43107	A	12817	1	756	
12740	43108	A	12818	1	1428	

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12741	43109	A	12819	1	2377	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPMGQWGFNIRKSI NIVQHINRTNDKNHIIISDAEK AFDKIQQRFMLKTLNKLIGIDGT YLKIIIRAIYDKSTANIVLNGQKL EAFPLKTGTTRQGCPSPLLFNIV LEVLAIRAIQKEFIKGIQIRKFE IKLSLFADDIMVHLENPIVSAQN LLKLIDNFSKVSQYKINVOQSQ AFLYTNNRQTESQIMSELPFTIA SERIKYLGILQTRDVKDLFKEN YKPLNDIKEDTNKWNTPRS WVGRINIMKMAILPKVIYRFNA IPIKLPMTFFTELEKTTLKFIVN QKGARIAKSILYRFNAQELEKT TLKFIWNQKGARIAKSILSQKN KAGGITLPDFKLYKATVIKTA WYWYQNRDIDQWNRTEPSEIM PHIYNHLIFDKPDKNKKGWNGDS LFNKWCWENWLAICRKLKLDLP FLIPYTKINSRWIKDLNVRPKTI KTLLENLNGTIQDIAMGKDFMS KTPKAMATKAKIDKWDNLNLK SFCTAKETTIRVNRQPIEWEIF AIYSSDKGRISRIYNELKQIYKK KTNNPIKKWAKDMNRHFSKED IYAAKRHMKKCSSLAIREMHI KTTMRHHLTSYRMAIIKKLGN DWCWRGCGEIGRLLHCWWD KLVQPLWKSVMWFRFLRDELET PFDPATPALLGIYPKDYKSCCYK DICT/RVCVPAALFTIANTWNPT
12742	43110	A	12820	1	4840	
12743	43111	A	12821	578	630	EYKNR*GLSLNPWGKTVHISW DVWSVGSSKAKRNWESWES*C RGIQKASLSRSTGNHSASSGI* ESRV*GLGTTGYRGITASLSL RSCTRLH
12744	43112	A	12822	8	214	EEWPKRKSEIRERPRP*SWPSDK QTLVVQRGQKMEQANHPDPTD HMSQLMWTACPKGLGIALICL VRH
12745	43113	A	12823	33	240	GGGRTNLQAVPGFPGW*RTL RTAVWDRRLTLRKPHHCPPGS QFPGPQRQVIGLLHLFSSLNHQ GWFV

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12746	43114	A	12824	1	411	MSTITQRKEENPSVFLEWLWEA /CKKIYSPVTRLTRGSDPKR*V YYAISHRYQQKAPKPSGPG*TK SGGIIKPGNLGVLY*GPRGTGQ KGKARSEKGCSSLHGPGQTNKP WWFREDRKWSRPITWYGFSLV WFARTP
12747	43115	A	12825	1	611	
12748	43116	A	12826	120	493	KYRAQRMMIARWLPQDLERGE AMLPNSSGWYKSLKGI/VLISEA FSCCKRAASLTADWL*VKQHS SPKKVQSPFSAVRRSKPWQFW RVTAAKQSIWDCRVRFIDVISC KLRLPLRVCGSRILK
12749	43117	A	12827	1	2195	VGEEGPAGVEGLNFFPAQSRRLP GPQQCSPGAEGGASARARRPRP RPRPAAAMVPGVPGA/VLTCLW LAASSG/SWRPAPARL/CAAAG RVAVCRERPARS/CASRCLSLQI TRISAFFQHFNNGSLVWCQNH KQCSKCLEPCKESGDLRKHQ QSFCEPLFPKKS YECLTSCEFLK YILLVKQGDCAPEKASGFAAA CVESCEVDNECSGVKKCCSNG CGHTCQVPKTLVKGVPLKPRK ELRFTELQSGQLEVKWSSKFNI SIEPVIVVQQRWNYGIHPSED DATHWQTVAAQTTDERVQLTDI RPSRWYQFRVA/VNVHGTGRF TAPSKHFRSSKDPSPAPPANLR LANSTVNSDG/AV*TVTIVWDL PEEPDIPVHHYKVFWSWMVSS KSLVPTKKRKRRTDGFQNSVI LEKLQPDQDYYVELQAITYWG QTRLKSAKVS/LHFTSHATNNK EQLVK/ITRKGIGITQLPFQRRRP TRPLEVGAPFYQDQGLQVKVY WKKTEDPTVNRVHVRWFPEAC AHNRITGSEASSGMTHENYIIL QDLSFCKYKVTVPQIRPKSHS KAEAVFTTTPCSALKGKSHKPI GCLGEAGHVLKSLVAKPENLS ASFIVQDVNITGHFSWKMAKA NLVQPMTGQVTVAEVTTESR QNSLPNSHSQSLPSDHYVLT PNLRPSTLYRLEVQVLTGEGG
12750	43118	A	12828	1	1410	
12751	43119	A	12829	2	299	
12752	43120	B	12830	81	510	
12753	43121	A	12831	3	436	
12754	43122	A	12832	1	769	

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12755	43123	A	12833	15	413	ERM CAGPWRKGAETGPYFCND TVRHRKASLLCPF*RMNGDQN SDVYAQEQDQFVQHFSQIVRVL TEDEMGHPEIGDAIARLKEVLE YNAIGGKYNRGLTVVVAFRELE VEPRKQDADSLQRAWTVGWC VELLQA
12756	43124	A	12834	1	795	MNGDQKSDVYAQEQDQFFQH SQIVGVLTEDMGHSEIGDAIA RLKDVLEYNAGGKYHRGLTV LVAFQELDAINYAILLEACIYYL LKLYCQAQPYLYNLIELFLQISC QPEIGQTLDLITAP/QDNVDFGR FT/EKQHANA*KILLEI/GEFFQI QDGYLDLFGDPTVTRKVGTDIQ DNKCSWL VVQCLQRSTLEQYQ ILKENYGGKKAKKV VQVKALY EELDLPVFLQY EEDGYSHIMG LTEQYAAPLLPAMFLGLVYKIY
12757	43125	B	12835	1	328	
12758	43126	A	12836	2	868	
12759	43127	B	12837	118	1138	
12760	43128	A	12838	100	374	KHISPALKALELPFRNLII/PLQ LLKVRILKEGEM/LDI*HWFL** GMGT VQKGMPHKCYHGKTGR VYNVTQHAVGIVVNNKQVK*VV
12761	43129	A	12839	1	1035	
12762	43130	A	12840	13	600	INPPPPFRPELPSSNSPKMTDH KGERGEATRYMFSRPFKKTMG VVPLGHNN*RFYKKGDDIVD/IK GMGYCVQNGMP/HKCYWPVKL EGVLQLLPQHA\VAIVVNQPV GQSFFPRE*IVRIEHIKHF*EPEIS FLK/RVLKENDSEKERSPNEKG TWGSNLKRILAPPQKKHTL*R TNGKEPELLEPIPEFHGHN
12763	43131	A	12841	1	317	QRPSEAKEIKLYAQIPPIEKMDA LSMLANCEKLSLSTNCIEKIAN LNGLEAVGDTLEELWISYNFIE KLKGIHIMKKLILYMSNNLVK DWGTPVIKGDDEEDN
12764	43132	A	12842	155	588	
12765	43133	A	12843	1	954	
12766	43134	A	12844	1	486	
12767	43135	A	12845	1	367	
12768	43136	A	12846	1	190	LISRAKEDMTLNIAEGVHPSY NIVLNTLHTCGISVKSTWRPSK GAAP*ARMPGGTAGPCLAS

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12769	43137	A	12847	1	2376	MRGAQKATNVNKLSEDIQGKE ESPTQFYERLWEAYRMYTPFDP DSPENQRMIPMALVRQSAEDM RRKLQKQAGLAGMNPSQLLEI ASQVFNDRDAVSRKENGKENG GQARRYADLFSRTKNYQPVQD LRLLHQAKLTFHPTVPNPSTLL GFPPAEDSWFTCLDLKDAFFPIR LAPERQKLFAFQWEDPESGWPP CWRA/WQQLPC*YKIVPSILRIS SSDGKYKAFSTCGSHLAVVC
12770	43138	A	12848	1	636	MRGAQKATNVNKLSEDIQGKE ESPTQFYERLWEAYRMYTPFDP DSPENQRMIPMALVRQSAEDM RRKLQKQAGLAGMNPSQLLEI ASQVFNDRDAVSRKENGKENG GQARRYADLFSRTKNYQPVQD LRLLHQAKLTFHPTVPNPSTLL GFPPAEDSWFTCLDLKDAFFPIR LAPERQKLFAFQWEDPESGWPP CWRA/WQQLPC*YKKQIS
12771	43139	B	12849	180	811	
12772	43140	A	12850	1008	1265	FLGVPTLGGWRPIQHRLK/PRE VTPVLLRDLIRRFPLWIGSDN GPAFLAALVQKTAQGIQNNITG GVYTLCDIDSHILFRSGY
12773	43141	B	12851	1	996	
12774	43142	A	12852	1251	1424	DSPRGEAES*A*LPEKLEMSG NRLVDNKDPGKKQTQRRIPHSP SQIPVPLPEIWCT
12775	43143	A	12853	1	1121	
12776	43144	A	12854	189	621	
12777	43145	A	12855	2207	2308	
12778	43146	A	12856	1	762	
12779	43147	A	12857	1	678	
12780	43148	A	12858	3	496	
12781	43149	A	12859	107	258	NALGKRSTFTNRNFLASGRFLD SVTYARRLQYQYAPAL*KTAI*SF SLLNH
12782	43150	A	12860	2	410	SPDPVWVSTYKSTCHIAQEAKEI HLRNQYERKGE*APRSNLMSE DANGGAPNPWFEEPEETIGW GFDEIRQQQHNIIR*QDAGLDA LSSHSRQKQM/GIEIGNELHEQN EIHDDLANLMENTDEKLRNETR RVN
12783	43151	A	12861	3	1402	

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12784	43152	A	12862	1	711	MAPDPWFSTYDSTCQIAQIEAE KIQRNQYERKGEKAPKLVTVI RALLQNLKEKIALLLKDLLRAV STHQITQLEGDRRQNLDDLVT RERLLASFKNEGAEPDLIRSSL MSEEA KRGA PN PWLFEEPEETR GLGFDFIRQQPKINQEQDARL DALSSIISSQKQ/MGQIEGNELD EQNEIIDDLANLVENTDEKLRN ETRRVNMVDRKSASCGMIMVI LLL.LVAIVVVAVWPTN
12785	43153	A	12863	1	936	
12786	43154	A	12864	1	1023	
12787	43155	A	12865	1606	2238	
12788	43156	A	12866	3	347	
12789	43157	A	12867	1	1665	
12790	43158	A	12868	1	589	
12791	43159	A	12869	19	1677	
12792	43160	A	12870	1	906	
12793	43161	A	12871	1	228	
12794	43162	A	12872	1	320	
12795	43163	A	12873	1	398	TSKAPGAQGEQGFEECLAVALL AGRPLPSLWALFQATTPVLQ LKEAFFRPEVPLRRDLPLLLFR TQTSDPAMLPTMIGLLAEARR AGCLSYQTSLSVDGETWHVMG ISSLLPSLEGWKQHVTEAFQF HF
12796	43164	A	12874	3	322	SAGGSGRRTLHSRTMAQFVRN LVEKTPALVNAAVTYSKPLRAT FWYYAKVELVPPTPAEIPRAIQS LKKIVNSAQTSFKQLTVKVTT G*MKT DVHNRKCLPLGFF
12797	43165	A	12875	91	425	WTFHPTTMAPFVRDLGEKTPA LGKAAVTVLKPRLAFAFWYYH QVELVPPTPAEIPRAIQSLKKIV NSAQTSFKQLTVKEAILLNDL VATEVSTWFYVREITGKRGIIG* NV
12798	43166	A	12876	179	664	HSSPAVPGRTDFSHSQNPWPQF CPVTLVGEDPRALVNAAVT/YT RKPRIGLHFWYYAKVELVPPT PAEIPRAIQSLKKIVNSAQTTG LANSSHVKEA/VL*NLVATEV LMWFLCSERLLGKRGHSLGYG CFEDQSFNIIWILFILELFVW DHVDPDC
12799	43167	A	12877	25	164	
12800	43168	A	12878	2110	2260	
12801	43169	C	12879	32	1429	
12802	43170	A	12880	172	322	

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12803	43171	A	12881	1060	12039	
12804	43172	A	12882	1	810	
12805	43173	A	12883	3	146	
12806	43174	A	12884	1	1211	GPQDGNQQAPPEKVGWVRKF CGKGIFREIWKNRYVVLKGDQ LYISEKEVKDEKNIQEVFDLSD YEKCEELRKSKSRSKNHKFT LAHKKQPGNTAPNLIFLAVSPEE KESWINALNSAITRAKNRILDE VTVEEDSYLAHPTDRRAKIQHS RRPPTRGHLMVA VASTSTSDGM LTLDLIQEEDPSPPEPTSCAESFR VDLDKSAVQLAGSRRRADSDRI QPSADRASSLSRPWEKTDKGAT YTPQAPKKLTPTEKGRASLEEI LSQRYAASAHTLQLRAEEPPTP ALPNPGQLSRIQDLVARKLEET QELLAEVQGLGDGKRKAKDPP S/RSPDPSES/EQLLETER/LLG EASSNWSQAKRVLQVRELRLD LYRQ/MDLQTPD/SHL/RQTTPH SQ/YRKSLM
12807	43175	A	12885	617	1041	TTLINPGGPAPLLSLPTSSITGFT TFYHPNLKPLRTCPSPVQAWPC RHPPI*SRDYQRDAEPTTCISKLL GENIRRDDEFWKVQIKARSGETE QNPRSTAFAGELPLANREELN LLLNKGILPLCDQRQEIESECAF TIFCAGDANCFFPSPHTLPLTAL QQRPCGLSGSASKEAWGNSLV CGPRGDTLPMAIAKPHRSASKH STLHQYPTPPRSLCHQHRDEQP TNHLQTLNTIPA WHITKWVPL DHINKPWRS CSSQSAYLFYHW LHYFLPPKLKTSKDL SILSAGLA MSAPHILFRVSAITNSNCKPSS TSKACEELFKHQCLGSTDIPHI IQGGAPFSAVSPQRLVLRGSQD GSHMVRPRLPPFDSAGLANFHL FSKFLD
12808	43176	A	12886	1	606	
12809	43177	A	12887	174	350	VSWRFVQVFI*VAGGSRICAAA GLSPGTPPCATSLIGACSLIFIP RLLSLFCGDEAL
12810	43178	A	12888	3	265	
12811	43179	A	12889	1	1209	
12812	43180	A	12890	53	369	VAHQEKGIAEPLRPTGDSRQT HRRLDVERSTSVQEHMGGCHF SPFPEREKLSTLRGIHQAPAL WQATDQWIDIEF/GLGQPEESL GR*ITRLQGGKTLFPFGSPIC

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12813	43181	A	12891	1	345	
12814	43182	A	12892	2	451	
12815	43183	A	12893	2	286	
12816	43184	A	12894	217	1071	GENPRSENTRLATILEVACCHF GSSPPPSIGSSGRKDPPLTFGDH EGTSKAEPSPALGLTPEHKGNV GHAARIQQPGPLSLWSRKAGK GVQDCYIDLKQIKIDLDKFSND PDGYIDVLQGLGQSFDTWRNI MLLLNQTLTPNERSATTTAARE FGDLWYLSQVNDRIAAEKREK FLTGGQAVPSVSGSHWDTESEH GDWCCRHLITCMLEGLRKRTRK KPMNYSMMSTITQGKEENPTA FLERLREALRKHTSLSDSIEGQ LILKDTFITQSAADIRK\NFKSPP
12817	43185	A	12895	1	756	
12818	43186	A	12896	473	1015	
12819	43187	C	12897	152	322	
12820	43188	A	12898	146	1079	PPCAVVCLLWIAAVYCLSTTFC APLCGQNTWLPKPCRHVNRRA SNASVSLSTVTLFSRLS*PQRKG SELLDSSGPLPASPLPLCSGVS PRAGLGSAPWKIPFLGIREAKN PRSENTRLATILEAGHRHLGTS VSKDHPVTFWRPRRDLQSDLK QIKIDLKGFSDNPDGYIDVLQEL GQSFDTWRDIMLLNQTLTPN ERSATTTAAREFGDLWYISQVV AAVAGLVSEAVKIIQGSYCVDI HDVNGILTAKGDLWLSDNHLL KYQALLLEGVPLRLRATCATLNP ATFLPDNEEKIEHNCCQVIAQT
12821	43189	A	12899	189	1798	

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12822	43190	A	12900	194	1729	NPAAQTFFVVKKGGRGAGL LHRQYPLRLEAKQGLKKIVKDL KAQGLVTPCSSPCNPTLAVQK PNGQWRLVQDLRIINEAVVPLY PAVPNPYILLSQIPEEAEWFTVL DLKDAFFCIPVHPDSQFLFAFED PSNPMSQLTWTVL PQGFRDSLH LFGQALAQDLSQFSYLDLTVLQ YMDLLLVTHSETWCHQATQA LLNFLATCGYKVSQNAQLCS QQVKNLGLKLSKGTRALSEERI QPILAYPHPKTLKQLRGFLGITS FCRIWIPRIKAVKLQILQMEPQ MQSMTKIYHGPLDRPTSPSSNV NDIEGTNASDFPFLSQVLEQVV SPKGSKEAQCCVLRPLGCESNL KQIKIDLGKFSDDPDGYIDVLQ GLGQPYLLTWRDIMLLLDQTL TPNERSAAITAVREFGDLWYLS QVNDRKITEEREQFPTGQQA VP SVDPHWDTESEHGDWCHRYLL TDVLEGLRKTRKKPIN*SMISTI TQKKEENPTAFLERLREALRKH
12823	43191	A	12901	1	642	
12824	43192	C	12902	54	254	
12825	43193	A	12903	32	221	NGVGHNRMTNGSGGGGEWGP PAPASA*GCSLASAFASAPRW WFEMGCRGIYDAQVALSRSF
12826	43194	A	12904	203	538	
12827	43195	B	12905	131	536	
12828	43196	A	12906	1	1251	
12829	43197	A	12907	38	475	ESERRGEFCLCKIIESEGRAVCV EDEQTSHFALTGNNGIYRKSSQ QWQQLSDLARDPPAQCSAGP VGDDMFHWQATIMGPNDSPYQ GGVFFLTIHPTDYPFKPPKVA F VTTRIYHPNINSNGSICLDILRSQ WSPAFNQFPKSS
12830	43198	A	12908	282	849	QSCPAAGIISFGRTFEHTPREV RKPDCKHTLLALKRINKDLSL ARDPPAQCSAGPVGDDMFHW QATIMGPNDSPYQGGVFFLTIH FPTDYPFKPP*GLHFTTRFYHP NINSKWAACFLRYS*DSQWSP ALTFKVLLSICLLCDPNPD DPLVPGDWHGYS*NRGTGDKYN RISREWTKQYAM
12831	43199	A	12909	1	397	
12832	43200	A	12910	245	535	
12833	43201	B	12911	68	333	
12834	43202	A	12912	265	562	

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12835	43203	A	12913	1	872	MVNTCEQLDWIEGCKVLILGVS KEASQGLGGRSRGRNVQRSTD ADIRPTSEKDARSLMTTRQEDN ISVDQRGFLSGVQKKGSCANGL KGSVCGGFYVWMAVIRMGVG KAMGLNLKLGKFEIKKGYLKG CRDSLRLSPTGFGKFTATSHV AATVPKVVLELTLQTHKILRG VFAHLTSLQLHSLPPGSSMDS AKARRQLQVAGQGHSLVKQK GFHVEAPDHHVPQLSDISCKSY RWGHKLIKINFLIPPLWYYDL EEVKREQSEKQQAAMADIIIG DALNAQKAFKGNPKGHKPLPF SAGQMENW*CCECPKSI
12836	43204	A	12914	7	231	
12837	43205	A	12915	1	223	MEILITCDKGLIFTGNTRKSETS TSECTCPDLINCSLSHSPSPSDE ETQHHTDLSLHVRPRKGYLLCIY HIPDIVAVMVNIQCQLDWIEGC KVLFLGVSVKVLPEINTGISGL GKADPPSIWKS*QHVTKDLYLQ VILENQKLVANALVRWLTVP FPTLLRALQMRKHSTTLTVCMS DRGKDICYCASTIYQI
12838	43206	A	12916	1083	1273	NKMSFKLKEDCFGRSKCNLT* CWKSINEA*/K/DLELQLQFGPQE KLFALEQQVKKKLNLPDA
12839	43207	C	12917	1	1506	
12840	43208	A	12918	3	1219	
12841	43209	A	12919	1	735	
12842	43210	A	12920	2	94	
12843	43211	A	12921	362	460	WLILSVNLIGLKDAKYCSCVCL *GCCQRRLTF
12844	43212	A	12922	1235	1474	
12845	43213	A	12923	1	250	
12846	43214	A	12924	1	261	
12847	43215	A	12925	2	85	
12848	43216	A	12926	1	291	
12849	43217	A	12927	1	321	
12850	43218	A	12928	1	370	
12851	43219	A	12929	1	684	
12852	43220	C	12930	1	210	
12853	43221	A	12931	2	91	
12854	43222	A	12932	1	243	
12855	43223	A	12933	2	353	WMKLETHLSKLS*GQKTKHRM SSLIGSTDQQLRVVKNVQGRVC PGSTGHGAWEAWTAMRKVDS PLQTGSLRPGWCRQVGSNARS GSAEAGNPGLHPGICPRVEDG IQVAENFFEV

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12856	43224	C	12934	1	289	
12857	43225	A	12935	1	1194	
12858	43226	A	12936	140	237	
12859	43227	A	12937	1	292	
12860	43228	A	12938	2	178	
12861	43229	B	12939	1	1245	
12862	43230	A	12940	2	241	
12863	43231	A	12941	1	675	
12864	43232	A	12942	1515	1920	TPTNLQEKNKQPHQKVGEGYE QTLKRRRLCSQKTHGKNAHH HWPSEKCKSKPQWIPSIHQLE WQSLKSQETTGTWWMKLETHLS KLLQGQKTKHHMFSLIGGNRT RRTHGHRKGNITLWGLSDSV NCASSG
12865	43233	A	12943	608	891	
12866	43234	A	12944	1	3956	MGSCPGGFTAIFYQRYKEELVP FLLLKLFQSEKQGTLPNSFYEAS IILIPKPRDRTTKENFRPISLMN IDAKILNKILTNRIQQHIKLLIHH DQVGFHGMQGWFNIRKSNVI QHINRTNDKKHMIISDAEKAF DKIQQPFMLKTLNKLGTWMLK ETIILSKRSQGQKTKHRMFSLV NIIPITIKILKQNMATMETLCPIF KLEGDTMDNPIANRRVRTAVP TSVVCLHVGTEPEARLPHGPMI TAQSPFG
12867	43235	A	12945	1	855	
12868	43236	A	12946	1	255	
12869	43237	A	12947	273	3484	
12870	43238	A	12948	3	377	
12871	43239	A	12949	85	333	
12872	43240	A	12952	22	308	
12873	43241	B	12953	30	383	
12874	43242	A	12954	3	448	
12875	43243	A	12955	1	453	
12876	43244	A	12956	3	491	
12877	43245	A	12957	2	749	
12878	43246	A	12958	155	637	
12879	43247	A	12959	1	510	
12880	43248	A	12960	2	559	RPHASAHASGRQSQDVTTMV WALLLLTLTQTGTGSAQSAL TQPPSASGSPGQSITISCTGLIND VASYNFVSWYQQHPGKAPKL MIYEVTKRPSGVPDRFSGSKSG INTASLDHLWGSRLDEADYYC LLICRRLHPGGIRRDWPRVTV LGSAQRPTPTVTSGSRPSSEGAP SQQGHTSVSDQ

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12881	43249	A	12961	1	1958	MSVQRKDRVRTQQGGSVASSM LTQEPVGSVALGQSARDRDPD CSDSVSVYLMDTWQSVIIGFAE SAATLGDPPELPMHPEGSEASY ELTQPPSVSVSPQQTARITCSGD ALPKQYAYWYQQKPGQAPVL VIYKDSERPSGIPERFSGSSGTT VTLTISGVQAEDEADYYCQSAD SSGTYPTVTQADRETPTHQYSR HPSYAKGFVFLWGSWAQSALT QPASVSGSPGQSITISCTGTSSD VGSYNLWSWYQQPQKAPKL MIYE/VDSKRPSGVSNRFGSKS GNTASLTISGVPGLRDEGDDY CCSYAGSVASYELTQLPSVSVS PGQTARITCSGDVLGENYADW YQQKPGQAPELVIYEDSERYPG IPERFSGTSGNTTTLTISRVLTE DEADYYCLSGDEDNPSVTQAD GEDTGIRSHYEGTLALYLYPEP VKATCSVTSYVLTPPPSVSVAP GQTARITCGGNNIGSKSVHWY QQKPGQAPVLVYVDDSDRPSGI PERFSGSNSGNTATLTISRVEAG DEADYYCQSLSTLGPCTLGDTV LRPMIYSVSIQASGVDPGFSGSK SGNTASMTISGFQAEDEADYYC NSHRRGSVVSELTDQPAVSVA LGQTVRITCQGDLSRYYASW YQQHPGKAPKLIYDGH
12882	43250	A	12962	2	367	
12883	43251	A	12963	2	376	QTYSLRRATPRHIIVGFTKVEM KEKVLRAA/NKPIRLTVDLAET LQARKEGGPIFNILKEKNFPRI SYPAKLSFISEGEIKSFTDKQML KDFVTTRPALQELLKEALNME RNNQYQPLQKHAKW
12884	43252	A	12964	2	1178	
12885	43253	A	12965	1	732	
12886	43254	B	12966	99	716	
12887	43255	A	12967	1	1011	

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12888	43256	A	12968	3	1263	GRTIQTKGKEVENFEKNLEECI TRITNTEKCLKELMELKTKARE VREECRSLRSQCDQLEERSAM EDEMNMKQEGKFREKRIKRN EQSLQEIWDYVKRPNLRLIGVP ESDVENGTKLENTLQDIIQENFP NLARQANVQIQERQRTQRYSS RRATPRHIVRFTKVEMKEKMG LLVPNWTNHSPLFRALFDYKG FCRFGTTHQTGFSPAGANQRGP LAATLSPGGEQSAVARLTGL IGVPESDVEKETKLETTLQDIIQ ENFPILARQANVQIQERQRTQRY YSSRRATPRHIVRFTKVEMKE KMLRAAREKGRVTLKKGPIRL TADLSAETLQARREWGPIFNIL KEKNFQPRISYPAKLSFISEGEIK SFTDKQMLRDFVTTTPALKELL KEALNMERNNRYQPLQNHAK
12889	43257	A	12969	1	1392	
12890	43258	A	12970	1	1224	
12891	43259	A	12971	1	970	
12892	43260	A	12972	1	954	MDGDLHKGVAVFWPPDAAGG HTCCRSVMVCRSLGGAQWKFH SFRCRIRFELILHMIQERNISIN QKDVHTETPSETHHHQRPKVD KSMKMRRNQCKKAENSKNQK ASSPPEKHNWSRAREQNWTE EFDKLTVEGFRRWVITNSSELK EHILTQCKEAKNLEKTLLELLT RITSLEKNINDLMKLKNTA*EL REAYTSINSQISQAERISEIEDQ LNEMKHEHRIREKRMKRNKQS FQEIWDYVKRPNLRLISVPESD GENGNK*ENILQDIIQENFPNL ARQANIQIQEIQRTQRYSSRRA TPRHIVRFTKV
12893	43261	B	12973	1	1346	
12894	43262	A	12974	1	318	GSRGELLSLCYNPSANSIIVNII KARNLKAMDIGGTSDPYVKVW LMYKDKRVEKKKTVTMKRNL NPNFNES\FAFDIP\TEK\LRRETTII ITVMDKDKLSRNDVIGK
12895	43263	A	12975	17	389	SWGPHCTHKLKSFSLMPMT DAMDREMR/RGSKKDVR/*VLG GCAATWTPRAGGRQQSPGTTV DKREDTPDCAMDQSTSHIPISA SSPSLLPGSSFTQTTPPGIAHYR ASFLIVAYYPSNKNKSK

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12896	43264	A	12976	84	282	GEGQVGWVPQGEVQQDEEVIEE VGA* DAGSGYQEEEEGPQLRR EVVGVELVVGADPSGEGPKED
12897	43265	A	12977	1	1179	
12898	43266	A	12978	3	634	
12899	43267	A	12979	234	619	CYVVQEVLPDLLCHLVICSRP GRTAEWPPG*GF*SPPHRGW/ GC*GHD/HRRGTSIFPTH/V*SPP ASYPGSLCRPGGQEEEREREGEW QREGRRPGTR*CGAAEARGW RAAAKATAVAGARRRRPGISG
12900	43268	A	12980	1	1182	
12901	43269	A	12981	3	763	
12902	43270	A	12982	32	949	
12903	43271	A	12983	1	1299	
12904	43272	A	12984	1	1176	
12905	43273	A	12985	1	421	
12906	43274	A	12986	81	404	VKFGPEIWCRRSDQGRGGVGT SLGRSIPCPALCSVRKIYLRPL VLRPTSPRNISPIINRDPTVQLT WQPLPEPLELWPKAL*LTSPQIY SA*RLKTDAAARLPKPPR
12907	43275	A	12987	1	378	
12908	43276	C	12988	1	751	
12909	43277	A	12989	302	629	ICLSYPAPPKCRFPHYTRVLYH* SLFNENTSQSCFTSR/WKLESFT TRAIERHQIFLL*ATLTLIRWLD KKLAFQLLSLTASFSPSYQLSP TPPLKLPIISSHTRQMV
12910	43278	A	12990	14	380	
12911	43279	A	12991	189	608	QSDLSASQHGFLPLATEVRSSG AASCPDSISCPAPTAPGRATP PQANCWASEGLTRYQALPGNR APVSQVSQAGGANLCVQQPKK HLTNFKSGKRPLFTLSNLQGP RSRPVAFLSKQLDLTVLWGPSC LVVQQLPP
12912	43280	A	12992	1	513	
12913	43281	A	12993	2	462	WSMGLPRRSGCVSLQPLSQEDL GRSQSES LGPEFQGLWEWLPEQ LPRSFQALGSLSYFPRTLNLNLS WPLCLRKGWYL/SLYLPFQVGL PSTVPWPLILPSKVPEEEGQLQS TLPCGIKLLPVFTSHHAF LGVFC NQWVSDVFLALFLMKLLGAQ
12914	43282	A	12994	59	213	
12915	43283	A	12995	1	1159	
12916	43284	C	12996	1	864	
12917	43285	A	12997	1	1155	

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12918	43286	A	12998	879	1163	SRRPLFMGLVRVLCCKMSGRGP LCFPGGHWIVFLWGGTVLWLW T*SPHWHRRKAN*DLFLQKLPRL *VSHQCDPCLPVCHLWNCLFL PLWGPPAG
12919	43287	A	12999	1	179	
12920	43288	C	13000	1	410	
12921	43289	A	13001	42	365	FGLRLSLAPPFCMFPLTT*HS*P SVLPASFPAAALGIPQARAVTFV SP*LLASLSFWAPPCSLCLDASV *HGSHLWHAQSSCRLRWSFGL AASQMQPEEPHGP RRK
12922	43290	B	13002	1	741	
12923	43291	A	13003	8	265	
12924	43292	B	13004	1	646	
12925	43293	A	13005	1	1158	MKLVTIFLLVTISLCSYSGYWFE NEQMSVGGGDDNGEVLYSALR GASEVIGQCQSSATKPRRSGKE SVREPWARVPGALGVGVREID QTLGIDTILCHHERLLQSHYGI HKSSLSMVGNSQVAALYQLNV YVVADTVGLIKNSISLDSVQPN YCSNKHIELRTQVGGARNLRA NSPMTSSYNQESSMENVVALS LLTVESPTSMFDYCDDSL ERVK SALDIFSMIIYTVTFFLAGNG LVIWVVG FHM SCTVNTCLPSPDP HLHGPLTCDPVANLVLEQLHTS KGN SGALEDLAFGNLFLCSLLD LQGN S W W K V S P S L Y N Q Y D L Q NETQGSQHLWKEIHPW*PSAFV V/SSGYWPENEQMSVGGGDDN GEV/RVFRPEGGFRGDRAVSFV SH*AEKIWEGISQRAL/VPEFQG LWEVW/CREIDQTLGIDTILCHH HERLLQSHYGIHKSSLSMVGNS QVAALYQLNVYVVADTVGLII KNSISLDSVQPNYCSNKHIELRT QVGGARNLRANSPTMTSSYNQE SSSMENVVALSLLTVESPTSMF DYCDDSL ERVK SALDIFSMIIYT VTFFLAGNGLVVIWVVG FHM SCTVNTCLPSPDPLHGPLTCDP VANLVLEQLHTSKGN SGALED LAFGNLFLCSLLDQGN S W W K VSPSLYNQYDLQNETQGSQHL WKEIHPWHQTLVTTAHFFFGFF

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12926	43294	A	13006	3	371	AGARFNVRSR*RNDRVRPHRD VYSLQGRSLSDHSPTFGCQQTQ GRLPWSFTLSGKFRFSGEGATT SPAHIKNFQTPEPQWP GIPPEPPP TGACYTCRKS GHWAKECPQAR IPPKPHPICVGP
12927	43295	A	13007	77	332	RWKKNCNLSPPRMS*QR*WKP* MQQAACSVGETQPPCTQVK*T ALLLTQSLFGGLFTRTHMKFGA VTRIGGPPLDQSPVLLLFAP
12928	43296	A	13008	1048	1349	RVVEQDDAERLFRFRFAA/GDL PYGAFFEIF*ETQCEMQQLAE DHASVTMISLEAWRLYRKMVC RIWASMLRLSVCHLCAPKR VV SLISRNGYHLP GSIH
12929	43297	A	13009	213	499	PEQRTSHRQQRRQPPQSRSP FCPLSPRSALSLFLCDGYAAP* AYRE*IPVTEDHFAE*/ISWCP *YREALGQLLAKMRR*SARKRF QLSP
12930	43298	A	13010	2	431	
12931	43299	A	13011	2	367	
12932	43300	B	13012	1107	2083	
12933	43301	B	13013	1	627	
12934	43302	A	13014	712	2671	AHVGRGST*ALPRAMGSDAF*C PLQ*MTPASFGSKAALS RVFIKE ALMMEDPCVVRKPLSAHMTA WWCRIWKAYLESV
12935	43303	A	13015	50	1362	WEQIPHGLVLSLQQLPRRSGSIS LQPLSQEDLGRSQSSELGPEFQ GLWQWLSDFQT*HQWVVS GFQ AFSDRLKAALSASLLRF GDSD WLPS SACKCLMLGLHFVIVGN ICATLKEKYSSMLHLDVTMKK NGEKRTLQKRKKGMPPHPAY EDLNIAAITLPANVVLHQPSGFR TSGQLDPVWWSLDTDAHEIWC QDPGLGSGDFPWEITPLSSYSLL HEKDPPTTSGPQTDQPKKHLTN FKSKTKETGFIHGPKTPAPVTD WEGSLPLVFNHCRDTS LIIHPCF KGVRRRDACLGPSPLAASPAF LEKGQDLINLAFKVYNNRKKL QFLASTVRQTPATSPA HKNFQT TEPQQPGVPPPEPPTGACYMCR KIWPLGQANARSPGFLSRVPS VWDPTGNRTVQLTWQPLPEPL ELWPKALCLTDSFPDLLGLAA
12936	43304	A	13016	1	507	
12937	43305	A	13017	5	271	
12938	43306	A	13018	1	618	

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12939	43307	A	13019	1	429	
12940	43308	A	13020	1	3567	
12941	43309	A	13021	1	353	
12942	43310	A	13022	1	338	
12943	43311	A	13023	1	1175	
12944	43312	A	13024	3	326	
12945	43313	A	13025	150	494	PSPSLGYLVGTRGTALRL*DAR AAMRPFDPSTLLPTCWDYWTY AGSLTTPLTESVTWIIQKEPVE VAPSQLSAFRTLLFSALGEEK MMVNNYRFLQPLMNKRVWAS FQATNEG
12946	43314	A	13026	2	975	DSREHHPLQTGVSGNRPKMLG RNTWTKTSAFSFLVEQMWAPLW SRSMRPFGRWCSQRSCAQWTSN NTLHPLWTVPVSPVGGTRQSPI NIQWRDSVYDPQLKPLRVSYE AASCLYIWN TG YLFQVEFDDA TEASGISGGPLENHYRLKQFHF HWGAVNEGGEHTVDGHAYP AELHLVHWN SVKYQNYKEAV VGENGLAVIGVFLKLAGHHQT LQRLVDILPEIKHK\DARAAMR PFPDPSTLLPTCWDYWTYAGSLT TPLTESVTWIIQKEPVEVAPSQ LSAFRTLLFSALGEEKMMVN NYRFLQPLMNKRVWASFQATN
12947	43315	A	13027	1	1233	
12948	43316	A	13028	761	1000	IPFISFSLIALARTSNTMLNKG ERGHPSLVVPFIGNASSFCPVSM ILAVGLS*IALIILRYVPSIPNLLR VFSMKGC
12949	43317	B	13029	697	1527	
12950	43318	A	13030	1	1695	
12951	43319	A	13031	434	925	VAKIFSHFVCCFLTLMVVSFAV QKLFSLIRSHLSILSFVAIDFGVL DMKSLPMPMS*MYMPRFSSRV FIVLGLTFKSLIHLELIFV*GVRK GSSFSFLHMASQFSQHLLNRE SFPHCLFFSGFSKIR*L*ICGIIE GSVMFH*SI SLFWYQYH AVLVT VAL
12952	43320	A	13032	1124	1234	KITPKKQIRQSPNLTQNTGQQ*S LQLWEHFQISTHF
12953	43321	A	13033	929	1261	
12954	43322	A	13034	1118	1354	IPFISSCLIALARTSNTMLNRSGE RGHPCLVPVFKGNASSFPFSMI LAVGLS*IALIILRYIPSIPSLLRV FSVKGK

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12955	43323	A	13035	2	348	HQHLLFPDFLMIALTGMRWYL IVVLCISLRASDDEHF/YHVS GCINVFF*EISVHILRPLFDGVV* FFLVNLFKFFVDSGYEPFVRWV DCKNVLPFCRLPVIHSDGSFFCC AFAAL
12956	43324	A	13036	578	712	LISNFSKVSQYKINVPKSAFLY TKNRQTAKS*VNSHSQLQRE
12957	43325	A	13037	1	1833	
12958	43326	B	13038	1	1587	
12959	43327	B	13039	1	1851	
12960	43328	A	13040	1349	1444	
12961	43329	A	13041	953	1277	MVLPRESSRVFVVLGLTFKPLI HLELIFV*GVNFV*GSSFSFPHM ASQFSQHLLNRESFPFLFLSG LSKIR*L*MGHISEGSLFHW ESLFWYQYHVLVTVAL
12962	43330	B	13042	804	4236	
12963	43331	A	13043	1	744	
12964	43332	A	13044	137	797	
12965	43333	A	13045	210	418	
12966	43334	A	13046	1	927	
12967	43335	A	13047	1	1415	MGFLGTGTWILVLPQAQPK PGGSQDKSLHNRELSAERPLNE QIAEAEEDKIKKTYPPENKPGQ SNYSFVDNLNLLRAITEKEKIEK ERQSIRSSPLDNKLNVEDVDST KNRKLIDDYDSTKSGLDHKKFQ DDPDGLHQLDGTPLTAEDIVHK IAARIYEENDRAVFDKIVSKLLN LGLITESQAHTLEDEVAEVLQK LISKEANNYEEDPNKPTSWTEN QAGKIPEKVTMPMAIQDGLAK GENDETVSNTLTLTNGLERRTK TYSEDNFRDFQYFPNFYALLKSI DSEKEAKEKETLITIMKTLIDFV KMMVKYGTISPEEGVSYLEGL DEMIALQTKNLEK/NATDNIS KLFPAPSEKSHEETDSTKEEA KMEKEYGSLKDSTKDDSNPG GKTDEPKGKNRSPWPKIRK/N EWLKKHDKKGNKEDYDPFQR* EVSFNNKADAIYVEKGILDK AEAIRIYSSL
12968	43336	A	13048	1	879	
12969	43337	A	13049	3	640	
12970	43338	A	13050	134	382	DGRQLRRGSLGGALTGRYLLP NPVAGQAWPASAETSNLVGMR SQALGQSAPSLTASLPCVSKCW ENIPPPWMN/WPPH*IKHIQS
12971	43339	A	13051	87	500	

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12972	43340	A	13052	1	1356	
12973	43341	A	13053	1	447	
12974	43342	A	13054	3	107	
12975	43343	A	13055	3	2377	
12976	43344	A	13056	1	2193	
12977	43345	A	13057	1	2724	
12978	43346	A	13058	253	490	QSSIPAIMSSFLGTGAETMPVPL GAGMRRTSTEPQVCFCTGIIF KTSSLREAPRKKSMSISLMGR E/WMPVTKLGRLLVKDMKIKSLE EIYLFSLPIKESIIIDFFLGASLKD EVLKIMPVQKQTRCGSVLVRLL PAPRGTGIVSAPVPKLLMMA GIDDCYTSARGCTATLGNF/AK ATFDAISKTYSYLTPDLWKETV FTKSPYQEFTHLVKTHTRVSV QRTQAPAVATT
12979	43347	A	13059	1	819	
12980	43348	A	13060	1	623	MARRKNGKWESEIDFCLGGSL KDEVLMKIMPVQKQTRAGQCTR FKAFVAIGDYNHGILGIKCSK E/LATAIRRAILLAKLSIVPCRG YWGNKISKPHIVPCRGTGIVSA PVSKLLMMASINDCYTSARG CTAILGNFDKATFDAISKTYSYL TPNLWKETVFTKSPYQEFTHLV VKTYTRVSMQSTQAPALAKLP RVAVQPAEAV
12981	43349	A	13061	1	949	KWRITPVPTGRP/GGPGGPGMG KPRCF/RGEVFGIVIRAGSPGPG TGPGRG/GEAAGAKAED*E/WMP VTKLGRLLVKDMKIKSLEEIYLF FSLAIKKSEIMSFLGLLGRDE VFE*LCPVQEQ/TRAGQ/RATRF KAFVALTTLGTTNG/HVGLGC* VPPREVATGNSWGPFLGQALH SSPVRRLGLLGGTKNSAKPPTLV PWQR*PRAACGLCAGYAFIPLQ PRGQLASVSA/PVP/KKLLMMA GTDG/CNNSQRRGCTATVG/NL AKATTFDAISKTYSYLTPDLWK ETVFTKSPYQEFTHLVKTHTR VSVQRTQAPAGATT
12982	43350	A	13062	92	265	SFELFADKVPKTA/WLDGKHVV FGKVKEGMNIVEAMERFGSRN GKTSKKITIDACGQLE

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12983	43351	A	13063	2	797	NRVLLAMVNPVTFFDIAVDGEP LGRVSFEVRGLDTKK*LLI*SIK LC*QIGLFAKVPKTAENFR/A L*SIEEKGFGL*GVPCFHRLFPR VLCVRGGDFHTAINGTGGKSI\ YGEK\FEDENFILKHTGPGILSH GKMLDPNTNGSQFFICTAKTIE WLDGKHV\VFVKVKEGMNIVE AMEA\FGSRDCKTSKKITIA\DF GQLRIKFDFVFLSLTTKIISFCAL LSGEHPLHPIWLGVILESMWLS LAVPFVVPCFCSLPCLAGLQS
12984	43352	A	13064	1	720	
12985	43353	B	13065	98	2074	
12986	43354	A	13066	596	841	
12987	43355	A	13067	66	326	
12988	43356	A	13068	1	441	
12989	43357	A	13069	2	325	WCPSQAAAAGARATRDMPGGS MTCLCRALWWLFSWLKVHR*R QQQQGRPAAPSAGPAKPTPTRN SSWLLAAPVPTRTSPSTPPCKL REPAPALASPERGSHSAAVG
12990	43358	A	13070	38	1066	
12991	43359	B	13071	1	324	
12992	43360	A	13072	2	680	
12993	43361	A	13073	2	165	
12994	43362	A	13074	1	1110	MASLLKSARPTQHWKEETPETS KRLKEQTPDIPSLRAVTLIAKVH SFIPEVCETKNPLEGIHSGHILAP NVGSPSPRRQARVQVFENVSVR ATKSDLPQSSLWSRRKTTVSAA ASKKTSKEISKGPQKPPGY/PVT SPSSCRGRGIWPNP/EYMTSPS LI*/SQIKVDLGKISDDPDRYIDV LQGLGQTLDSLWRDVMLLLDQ TLAFNEKNAALAAAEQFGDTW YLSEVNDRMTAEERDKFPTED GEPIKDCQQIIVQTYAAQDDIL EVPLANPDNLNLYTDGSSFVENG IRRAGYAIVSDVTILERPNLFRA IQQVVKACEVCQRKNPLVHPP NYLYKTLNLTHSLNLQSNPSLA NDCWLCSSLVSVAEPYN

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
12995	43363	A	13075	450	1776	RGGRACLRP*AA/SPGPSTP*WP PPRGVQAAAILSGPPRPAPPKG AASQRLCGGFVEARQAWVGRR GRRGVPVGETQPPPSVIQPPSRG AG/PRDQQPAMPEPPTPSVGSC AARASQISAAPCSTAPSPIDHPR AECCRRTVWDWQAAPPAQV RDPLGEASWAPESGGDVENLY VLLRDCKYTSQHPVSSSGSVNA PIDTLYLATLLRDCKYTNRHVS SSSRFVNTPISTVSSEFANAPID TLHLATLKEETPNTSEHQKEQT PDMPLRTVTVTARVRGFILDV SETKNPPIPDITWRPWRDLRQS PSNQTLAFNEKNAALAAQEF GDTWYLSQVNDRMTAERDKF PTEFIPSSGFLVLLTSRMKPQTF AASVTALKDGVSRVCSFRCVQS FFLPSADWCIYKPLARYALIG AFLQSAHWCVYKPLARHSVL GAFTNL
12996	43364	B	13076	1	1999	
12997	43365	A	13077	3	469	
12998	43366	A	13078	224	410	
12999	43367	A	13079	478	675	
13000	43368	C	13080	55	237	
13001	43369	A	13081	109	239	
13002	43370	A	13082	2	88	
13003	43371	A	13083	2	178	
13004	43372	C	13084	278	460	
13005	43373	C	13085	50	217	
13006	43374	A	13086	3	251	
13007	43375	A	13087	1	759	
13008	43376	A	13088	2	604	
13009	43377	A	13089	1	558	
13010	43378	A	13090	3	1055	
13011	43379	A	13091	1	466	MDKFLDTYTLPRNLNQEVEESLN RPMITGAEIVAINSLPTKKSPPGD GFTAIFYQRLISNFSKVSQGYRIN VQESQAFLYTINRQTESQIMSA LPLTIASKRIKYLGIQLTRDVKD LFKENYKPLLNEIKEDTNKWK NIPCSWVGGRINIVKMAILPK
13012	43380	A	13092	2	848	
13013	43381	A	13093	458	625	
13014	43382	A	13094	482	745	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in US 9,540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
13015	43383	A	13095	1	742	MNIDAKILNKILANRIQQHIKKL IHHDQVGFIPGMQGFNIRKSI NVIWHINRTKDKNHMIIIDAE KVFDKIQQPFMLKTLNKLIGDG TYLKILRAIYDKPTANIILNGQK LEAFPLKTGTRQGCPSPLLFNI VLEVLAIRQEKEIKGQLGKE EVKPSLFADDVIVYLENPIISVQ NLLKLISNFSKIKYLGQLTRNV KYLKFNKYKSLLEIKEDTNK WKNIPCSWIGRINIVKMAILPK
13016	43384	A	13096	1	1458	
13017	43385	A	13097	2	1624	
13018	43386	A	13098	1	1095	
13019	43387	A	13099	1	2913	
13020	43388	A	13100	2	1887	
13021	43389	A	13101	1	972	
13022	43390	A	13102	1	873	
13023	43391	A	13103	1	1365	
13024	43392	A	13104	1	867	
13025	43393	A	13105	1	591	
13026	43394	A	13106	1	990	
13027	43395	A	13107	1	2109	
13028	43396	A	13108	1	843	
13029	43397	A	13109	1	1203	
13030	43398	B	13110	1	1221	
13031	43399	A	13111	1	1092	
13032	43400	A	13112	1	931	
13033	43401	A	13113	1	1293	
13034	43402	A	13114	1	544	
13035	43403	A	13115	3	718	
13036	43404	A	13116	693	1397	ARAEVKLSLFADDMIVYLENPII *ARAEVKLSLFADDMIVYLENP IISAQNLKLLISKFSKVSRKYNV QKSQAFLYTNRRQTESQIMSEL PFTIATRKIKYLGQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWIGRINIVKMAILPKVIYRF SAIPIKLPMTFFTELEKKNWLAI CRKLKLDFFIPYTKINSRWIKD LNVPRKTMKTLEESLGNITQDI GIGKDFMTKTPKAMATKAKRA SAQQKKLPSE
13037	43405	A	13117	1	2814	
13038	43406	A	13118	1	1302	
13039	43407	A	13119	1	1542	
13040	43408	A	13120	3	1327	
13041	43409	A	13121	1	1023	
13042	43410	A	13122	1	1448	
13043	43411	A	13123	1	1038	
13044	43412	A	13124	3	1711	

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13045	43413	B	13125	1	1756	
13046	43414	A	13126	1	923	
13047	43415	B	13127	1	1515	
13048	43416	B	13128	1	1560	
13049	43417	A	13129	1	4032	
13050	43418	A	13130	1	2684	MVKGSIQEEELTILNIYAPNTG APRFIKQVLSDLQRDLDSHTLI MGDFNTPLSTLDRSTRQKVNK DTQELNSALHQADLIDINRTLH PKSTEYTFSSAPHHTYSKIDHIV GSKALLSKCKRTEIITNYLSDHS AIKLELRKLNLTQSRSTPWKLN NLLNDYVWHNEMKAEIKMFF ETNNKNDTTYQNLWDAFAV CRGKFIALNAYKRKQERSKIDT LTSQLKELEKQEQTSHKASRRQ EITKJRAELKEIETQKTLQKINES RSWFFERINKIDRLPLARLIKKR EKNQIDITIKNDKGDITDPTIEQ TTIREYYKHYANKLENLEEM DTFLDTYTLPRLNQEEVESLNR PITGSEIVAIINSLPTKKSPGPG FTAIFYQRAIYDKPTANIILNGQ KLEAFPLKTGTRQGCPLSPLLF NIVLEVLARAIQKEIKGIQLG KEEVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSQYKINV QKSQAFLYTKNRQTESQLMSEL PFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNI PCSWVGRINIVKMAILPKVIYR FNAIPKLPMTFFTELEKTTLKFI WNQKRAIAKSILSQKNKAGGI TLPDFKLYKATVTKTAWYW YQNRDIDQWNRTEPSEIIPHIYN HLIFDKPEKNKQWGKDSL FNK WCWENWLAICRRLKLPFLTP
13051	43419	A	13131	1	1149	
13052	43420	A	13132	127	329	
13053	43421	A	13133	1	1132	
13054	43422	A	13134	1	1020	
13055	43423	A	13135	803	2009	
13056	43424	A	13136	1	1944	
13057	43425	A	13137	1	1282	
13058	43426	A	13138	1	2423	
13059	43427	A	13139	1	2694	
13060	43428	A	13140	1	1195	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,954,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
13061	43429	A	13141	6082	6984	KLAQDRDALSPPLLFNIVLEVL ARAIQKEIKEIGIQLGKEEVKLS LFADDMIVYLENPIV/SAPKSPL RLISNVSVK*GYKINVQKS/QA FLYTNNNTDKQESQIMSELPFTT ASKRIKYLGIQLTRDVKDLFKE NYKPLLKEIKEDTNKWNIPCS WVGRINIMKMAILPKVNYRFI NSMPSIPIKLPMTEFTTELEKNYF KVHMEPKKSPHCQVNPKTKEQ SWRHQRYLTSNYLQGYSNQK STISMVLVPKQHGTGTKEIIDQ WNRTEPSEITPHIYNYLIFDKPL LEKNKQWGKGFI
13062	43430	A	13142	193	335	MVEEKLTLPKDEK*KSKQRSY RKTLLQELKNKNEKRNKKNKW QVKTH
13063	43431	A	13143	131	427	
13064	43432	A	13144	1	360	
13065	43433	A	13145	2	376	
13066	43434	A	13146	1	360	
13067	43435	A	13147	2	376	
13068	43436	A	13148	3	469	
13069	43437	A	13149	224	410	
13070	43438	A	13150	478	675	
13071	43439	A	13151	32	161	
13072	43440	A	13152	1	1671	
13073	43441	A	13153	1	1656	
13074	43442	A	13154	62	1295	
13075	43443	B	13155	149	320	
13076	43444	A	13156	12	89	
13077	43445	A	13157	28	417	
13078	43446	A	13158	2	440	
13079	43447	A	13159	190	553	EIVREGASFIRHLRWSRHRKC RFSVKTLTGEDPSTLEVEPS/DT IE/NVKAK/IQDKEG/PPDQQR/L/ VSFAGKQL/EDGRDSLGSY/NIQ KGSLLHPCV*DFRGGAKKKEE ESLYTTSRPRKD
13080	43448	A	13160	3	415	PVK/VGA*GGQVINGVLAQV*L TVGPVGPRTHPVVFIPVPECRIG RDILSSWQNPHTGSLTGRVRAF MVGKAKWKP*ELPLPRKTVNQ KQYRIPGGIAEIS/A/TIKNLRG VVIPTTSRFNSPIWPVQKTDGS W*TAADY

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13081	43449	A	13161	5	405	HCCGIPHSIAEQDTYFMAKEV WQWAHAHGIHWSYHVPHHLE AAGLIEQWNGLLMSQLQHQLG DNTLQGWGKVLQKVYYALNQ RSIYGTVSPIRIHGSRNQGVVE EVALLTVTPNDPL/GKY*L.PVPV TLHSDR
13082	43450	A	13162	138	387	
13083	43451	C	13163	184	297	
13084	43452	A	13164	1	430	
13085	43453	A	13165	1	867	
13086	43454	A	13166	35	601	CLSRRAAPVYLASMSGRGKGTG G/KARAKAMSRSSRAGRPSQ VGR/VHRLLRKGHYAERVGR QPCCYLG*CMYELT*ESWS MAGNAARN\KKTRIPIRHLQ LAIRNDEELNKLA WAALTIAQ GSR/VLPNIQARCCGPR*TSATV GPKAPSGGEERATQASARSTK RARAAAGRPSVPMPPQRP
13087	43455	C	13167	11	313	
13088	43456	B	13168	1	552	
13089	43457	A	13169	1	621	
13090	43458	A	13170	55	296	
13091	43459	A	13171	959	1182	WVYLF*PSCKGVIYP*AAGFESI FWWVTINKNIDWINIYYNQ QFMNYTRDAVKGIAEQLGTNC QMAWENRIALDMILAEGRGVC IMIKTECCAFIPNNTAPNGSITK ALQGLTALSNELASSSGVNDPF TGWLEKWFGKWGITASILTSL TAVMGVLILVGCCVPIICGLV QRHRGPPLVVIETKPLGLERLA GLPVGHALKLSGIQATPQNGE NADRREAFPAAS
13092	43460	A	13172	1	540	
13093	43461	A	13173	2	142	
13094	43462	A	13174	42	384	
13095	43463	A	13175	102	329	
13096	43464	A	13176	1	1257	
13097	43465	A	13177	1	378	
13098	43466	A	13178	1	1143	
13099	43467	A	13179	1	481	SDSELNRPVMTMKNFPVFTSDR SKNRKRHFNAPSHVRRKIMSSP LSKELRQKYNVRSMPIRKTDEV IQVVRGHHYKGGQIGGQSPRCTR KKYVIYIERVQREK\ANGTNC TWGISPKARWLFTRLKLDKDR KKILERKAKSRQVGKEKGKYK EELIEKMQE

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13100	43468	A	13180	39	556	AAAGYFAEDCEASCVCVKHPP SVKKARCFLSELIKKPSGGSVTL SESTAIISHGTTGLVTWDATLYL AEWAIENPAAFTNRTVLELGSG AGLTG/VAICKMYRPRAFIFSDC HSRVLEQLRGNVLLNGLSLEAD ITANLDSPRVTVAQLDWDVAT VHQLSAFQPDVVIAADVLY
13101	43469	A	13181	46	231	
13102	43470	A	13182	1	1503	
13103	43471	A	13183	3	340	FFFANTFYCVFNVLVNAPLRF SLPSTQSLKLRDSSDSELRRD ILQKVRIPESLGLMTLPPELRLK T*EKNRRCACTL*K/TPVQRTKP LSQHCRVWVWAPPTAPALSFSTK
13104	43472	A	13184	2	594	
13105	43473	A	13185	1	1470	
13106	43474	B	13186	79	1355	
13107	43475	A	13187	248	540	
13108	43476	A	13188	386	1388	
13109	43477	A	13189	386	1334	
13110	43478	A	13190	3873	4070	
13111	43479	A	13191	146	510	PPCAVCLLWIAAVYCLSTTFC APLCGQNTWLPKPCRHVNRRA SNASVSLSTVTLFSRLS*PQRKG SELLDSSGPLPASPLPLCSGVS PRAGLGSAPWPKIPFLGIREAKN PRSENTRLTT
13112	43480	A	13192	21	95	KCSSNGAPDAVHE*DLPWTGPG AC
13113	43481	B	13193	1	477	
13114	43482	A	13194	228	935	PLSSSMAAELEFAQIIIVVVTV MVVVIVCLLNHYKVSTRSFNIR PNQSRREDGLPQIMHAPRSRD RFTAPSFQIRDERSRFQPTYPYV QHEIDLPTTISLSDG/EEPLLYQV PCTLQLRDPQQMELNRESVRA PPNRTIFDS/IDLDIAMYSGGPCP PSSNSGISASTCSSNGRMEGPPP TYSEVMGHHPGASFLHQRSN AHRGSRLQFQQQNAESTIVPIK GKDRKPGNLV

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13115	43483	A	13195	526	1629	FYSFDSARGEAPRPWRVRGLEGRVELGQQLGLLTLGPAPFPGGLGTQQRVGLPGPAGPGAGEGQAGPAEAGQVPVGGLADEAVEHGVGDVAEAGEQEGEVVGVENALGEVAAGLPDAAHQQQHVVGQEAGQEDDHGAHQPLDLVLAALLGAVAPAHGAQDALVGRQQQADGEEEA/LPGSGSS*WHAAMPGWGSAQSTRGAGSRPR*PPRASGSRCSWAAPWR*PR*RRRPPSGSGTGGSGRDPQPGSGRPTMQQRKPTLM*MFYRRTPTGRTGRRETSCRAAARTAAARRASRCRRGRPPSGCTGTRPARSGP*SAGSEVEGQAVGREAHHQHGNIDHRGQRLVDGMVDGTAHRRGVVCSDDVPH
13116	43484	B	13196	2699	7361	
13117	43485	A	13197	67	1523	
13118	43486	A	13198	1	287	
13119	43487	A	13199	2	563	
13120	43488	A	13200	96	401	
13121	43489	B	13201	1	480	
13122	43490	A	13202	1	924	
13123	43491	B	13203	13	1512	
13124	43492	A	13204	1	402	
13125	43493	A	13205	609	803	RDPRNPSSA\FQAGGIALMLITRGEDLTGGVIHQYPPGGMNLWMQGTAGNQRRRAENAAQQQ
13126	43494	A	13206	3	526	VTETALTLPYLVAKHGYFLPQDLAKRTETMNWLFWLQGAAPFLGGGFGHFYHYAPVKIEYAINRFTMEAKRLDLVDKQLAQHKFVAGDEYTIADMAIWPWFNGNVVLGGVYDAAEFLDAGSYKHVQRWAKEVGERPAVKRGRIVNPTNGPLNEQLHERHDPDFQNTNENNRQG
13127	43495	A	13207	1	250	
13128	43496	A	13208	1	489	
13129	43497	A	13209	209	601	
13130	43498	A	13210	1	96	
13131	43499	A	13211	1	1110	
13132	43500	A	13212	1	595	
13133	43501	A	13213	1	240	
13134	43502	A	13214	1	675	
13135	43503	A	13215	1766	1957	
13136	43504	A	13216	1	426	
13137	43505	B	13217	94	3238	
13138	43506	A	13218	1	2370	

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13139	43507	A	13219	1	2796	
13140	43508	B	13220	43	566	
13141	43509	A	13221	1	903	
13142	43510	A	13222	3	110	
13143	43511	A	13223	2	755	
13144	43512	A	13224	1	1338	
13145	43513	A	13225	1	807	
13146	43514	A	13226	1	918	MARADTVSVPMFMGLAAKPC WRDTEPNTGYRGPHVNRNIQLT HDPRLDYRSI/LIDINDIGQTFHE RLHPDAC/LSNAILVHNKKGPP LADGIVITPSHNPPEDGGIKYNP PNGGPAVPTSLKWWKTGPTHC WPMMA*KA*SVSPARRSDGIRSKN DVIDTSDDDM**QCLSRSSNG HPGAKVANLVPKTTTFIDGVDQT SFFLGTNGQSNRKAHEYFLNGK LAAVRMDEFKYHVLQQPYAY TQSGYQGGGTGTVMQTAGSSV FNLYTDPQESDSIGVRHIFMGV PLQTEMHAYMEILKKYPPRAQI
13147	43515	A	13227	1475	2904	FWRAAAPIDCWRSGAVKKQH VEVTQLDWTTPGRQYAGPIPCS RRGYCPLPRSGSVRWADL/FPP A/LD/LAGHPG/AKVANLVPKTT FIDGVDQTSFFLGTNGQSNRKA EHYFLNGKLAAVRMDEFKYHV LIQQPYAYTQSGYQGGGTGT MQTAGSSVFNLYTDPQESDSIG VRHIFMGVPLQTEMHAPGLPLA SSMKRWIRRTGFIKGKEQFED VVPVLGSKVNGVQFNALVAD SLGISQIRCRCAIFLTVVFPVLH KQAFDLISLLQQPGRNGGIDT AGHADDYFFCGFRHWITHDIEL QGGARQKDAADHYLAGDIESL PLATATFDLAWSNLAVQWCGN LSTALRELYRVVRPKGVVAFET LVQGSPLHQAQVAVDERPH ANRFLPPDEIEQSLNGVHYQH IQPITLWFDDALSAMRSLKGIG ATHLHEGRDPRILTRSLOQLRQ LAWPQQQGRYPITYHLFLGVI
13148	43516	A	13228	215	525	LAWARRCRLLAKATSLIRAPS SEMRASTPCRQRRPSGYSWY GRSPRAVLEGLRVGAHLRSAN CPWPSR/SQVVELIPDGPVFLD FTKIPGRDTQNEHIVLLH
13149	43517	A	13229	1	942	
13150	43518	B	13230	1	1201	
13151	43519	A	13231	685	921	

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13152	43520	A	13232	2	251	
13153	43521	A	13233	2	100	
13154	43522	A	13234	5	1093	
13155	43523	A	13235	2	482	
13156	43524	A	13236	1	2496	
13157	43525	A	13237	572	912	RCRPDKAFTPHPAIGARCLMRR LRVLSCLQPLPNVGWIRRLRRIR QFSAPDEGAKCRVAIQ/DFDA QYGRFLEVTSGAQQRFQTD*K HAAALPFFFPSSAYSLAAISVVF GFR
13158	43526	C	13238	5	127	
13159	43527	A	13239	1	444	
13160	43528	A	13240	17	261	
13161	43529	A	13241	173	397	
13162	43530	A	13242	169	421	LKPKNLDEKLLPASSSSCRIWA TSPVHHLWQVLKKILFGWNP KSPRCLS/TRQAMFSLSKKASLP WTIAARSADQRCRTIAEL
13163	43531	A	13243	17	744	RPHQEORAGCGVNALSSLRSA TAVGMIRASVASG/DRAPIAG CGVNALSGLHRHFIEVTCTHFL LVRYEGIAIFRGGKFRLHLFLN VVLHTLALGIGVCQVKHVEPH AVDTCQGDELELVAHIRQLLLE AGNSFVVEVYLPVERRRAVISQ QFARIFRVDSLCKATRFQIRRG RSHQTGQHMGIIRRVDAAHAD DRRTSGRVPPLIQVCPAHSSEA VVVVDVDVDVDVDVDVIGAV
13164	43532	A	13244	954	1104	
13165	43533	B	13245	54	1169	
13166	43534	A	13246	35	3066	VGHSTRPAASGPAAGIGRSPA RLVQQPQORSLAKPLNRPAAQR GLLPQRRHPKRTKRRKQAQN PQKRLPHRQPVRRRRHHRRLL QKMRRPDKRQORRAAPRRHPR RRQRLLA VRRRLRAKVRNRP RQRA PQQLNGQRILHPPWRRLR MQVRRKRG*YSSAVRPTVRLK RWRQRQRQ*NQPMTMQRNV RKTRTALIYP/YKGCFLNNINAV SKDTFADKRGMRVYRVNAPAG ATSGKYYPPVVMRSAGSFHI
13167	43535	A	13247	1	2919	

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13168	43536	A	13248	1	3211	MEFTSLTPDDLRLVLELYRTPFS DGYVFHSMQFHIFDLLKSGQN VVLASPTSMGKSAIVDSLLGMG TLKRLVLVPTVALADETRRRL QERFGDRYQIIHSSQVCHSDQ AVYVLTQERVNERDDIVIDLF VIDEFYKLAFRQLKSGDIDHQD ERVIELNIALSKLLKVSRQFYLT GPFVNSIRGLEKLGYPHTFVST DFNTVALDVKTSASKRMTTKP SSKRWGKSRTCVDADHIKNGIG LHFGALPRALQQYT
13169	43537	A	13249	486	3882	LRLRGEALPVASGCLANATDTP AGTTLWATERHAVQ**TCEA DTLGSCGYAAKPCLSPPVAVWQ MLLTRLLEQHYGLTLNDTPFSD EPVLTAPIDAAALRGIEFGKFQ GNMVGDIIECGSDVTDYAVG DSVCGYGPLSETVIHNAVNNYK LRKMPQGSSWKNAVCDPAQF AMSGVRDANGARRGFWWGGL GAIRVQLAFKWLNAAGRLPGG GLGGPIPSAHRCDIARRHGAD FCLNPIGTDVGKEIKTLTG
13170	43538	B	13250	1	1116	
13171	43539	A	13251	729	985	SAPPQLAPSLPDRATDPDTCWP PG*RP*RYLPSRQIDCFNTRFRLL QRLTASQCAEAVDVAFRLTV QQTPHFRCAQLRQRAFRID
13172	43540	A	13252	395	605	
13173	43541	A	13253	1	1140	MIYVFVTVKHRNDHFTKNTLA SYRGRTLLGLTFKGVYHLYKD ETYLQSGKGHTIQEVRIKGL NNPDLDAAVGEDLAQQLRDEL ELVKGASNEFDKELFLAGEITP VFFGTALGNFGVDHMLDGLVE WAPAPMPRQTDTRTVEASEDK FTGFVFKIQANMDPKHRDRVA FMRVVSQGYEKGMLKRVQRT AKDVVISDALTFMAGDRSHAY PGDILGLHNNHTIQIGDTFTQG EMMKFTGIPNFAPELFRIRLK DPLKQKQLLKGLVLQVLEEGAV QVFRPISNNDLIVGAVGLQFQD VVVARLKSEYNVEAVYESVNV ATARWVECADAKKFEFKRKN ESQLALDGGDNLAYIATSMYV LRLAQERYPDVQFHQTREH
13174	43542	A	13254	1	1495	

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13175	43543	A	13255	372	1365	IRYFENRGLFAHCATRTGQFPP HCILASYKCGEQPDSSSNHPRN LFVWRSNLLGSSG/KGHEYMQ KYL LGTESGIQGEELGASDGIKP EEVEWQTA AIEGKLDLVLTLDF RMSSTCLFSDIVLPATWYEKD DMNTSDMHFPFIHPLSAAVDPA WESRSDWEIYKGIKAFSQCVCV GHLGKETDVVLQPLLDHSPAEL SQPCEVLDWRKGECDLIPGKTA PNIVAVERDYPATYERFTSLGP LMDKLGNGMDLTDYANMALSI PSANTDIWNLEQDVTGTRLTNS RHGLADNGGAWVS YFGGNFN GDNGTINYDQDVNGIMGVVD KIDGNDG
13176	43544	A	13256	3	1444	
13177	43545	A	13257	61	1058	LPYLIALLARAWFNGLLTSRTR LYIKGNIGIVL PKLQEMVADVS HHFPLRLPAPT PKALYSPCEIRH LAINVNLEYDPTAAFRNQVVHF DFRKL DVFSFGENQNC LVGNV DLLYRNSWNEVRTLHFNGEQS MIEALKTILGKMHQDAAPPDSV EVFCYSQHLRLIRTRVQQLVS ECIELRLSSTRQETGRFKALRVS GQTWGLFFERLNVSVQKLENAI EFYGAISHNKLHGLSVQVETNH VKLPA VVDGFASEGIIQFFFEET QDENGFN IYILDESNRVEVYHH CEGSKHEELVRDVS RFYSSSHDR FTYGSSFINFNLD PPLYLARVSI
13178	43546	A	13258	1	1133	
13179	43547	A	13259	2	240	ISSARHFGALACTLELGKALT GQNDLRQFAVTA SAIAALL/SR HSPSFEMHMASD TLNFMPEFK GTLLAQDGEERFTVTH
13180	43548	A	13260	1	358	LPFLPSGLRGLA AENKIRRP GSFLGPCCGLRGKL V/ISAALM STTIPISRVQGLLQFLNSKSPISR AERSWSTFGASA AFLTTLASLL FLFPPLA ISSLANSAFA VFPPTPC AGSP
13181	43549	A	13261	1	1635	
13182	43550	A	13262	1	1363	
13183	43551	A	13263	5	249	
13184	43552	A	13264	15	280	
13185	43553	A	13265	6	363	

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13186	43554	A	13266	78	346	TRYAMLTRHDNHLKSFYLARG RYRADFHAPETNTGERCYRYK PLPYWLE*RRGRNRYPALQ*TM FLPADGPARCLSRQAAILKESV LPK
13187	43555	A	13267	568	831	ELQRHVLVVFAGFWIVKNSRN LFLVCAEHRKSVVKGLLRQQ GQGFWFHFQDGFAVEVGNAN VIGSE*IVFGIVFPHRERCLVDK
13188	43556	A	13268	3	419	
13189	43557	A	13269	1	561	
13190	43558	A	13270	1	741	
13191	43559	A	13271	2	1040	
13192	43560	B	13272	1	1974	
13193	43561	A	13273	2111	2340	EVFIRDKLMERRNRRTRGTEKA /RDRTVRTWIGEAVAAAAADG VTFSVPVTPHTFRHSYAMHML YAGIPVKVLQSQCI
13194	43562	A	13274	470	813	KTTSPAKLNFACRISLLASAEV NPNISAYLATWISQIPSCSCRVP SDFLIWSNTRYSRF*SRRRLVG EAV/AAAAADGVTFSVPVTPHT FRHSYAMHMLYAGIPLKVLQS LMGH
13195	43563	C	13275	440	1180	
13196	43564	A	13276	1	1290	
13197	43565	A	13277	1	1036	MKLMETLNQCINAGHEMTKAI AIAQFNDDSPKARKITRRWRIG EAADLVGVSSQAIRDAEAKGR LPHDPMENSRRDRFEQGFEPDV RILLTKYSNSNGSQSPWMEEQI RDAWGSMLVKNVRETDEVG KDPRPLPYLGHDEPYTFDINLS VNLKSMVVG GTDMGQEPKQ MGAWGPLSLKAMGFFIRGYG FFTPFGRITLPLGFGSTPPFTPL LTKTIGVFILDKLMERRNRRTG RTEKARIWEVTDRTVRTWIGEA GAAAAADGVTFSVSVTPHTFR HSYAMHMLYAGIPLKDLQSLM GHKSISSTEGYTKDFSLDVG/AR HRVQFAMPESDAVAMLKQLF
13198	43566	A	13278	366	672	RNGTHPRYIEAVPWGALPAD/G VTFSVPV/TPHTFRHSYAMHML YAGIPLKVLQSLALRELQQA VHAGLPQAKILFDGGSEIGKIPH IVLYKPVCQSLWAFVH
13199	43567	A	13279	2602	2976	
13200	43568	A	13280	982	1347	
13201	43569	A	13281	1	780	
13202	43570	A	13282	568	891	

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13203	43571	A	13283	1	718	MKEKPSSPRQYSYSLSSMILLG GGESWNLRLADQLRIFAKSWP RASRYQQGHQDLFILRSDLPSQ VFIRDKLMERRNRRTGRTEKAR IWEVTDRTVRTWIGEA VAAAA ADGVTFSPVPTPHTRFSYAM HMLYAGIPLKVLQSLMGHKSIS STEYVTKV/FALDVAAPHPSTP VHLPSPRENKIPPPIMRIPCGLPTS PIEQKQGISATGTQWRRLKQE TRLSSVSARLMSYVGVCMC
13204	43572	A	13284	1	496	AMFGFFIRGYGFFTPFGRTLFLP FGGSTPPFTFPLLTKTIGVFILDK LMERRNRRTGRTEKARIWEVT DRTVRTWIGEA GAAAAADGVT FSVSVTPHTFRFSYAMHMLYA GIPLKDLQSLMGHKSISSTEGYT KDFSLDVGARHRVQFAMPES DAVAMLKQLF
13205	43573	A	13285	2	545	
13206	43574	B	13286	1	735	
13207	43575	A	13287	1	1599	
13208	43576	A	13288	583	1005	
13209	43577	B	13289	31	1239	
13210	43578	A	13290	1	1023	
13211	43579	A	13291	1	933	
13212	43580	A	13292	1	1278	
13213	43581	A	13293	1	705	
13214	43582	A	13294	2	893	
13215	43583	A	13295	88	429	
13216	43584	B	13296	1	1419	
13217	43585	A	13297	1	2784	
13218	43586	A	13298	163	416	RNGTHPRYIEAVPWGALPAD/G VTFSPVPV/TPHTFRFSYAMHML YAGIPLKVLQSLRALRELQAV HAGLPQQA KILFDGGSEIGKI
13219	43587	A	13299	740	1431	CCQTLPVFHPHPSHLGPRPCPP TH/HLPSEHRS/LFLEAACHDS LEPLNLSGSKTSKPSLPPKAKK PKGLEISA/RPAGALRHRRLHR PQQSPPLGIPHPSL/TAQVFIR DKLMERRNRRTGRTEKARIWE VTDRTVRTWIGEA VAAAAADG VTFSPVPTPHTRFSYAMHML YAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
13220	43588	B	13300	1	858	
13221	43589	B	13301	1	1098	

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13222	43590	A	13302	1	1047	MNRQLSDSYTETDKPSDVTTS ETRSPPGSAKTTMIDTLKKLQ DVLKTEDSKNPTKSAADLLEQ YVKATGPHEILQKATKTMEMI MIVEEKASDELQDPPELQQRVI HSVRGKPGLVKQRTQEITRLR LAGLTVSSPLKRSHSLAKLGSL TFSTEDLSRPPGPPGPPGLHP GPPRRPPKLPAPPGCSVHC CHYPLHFVVSPLGFGYCSLMRI QIVFVTAHVHDSALLPLDASL APEALQNFQRYTGQIHVIRIGM AERMWCDNRNRHTVSSSGGN RLPNPAPLPNPGVL SAPPNLIQR PKADDTSAATIEKKATATISAK PQITNPKAEIT* NPRVWQGSWI GEAVAAAAADGVTFVSVPTPH TFRHSYAMHMLYAGIPLKVLQ SLRSQ*SVRGKPGLVKQRTQEI ETRLRLAGLTVSSPLKRSHSLA KLGSLTFSTEDLSRPPGPPGPP PPGLHPGPPRRPPKLPAPPP GCSVHCCHYPLHFVVSPLGFGY CSLMRIQIVFVTAHVHDSALL PLDASLAPEALQNFQRYTGQIH VHRIGMAERMWCDNRNRHT VSSSGGNRLPNPAPLPNPGVLS APPNLIQRPKADDTSAATIEKK ATATISAKPQITNPKAEITRFCL
13223	43591	B	13303	1	1185	
13224	43592	A	13304	529	774	
13225	43593	B	13305	1	1089	
13226	43594	A	13306	712	1024	GVESNLVVVVVALCHRLIYLVW GTRTVRTWIGEA VAAAAADGV TFSVAVTPHTFRHSYAMHMLY AGIPLKVLQSRVVALDVAARH RVQFAMPESDAVAMLKQLS
13227	43595	A	13307	556	1040	
13228	43596	A	13308	1	984	
13229	43597	A	13309	95	428	
13230	43598	C	13310	1	426	

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13231	43599	A	13311	116	1746	SSVTGRTEKARIWEVTDRTV/R RPWIGEAVAAAAADGVTFSVP VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEYTKVF ALDVAAARHRNRFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS CIVSLKIDWIERVQLPQSYQLY YFELAIPIVGYFYPGFSFSTASRL LLHPRGLRAITIAVFGKQNTYIR LEPFKINVLEQITKHIEKLQCGG VVKQLSRRGNNQHSISTYDINR ADTQVRRAVNNYDIIVMSNSFN GQSEHQVWIARLTWVIGTINVV CAADVLIPTPAELFDYTSALQ FFDMLRDLLKNVDLKGFEPPDV RILLTKYSNSNGSQSPWMEEQI RDAWGSMVLKNVRETDEVG KARLTWIGTINVVCAADVLI PTPAELFDYTSALQFFDMLRDLL LKNVDLKGFEPPDVRIILLTKYSN SNGSQSPWMEEQIRDAWGSMV LKNVRETDEVGKEPPSTNTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEYTKVFALDVAAR HRVQFAMPESDAVAMLKQLS
13232	43600	A	13312	1	1593	
13233	43601	A	13313	1	2536	
13234	43602	A	13314	887	1205	RPEKAR/IWGVTDRTVVRTWIGR AVAAAAADGVTFSVPVPPHTF RHSYAMHMLYAGIPLKVLQSL MGHKSISSTEYTKVFALDVAAR RHRVQFAMPESDAVAMLKQLS
13235	43603	A	13315	79	351	
13236	43604	A	13316	1	2320	
13237	43605	A	13317	187	798	
13238	43606	A	13318	2089	2610	
13239	43607	A	13319	1	1407	
13240	43608	B	13320	154	3682	
13241	43609	A	13321	1	1206	
13242	43610	A	13322	1	255	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, \=possible nucleotide insertion)
13243	43611	A	13323	3058	3160	GSAA*LPPLPAAFSGCWLSQLRHPDLHV*NEIYHLLH*KSFTSC*HNLSS*PRYPYLSSERVLW*CLSFISKI*SVTMP*DLISLW*KLEPLTCRSTSHFRQKLAQ/RLP/AYQQGHQDLFILRSDLP SQVFIRDKLMERRNRRTGRTEKARIWEVTDRTVRTWIGEAVAAAAADGVTFSVPVTPHTFRHSYAMHMLYAGIPLKVLQSLMGHKSSISTEYVTKVFALDVAARHRVQFAMPESDAVAMLKHYPEINALALYLKCGTEWIC
13244	43612	A	13324	1	1812	
13245	43613	B	13325	1	1776	
13246	43614	A	13326	583	751	
13247	43615	B	13327	826	2097	
13248	43616	A	13328	1810	4163	
13249	43617	A	13329	686	2939	
13250	43618	A	13330	1085	1690	SYFIMVKVGTSYVPINVSFSPKVGPASRYQQGHQDLFILRSDLP SQVFIRDKLMERRNRRTGRUIYKARIWEVTDRTVR/TWICRGLPAAAAADGVTFSDPGPPHTFRHSYAMHMLYAR*YR*KFLQSLMGHKSHPINGKATPKVFGPGMGLARA/HRGAGWQWPKSDAVG\MPKQLSLRINALGLYMETGKPEGIMLFFGC
13251	43619	A	13331	3	327	
13252	43620	A	13332	3	337	
13253	43621	C	13333	167	413	
13254	43622	A	13334	1	1256	
13255	43623	A	13335	1	1078	
13256	43624	A	13336	3	976	
13257	43625	A	13337	1	1004	
13258	43626	A	13338	2	291	WRKIYEANGKKRKRLQSL*SLMKQTLNQQRSKETKKASA/SMRIKYLGIQLTRDVKDLFKENYKPLLNEIKEDTNKWKNIPCSWVG RINIVKMAIPPK
13259	43627	A	13339	1	2022	
13260	43628	A	13340	1	2262	
13261	43629	A	13341	5	283	
13262	43630	A	13342	1	1245	
13263	43631	A	13343	1	1203	
13264	43632	A	13344	1	687	
13265	43633	B	13345	1	1371	
13266	43634	A	13346	1	2241	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13267	43635	A	13347	1	832	LKKCIKTP EIPSKHVRNWVPKV LEQRRQGLETYLQVASITLIPKA DEDTPKKKTTDKNSWTGTDAK VFNKILEIKFSSILKRLYWPVLE VLARAMRQEKEIKGIQLGKEEV KLSRFADDMIVYLENPVSAQN LLKLISNFSKVSQYKINQVKSQ AFLYTNNRQTESQIRIKYLGIGI LTRDVKDLFKENYKPLKEIKE DTNKWKNPCSWVGRINIVKM AILPKRYPFCQLCHQSAISTTKG VFTSILPLLMIEQLVSGRSCPSV AWSSMECTTV
13268	43636	A	13348	1	1314	
13269	43637	A	13349	1	843	
13270	43638	B	13350	1	1011	
13271	43639	A	13351	1	173	
13272	43640	A	13352	1	323	
13273	43641	A	13353	3	2020	
13274	43642	A	13354	1	1473	
13275	43643	B	13355	1	636	
13276	43644	B	13356	1	456	
13277	43645	A	13357	1	619	
13278	43646	A	13358	1	1293	
13279	43647	B	13359	79	1041	
13280	43648	A	13360	3	718	
13281	43649	A	13361	1	612	
13282	43650	A	13362	1	992	
13283	43651	A	13363	1	1236	
13284	43652	A	13364	1	1071	
13285	43653	A	13365	359	1250	KLPMGVAVVKLLHLPKVIIVFW LASWMMSRWLHYPDWVTIIAQ QVLMNVVSVMQADCRMNLLLEI FLRWLMRKIFHVRLLPAVSTPP NCLNQLLLFFLTPVNYLPGQVM HFKKPLQIKRNYLSSRHITFMS RKKLKGKVSQYKIHVQKSQAFL SANSQGOTESQIMSELPFTMASK RIKYLGIQLTRDVKDLFKEKYK SLLNEIKEDTNKWKNNPCSWV GRINIMKMAILPKVIYRFNAIPI KLPMTFFTELEKTTFFIWNQK RAHIAKSNLSQKNKAGGITLPD FKLYYKATVTKIT
13286	43654	A	13366	1196	2132	
13287	43655	A	13367	1	2271	
13288	43656	A	13368	2	1105	
13289	43657	A	13369	1	2117	
13290	43658	A	13370	1	1447	
13291	43659	A	13371	1	1669	
13292	43660	A	13372	1	2823	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13293	43661	A	13373	1089	2539	
13294	43662	A	13374	1	1787	
13295	43663	A	13375	1205	1207	
13296	43664	B	13376	1	2745	
13297	43665	A	13377	1	2063	
13298	43666	A	13378	1	4380	
13299	43667	A	13379	1	3347	MGDFNIPSLDRLSTRQKVNKD TQELNSALHQADLDSYRTLHP KSTEYTFPSAPHHTYSKIDHILG SKALLSKCKRTEITNYLSDHSA IKLELRINKLTQNCSTTWKLN LLNDYVWVHNEMKAEIKMFFE TNENKDTTYHNLWDAFKA VCR GKFIALNAHKRKQERSKIDTLT SQLKELEKQEQTTHSKASRRQEI TKIRAELEKETQKTLQKINESR SWVFERINKIDRLARLTKKKS EKNQIDAINKDK
13300	43668	A	13380	1	2367	
13301	43669	A	13381	1	1116	
13302	43670	A	13382	1	1095	
13303	43671	A	13383	670	1500	QTESSTSKSLSTMIKWASSLG WQGWFNIRKSINVIQHIKGIQR QKPHDYLNRCKSL*QNSTTLH AKNSQ*IAQNLLKLISNFKVS GYKINVQKSQAFLYTSNRQTES QIMSELPFTIASKRIKYLGIQLTR DVKDLFKENYKPLLKEIKEDTN KWKNI PCSWVGRINIVKMAILP KVYIRFNAIPIKLPMTFFTELEK TTLKFIWNQKRAHIAKSILSQK NKAGGITLPDFKLYYKATVTKT AWYVYQNM CYRSMEQNRALS YYVAYLQPSDL
13304	43672	A	13384	441	3131	
13305	43673	B	13385	1	5688	
13306	43674	B	13386	916	2165	
13307	43675	A	13387	1	1529	MDPPAGAARRLLCPALL*LPAG *PLRPRLAGAAPAGTALLHER AMPL*LRPGLHDVHGVDPDL
13308	43676	A	13388	1	714	
13309	43677	A	13389	3	457	
13310	43678	A	13390	2	492	
13311	43679	A	13391	3	1201	
13312	43680	A	13392	1	309	
13313	43681	A	13393	2	1073	

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13314	43682	A	13394	3119	6984	CIVKHAAMRSAMTSLAARITVL NPTRATTPTNT/RVADDQGFLRQ WSKVAKERKLQRLYIGEPSAEA VAAQMPDLILISATGGDSALAL YDQLSTIAPTLIINYYDDKSWHPR LSFNKADEITTVFCGSKKSLAN GIPMANILFPTSVIATQQTQHFR FVDDFNAQFLRFASLDPAASPA ITISGKATLEIPGTCLVFYAALE KKLNKPGQTTDFGRFTLLPTC CLGNCDKGPNNMIDEDTHAHL TPEAIPELLER
13315	43683	A	13395	3	587	
13316	43684	A	13396	1	315	
13317	43685	A	13397	430	636	
13318	43686	A	13398	1	84	
13319	43687	A	13399	1	1647	
13320	43688	A	13400	1	2652	
13321	43689	B	13401	1	1494	
13322	43690	A	13402	1	750	
13323	43691	A	13403	1	513	
13324	43692	A	13404	1	2254	
13325	43693	A	13405	1	746	
13326	43694	A	13406	3	428	LGDDFVRAANIILHCEGKVVS GIGKSGHIGKIAATLASTGTPA FFVHPAEALHGDLMIESRDV MLFISYSGGAKELDIIPRLEDK SIAL/GKPTSPLGLAAKAVLDIS VEREACPMHLAPTSSTVNTLM MGDALAMAV
13327	43695	A	13407	1	1431	
13328	43696	A	13408	943	2481	
13329	43697	B	13409	1	783	
13330	43698	A	13410	3	729	
13331	43699	A	13411	1	843	
13332	43700	A	13412	3	128	
13333	43701	A	13413	1	136	
13334	43702	A	13414	1	492	
13335	43703	A	13415	3	619	

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13336	43704	A	13416	1	1600	GQACHASSSPLKSGRGSPPNFEI LYGPIFEDSLAPD*PKVIAGQIT LRDAVTGPISSPNEAGKIYQLKP NPAVLICRVRGLHLPEKHVTW RGEAIPGSLDFALYFFHNYQA LLAKGSGPYFYLPKTSQWQEA AWWSEVFSYAEDRFNLPRGTIK ATLLIETLPAVFQMDIELHALR DHIVGLNCGRWYIFSYIKTLK NYPDRVLPDRQAVTMDKPFLN AYSRLLIKTCRKGAFAMGGM AAFIPSKDEHNNQVLNKKVA DKSLEANNHGDGTWIAHPGLA DTAMAVFNILGSRKNQLEVM REQHAPITADQLLAPCDGERTE RKFNALMESEKQSQNLWKFA VYSGLRHGELAAALAWEDVDLE KGIVNVRNLTILDMFGPPKTN AGIRTVTLLQPALEALKEQYKL TGHHRKSEITFYHREYGRTEKQ KLHFVFMPRVCNGKQKPYYSV SSLGARWNAAVKRAIGRRNP YHTRHTFACWLLTAGANPAFA SQMGHETAQMVVEIYGMWID DMSDEQIAMLNARVM
13337	43705	A	13417	2	278	
13338	43706	A	13418	3	662	GHLWIRIDLSQSAVSHSVKELE NHTGVRLDRRTREVVLTDAG QQIALRLERLLDELNSTLRDTG RMGQQLSGKVRVAASQTISAH LIPQCIAESHRRYPDIQFVLHNR PQQWVMESIRQGDVDFGIVIDP GPVGDQLQCEAILSEPFLLCHRD SALAVEDYVPAALPLPEGSPLVV KRITPVVERQLMLVRRKNRSL TAAEALWDVVRDQGNALMAA
13339	43707	A	13419	1	646	GQQLSGKVRVAASQTISAHLIP QCIAESHRRYPDIQFVLHNRPO QWVMESIRQGDVDFGIVIDP VGDLQCEAILSEPFLLCHRD LAGGDYVPWQALQGAQLVLQ DYASGSRPLIDAALARNGIQAN IVQEIGHPATLPPMVAAIGIGISIL PALALPLPEGSPLVVKRITPVVE RQLMLVRRKNRSLSTAEEALW DVVRDQGNALMAIGRE
13340	43708	A	13420	1	1068	
13341	43709	A	13421	1	381	
13342	43710	A	13422	3	938	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met bod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
13343	43711	A	13423	595	1630	CSWHDRFPDWKAGRILPISEPPS NRIFACWGKPAWTACCN/FSQG QAVKGNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQ VSRLESQGDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVKG NQLLPVSLVKRKTTLAPNTQTA SPRALADSLMQLARQVSRLESG QDFADFGTTIKQDFRLLGQTSV DRLLQLSQGQAVKGNQLLPVS LVKRKTTLAPNTQTASPRALAD SLMQLARQVSRLESQGDFADF GTTIKQDFRLLGQTSVDRLLQL SQGQAVKGNQLLPVSLVKRKT TLAPNTQTASPRALADSLMQLA RQVSRLESQGHYDHDYEFELGTR FRAVIIKLCNGDSLRFHMTSVY ALVKCFHEGDP LHKGTGCQHLIP KQQQNEKYQVPQFDQSTIKNIE SAKGLDVWDSWPLQNADGTV AEYNGYHVEMLLREAGKAGFC RFRNHHTGFSPAGANQRGPL AATLSGPGGEGQSAVARLTGE KKNHPGAQYANRLSPRVGRFIN AAGTTGNSYDHDYEFELGTHQ RLGAVARIVGDDLLNELRRDV VDARAGDVDQHAHAKEKGDFR
13344	43712	A	13424	1	1395	

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13345	43713	A	13425	1307	1992	DKLNPVAHQKAYLAQSSQCHP QNARLVQHTQIRILPISEPPSNRI FACWGKPAWTACCN/FSQGGQA VKGNGQLLPVSLVKRKTTLAPNT QTASPRALADSLMQLARQVSR LESGQDFADFGTTIKQDFRLLG QTSVDRLLQLSQGQAVKGNQL LPVSLVKRKTTLAPNTQTASPR ALADSLMQLARQVSRLESGQD FADFGTTIKQDFRLLGQTSVDR LLQLSQGQAVKGNQLLPVSLV KRRKTTLAPNTQTASPRALADSL MQLARQVSRLESGQDFADFGT TIKQDFRLLGQTSVDRLLQLSQ GQAVKGNQLLPVSLVKRKTTL APNTQTASPRALADSLMQLAR QVSRLESGQLKHKEVESPNRPI TSSEIQVLKLSPIKKSPGPDGFT AEFYERYKEELVPFLKLQFOTIE QERLLPNSFYEASILTSPSRD ATKKDNFRPTSLMNIYAKILNK IGQTESSSTSKSLFSTIKSVSSPE CKAGSTYANQDFADFGTTIKQ DFRLLGQTSVDRLLQLSQGQA VKGNGQLLPVSLVKRKTTLAPNT QTASPRALADSLMQLARQVSR LESGQETTPWSPFSDPVLAFDY KVFMAFVYNNVVRVSQRMVVA GCISAFNDKLLNDLICFPVAPVS SKQIFPSDVKVAEPDHSCVSSY RIGSMAPNLTISEMPRHNYFPA GNSVDHDNEFEL
13346	43714	A	13426	560	844	
13347	43715	B	13427	200	1519	
13348	43716	A	13428	950	1230	CSWIHDFPDWKAGRILPISEPPS NRIFACWGKPAWTACCN/FSQ QAVKGNQLLPVSLVKRKTTLA PNTQTASPRALADSLMQLARQ VSRLESGQDFADFGTTIKQDFR LLGQTSVDRLLQLSQGQAVK NQLLPVSLVKRKTTLAPNTQTA SPRALADSLMQLARQVSRLESG QDFADFGTTIKQDFRLLGQTSV DRLLQLSQGQAVKGNQLLPVS LVKRKTTLAPNTQTASPRALAD SLMQLARQVSRLESGQDFADF GTTIKQDFRLLGQTSVDRLLQL SQGQAVKGNQLLPVSLVKRKT TLAPNTQTASPRALADSLMQLA RQVSRLESGQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13349	43717	A	13429	695	1060	FRQRSVAFPTVPNACVSVRSR ERDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMLQARQVSRLESGQ*AQR N*CRKHRLSIPRK
13350	43718	A	13430	1	1558	MRDIFWVPDICKVMLYLVFRRS MGTPPLRAVAMGLVITSWKIAQ KPRDFADFGTTINQDFRLLGQT SVDRLQLSQGQAVKGNQLLP VSLKTDTKAKNLYLTKAYYGG GTNFFRKESQKLQSAKKRDA ELANGALGHIELNDYTLKKVM KPLITSNTGFAFGTTIKQDFRL LGQTSVDRLLQLSQGQAVKGN QLLPVSLVKRKTTLAPNTQTAS PRALADSLMLQARQVSRLESG Q*AQRN
13351	43719	A	13431	391	1676	FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMLQARQVSRLESGQ*AQR N
13352	43720	B	13432	1	1638	
13353	43721	A	13433	1	2430	
13354	43722	B	13434	1	1282	
13355	43723	B	13435	1	1225	
13356	43724	A	13436	350	709	
13357	43725	A	13437	1	2236	
13358	43726	A	13438	548	1698	RSWLRSSLSGSIPIATEISCSTCE ASTSS/VRDFPGVKDLTFQWHD RLIFAIALRLGRSACGVTFHKEQ LGTVKVLRGTISQFARQRAAG QLFTHHFFGRTHALGAGNRH LRQQFSRLNVLVQPQDKGIFHH ARNECALTRRETPAFFRIRAVF NSQLSQTQLHIFTARPAGLAS KCRKPPQACYLWDFADFGTTIK QDFRLLGQTSVDRLLQLSQGQ AVKGNQLLPVSLVKRKTTLAP NTQTASPRALADSLMLQARQV SRLESGQNIESAKGLHVWDSW PLHNADGTVDEYNGYHVVFAL AGSPKDAADTSIYMFYQKVG NSIDSWKNAGR/VFKDSKFD NDPILKQDTQEWSGSATFTSDG KIRLFYTDYSGEYHYG
13359	43727	B	13439	448	1116	
13360	43728	A	13440	97	1636	
13361	43729	A	13441	1	1296	
13362	43730	B	13442	1	2160	

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13363	43731	A	13443	485	865	FIRDFADFGTTIKQDFRLLGGQTS VDRLLQLSQGQAVKGNQLLPV SLVKKRKTTLAPNTQTASPRALA DSLMLQARQVSRLESGQS*NSS KTKNTKCLNSINQRLKILSLQK DLMCGTAGRCKTLTEQ
13364	43732	A	13444	816	1194	SLILFLRRRRRAVEKRGKVWQDS CPNGTTTLTSGAIFLFIREFADF GTPITQDFRLLGGQTSVDRLLHLS QQGQAVKGNQLLPVSLVKKRKT LAPNTQTASPRALADSLMLQAL RQVSRLESGQ*AQRN
13365	43733	B	13445	1	2710	
13366	43734	A	13446	2027	2934	NPRILPISEPPSNRIFACWGKPA WTACCNFSQQAQVKGNNQLLP VSLVKKRKTTLAPNTQTASPRAL ADSLMLQARQVSRLESGQDFA DFGTTIKQDFRLLGGQTSVDRLL QLSQGQAVKGNQLLPVSLVKKR KTTAPNTQTASPRALADSLMQ LARQVSRLESGQSRVHSHSLGP LPTTTTGLSLNQKGGVSGGPG SKEQAEISCLKERKDLGLGILGS TVGILKVKHQGASTKQGHSD LIKILLSDTSLTPAAPMVDSLIA RVGV MARGNAITLPVCGRDVK FTLEVLRGDSVEKTSRVWWSGNE RDQELLTEDALDDLPSFLLTGQ QTPAFGRRRVSGVIEIADGSRRR KAAALTESDYRVLVGELDDQ MAALSRLGNDYRPTSAYERGQ RYASRLQYMNLLPIFLRWLMR KIFHDEHVPQDQEEPISEITII EEEIPINSIDLGNELYFVKLPKF LSIEPKDFADFGTTIKQDFRLLG QTSVDRLLQLSQGQAVKGNQL LPVSLVKKRKTTLAPNTQTASPR ALADSLMLQARQVSRLESGQP HSTDASATHRKMTLSLADRCST QKIRILPMAGRDPECORTEMIK SSDLMAEIIQEHKEDQLPELEQL EHIGLFSHAEIKAIKKASDLQY RIQERALFKDDFINYVLHEIPLF EQIQRRTIGYSLKHGIRAVKA TIVRALYGRIPAGVVVTRSV
13367	43735	A	13447	1	5240	
13368	43736	A	13448	4733	4753	

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13369	43737	A	13449	299	761	LNTTATLCLLLREARKTLMTH QSTCFIKRDFADFGTTIKQDFRL LGQTSVDRLLQLSQGQAVKGN QLLPVSLVKRKTTLAPNTQTAS PRALADSLMQLARQVSRLESG Q*AQRN**PVPKEKRRRGDRQE HQQPCRNTEGTALRVWAARDQ
13370	43738	A	13450	3925	4190	FIRDFADFGTTIKQDFRLLGQTS VDRLLQLSQGQAVKGNQLLPV SLVKRKTTLAPNTQTASPRALA DSLMLQLARQVSRLESGQ*AQR N
13371	43739	A	13451	2	1040	
13372	43740	A	13452	58	350	HLASWVVALVLHWGCVVWTA ESSTSKTRSPFRARSWIGEAVA AAAADGVTFSPVPTHTFRHSY AMHMLYAGIPLKVLQSLMGH KSISSTGVPSSNS
13373	43741	A	13453	1	1290	
13374	43742	A	13454	289	1338	
13375	43743	A	13455	1	732	
13376	43744	A	13456	982	1347	
13377	43745	A	13457	116	1746	SSVTGRTEKARIWEVTDRTV/R RPWIGEAVAAAAADGVTFSPV VPTHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEYTKVF ALDVAARHRNFTQFRLSETKE ITNPYAMRLYESLCQYRKPDGS CIVSLKIDWIIERYQLPQSYQLY YFELAIPIVGYFYPGSFSTASRIL LLHPRGLRAITIAVFGKQNTYIR LEPFKINVLEQITKHIEKLQCGG VVKQLSRRGNNQHISSTYDINR ADTQVRRAVNNYDIIVMSNSFN GQSEHQVWIARLTWVIGTINVV CAADVLIPTPAELFDYTSALQ FFDMLRDLLKNVDLKGFEVDV RILLTKYSNSNGSQSPWMEEQI RDAWGSVMVLKNVRETDEVG KARLTWIGTINVVCAADVLI PTPAELFDYTSALQFFDMLRDL LKNVDLKGFEVDVRIILLTKYSN SNGSQSPWMEEQIRDAWGSVM LKNVRETDEVGKPEPSTNTFR HSYAMHMLYAGIPLKVLQSLM GHKSISSTEYTKVFALDVAAR HRVQFAMPESDAVAMKLQSL
13378	43746	A	13458	1	780	

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13379	43747	A	13459	116	396	SSVTGRTEKARIWEVTDRTV/R RPWIGEAVAAAAADGVTFSP VTPHTFRHSYAMHMLYAGIPL KVLQSLMGHKSISSTEYVTKVF ALDVAARHR
13380	43748	A	13460	3	514	
13381	43749	A	13461	2	545	
13382	43750	A	13462	1	1110	
13383	43751	A	13463	1	870	
13384	43752	A	13464	1	1422	
13385	43753	A	13465	1	1599	
13386	43754	A	13466	614	1236	TARVAAARRRCQCWGSACGS ALTLPTSSLTLTETPIVQQTRM VVRCPTASLPQWRSPSTWA VPKTPPTWTCWRNSAILSL/VVF IRDKLMERRNRRTGRTEKARIW EVDTRTVRTWIGEAVAAAAAD GVTFSPVTPHTFRHSYAMHM LYAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
13387	43755	A	13467	1	1023	
13388	43756	A	13468	1	699	
13389	43757	B	13469	1	1281	
13390	43758	B	13470	77	751	
13391	43759	A	13471	1	705	
13392	43760	A	13472	2	893	
13393	43761	A	13473	206	837	CAGAGGIARRRAEKEKALSAV NLDPTSSRLSSTSLPGAPPNPRV AAAGLSRRRPTSPSAGRKS/GR WPRASRYQQGHQDLFILRSDLP SQVFIRDKLMERRNRRTGRTEK ARIWEVTDRTVTRTWIGEAVAA AAADGVTFSPVTPHTFRHSYA MHMLYAGIPLKVLQSLMGHKS ISSTEYVYTKVFALDVAARHRVQ FAMPESDAVAMLKQLS
13394	43762	A	13474	1	1416	
13395	43763	A	13475	1	765	
13396	43764	B	13476	1	519	
13397	43765	A	13477	1	2784	
13398	43766	A	13478	1	624	
13399	43767	A	13479	2089	2454	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, ~=-Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13400	43768	A	13480	740	1431	CCQTLFVFHPPHPSHLGPRPCPP TH/HLPSEHRSFLFLEAACHDS LEPLNLSSGSKTSPSLPPKAKK PKGLEISA/RPAGALRHRRLHR PQQSPPLGIPHPSLUTAQVFIR DKLMERRNRRTGRTEKARIWE VTDRTVRTWIGEAFAAAADG VTFSVPVTPHTFRHSYAMHML YAGIPLKVLQSLMGHKSISSTE VYTKVFALDVAARHRVQFAMP ESDAVAMLKQLS
13401	43769	A	13481	2	2309	
13402	43770	A	13482	1	603	
13403	43771	A	13483	1	762	MVPHSTGKSWNGCDPTSATLD QLVTVFFMKLFSIGDARIPCLGP RSHSYRRSDYYSGTIIHSCRA DYWSGTTAHLRCRSDYHPVPS FILVTSTTNHQPLKPSISEASWN PLFASL/HHLQLITES/W/YMSLA TTVFIRDKLMERRNRRTGRTEK ARIWEVTDRTVRTWIGEAFAA AAADGVTFSVPVTPHTFRHSYA MHMLYAGIPLKVLQSLMGHKS ISSTEYTKVFALDVAARHRVQ FAMPESDAVAMLKQLS
13404	43772	A	13484	1	762	
13405	43773	A	13485	1	615	
13406	43774	A	13486	887	1203	RPEKAR/IWGVTDRTVRTWIGR AVAAAAADGVTFSVPVPPHTF RHSYAMHMLYAGIPLKVLQSL MGHKSISSTEYTKVFALDVAA RHRVQFAMPESDAVAMLKQLS
13407	43775	A	13487	1	855	
13408	43776	A	13488	1	927	
13409	43777	A	13489	1	921	
13410	43778	A	13490	1	3216	
13411	43779	A	13491	1	1974	
13412	43780	A	13492	1	1221	
13413	43781	B	13493	1	2337	
13414	43782	A	13494	1	1273	
13415	43783	A	13495	1	1251	
13416	43784	A	13496	1999	3237	
13417	43785	A	13497	1	1773	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13418	43786	A	13498	1	633	AQALIAITYGRDRDPGRPLWLG SVKSNIGHTQAAAGVAGVIKM VMAMRHGQLPRTLHVESPSPE VFIRDKLMERRNRRRTGRTEKAR IWEVTDRTVRTWIGEA VAAAA ADGVTFSPVPTPHTRFSYAMH MLYAGIPL/*VLQSLMGHKSIS TEVYTKVFALDVAAHRVQFA MPESDAGGPGTCACSQQCRL RGSSVSPGRQHPQPHRV
13419	43787	A	13499	101	1943	
13420	43788	A	13500	686	3925	
13421	43789	A	13501	1	2084	
13422	43790	A	13502	734	834	
13423	43791	A	13503	1	1075	
13424	43792	A	13504	1	357	
13425	43793	A	13505	795	1273	SHPFSTDWSTDTGFRSKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASWMMRWLHYPDWVT IIAQQVLMNVVSMQADCRMN LLEIFLRWLMRKIFHVRLLPAV STPPNCLNQLLFFLTPVNYLPG QVMHFKKPLQIKRNYLSSRLT FMSRKKLG
13426	43794	A	13506	344	449	SHPFSTDWSTDTGVRKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASCMMSRCPHYPDWVTI IAQQVLTPRKDVMQADCRMN LLEIFLRWLMRKIFHVGFM
13427	43795	A	13507	1197	1511	WHYREPLLRAQLTNPPSGQLV SITKYLQPVVE*AYVLE*QAHL HYQLKSVQDQWPVQKQFSSGSD LYQLHPFHVQHLEPCFPRHPE FAPPSTGTESHYYCCIW
13428	43796	B	13508	1	1494	
13429	43797	A	13509	1	554	MTARKARKITRRWRIGEAADL VGVSQAIRDAEKAGRLPHPD MEIRGRVEQRVGYTIEQINHMR DVFGRLLRAEDVFPVIGVAA HKGNPDQGTASMYHGWVPLD HIHAEDTLLPFYLGKDDVITYA IKPTCWPLDIIPSCALHRIETE LMGKFDEAQPNLGIGT/N*CRM CC*CADCSHAC
13430	43798	A	13510	1771	2068	DTYSVSWIGEA VAAAAADGVT FSVPVTPHTRHYSAMHMLYA GIPLKVLQSQYPIFKLSYKNPVT QTA WFWFNFRIFGPVPIVNSFS PKVGPGLPGII
13431	43799	A	13511	65	277	

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13432	43800	A	13512	327	748	VHQFHGSLHEGFCAGCGCPAP GTVCDAGGFCFRFRNHHQTGFSP AGANQRGPLAAATLSGPGGEGQ SAVARLTGEKKNHPGAQYANR LSPRVGRFINAAGTTGFPTGKR AKSIWCHRNCRW/RVAVVKLL HLPKVIIVFWLAS
13433	43801	A	13513	512	580	
13434	43802	A	13514	2096	2272	EWRNVCGVTGTENVTPSAAAA QPPQSRPFSWILRPF*RP*RKIS TSFIRPLFTFLPA
13435	43803	A	13515	402	2784	RKNPFILH*LFR*TLRQTKPDNS AGKCVKI*HTQNQRSGRSQSD F*RRRNISERSAAYR*RQLYIR RQPYAERPSHVEDKGHKYLVF EANTGTENGYQGEESLFNKAY YGGGTNFFRKESQKLQQSACK RDAELANGALGIHELNNDYTLK KVMKPLITSNTVTDEIERANVF KMGKGYLFTDSRGSKMTIDG INSNDIYMLGYVNSLTGPYKP LNKTGLVLQMGLDPNVDVFTY SHFAVPQAKGNVIVTSYMTN RGFFEDKKATFAPSFLMNIKGN KTSVVKNSILEQQGLTWLQVA KRAGLGGGQSGRTVLRERLPN YKNFKGTIQELGQNYAVSGEI FVVDNRNTVEITELPVRTWTQVY KEQVLEPMLNGTDKTPALISDY KEYHTDITTVKFVVKMTEEKLA QAEAAGLHKVFKLQTTLTCNS MVLFDHMGCLKKYETVQDILK EFFDLRLSYGLRKEWLVGML GAESTKLNNQARFILEKIQKII IENRSKKDLQMLVQRGYESDP VKAWEAQEKCDNLKTCHTSH GSVMAETA VINHHKRNKNSPRIV QSNDLTEAAYSLSRDQKRMLY LFVDQIRKSDGTLQEHGDICEIH VAKYAEIFGLTSAEASKDIRQA LKSFAGKEVVYRPEEDAGDE KGYESFPWFIKRAHSPSRGLYS VHINPYLIPFFIGLQNRFTQFRLS
13436	43804	A	13516	2	199	WRKKSLDIPPLIIPNGIVKNILRH FSQLLNVPIRPFWSWILRPF*RP* RKISTSFIRPLFTFLPA
13437	43805	A	13517	1	1887	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,409,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13438	43806	A	13518	125	828	ECKRHTKLKLPQTIWHVLI/Y NSEKLLVYRKLLQVLTLGYKRS NLGVRLYACCGLLCPAYPQH FAHGYYVDKIPGYPRAGTLTGL HPMQCDNLKTCHTSHGSVMAE TAVINHKKRKNSPRIVQSNLDT EAAYSLSRDQKRMLYLFVDQIR KSDGTLQEHGICEIHVAKYAE IFGLTSAEAILRVFIKHSADMEA ITNGMMNLNRQRHQHLVALRII FAHGENGGEEVVHIGHV
13439	43807	A	13519	504	755	EPCFPAIPEFAPLSTGAESHIIY CCIW*AKYVHQARTL*DQRS*A DHEAYRKTA VRRCSTTQQAWE EQLVHQHILPSSCRYPG
13440	43808	B	13520	1	1980	
13441	43809	A	13521	923	1063	
13442	43810	B	13522	1	1932	
13443	43811	A	13523	383	1383	RKVFFIALKRPAMKKAMNLF LGLSNVRTVHIEGFTVYISTHIS FPISLGYKTRLSFGLVKQKKS PILLEVLAREIQE/KEIKGIQGF KEEVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSQYKINV QKSQAFLYTNNRQTESQIMSEL PFTIASKRKYLGIQLTRDVKDL FKENYKPLLEIKEDTNKWKNI PCSWVGRINIVKMAILPKLSRM HGRPHQPPNAASTLPFPRRSH YGQKSERLSRSGDNRKSHPECR HWQSCAKKSRCLAFTRTVRHT PRSAYLLTRTIELLESSALWHV QTRQRIYAPLYETLDPGNRTHCE
13444	43812	B	13524	107	1000	
13445	43813	A	13525	1778	1897	
13446	43814	A	13526	273	421	SHPPFSTDWSTDGTGVRKSIWC HRNCRW/RVAVVKLLHLPKVII VFSSAS
13447	43815	A	13527	273	697	SHPPFSTDWSTDGTGVRKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASWMSRWLHYPDWVT IIAQVLMNVVSMQADCRMN LLEIFLRWLMRIIFHVRLLPAVS TPTNCLNQLLFFLTPVNYLPG QSGTTVPLVSSV

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13448	43816	A	13528	273	688	SHPPFFSTDWSTDGTVRSKSIWC HRNCRW/RVAVVKLLHLPKVI VFWLASWMMRWLHYDPWVT IIAQQVLMNMGVSMPADCRMN LLEIFLRWLMRKIFTTGLRSFGL VKQKKSPIRMPCVYTNPVCVSIV SRMGQASSL
13449	43817	B	13529	1	1053	
13450	43818	B	13530	1	1869	
13451	43819	A	13531	120	430	EDLSDTGVRSKSIWCHRNCRW/ RVAVVKLLHLPKVIIVFWLASW MMSRWLHYDPWVTIIAQQVL MNVVSVMQADCRMNLEIFLR WLMRKIFHSSLEDPRNWHL
13452	43820	B	13532	148	334	
13453	43821	A	13533	2	147	TSMDBKLGQALKKKI*DL*KK* LKNIPVDKWITPREVFSGIVCK QNI
13454	43822	A	13534	151	325	KAICHNTFSKPSMDKGL/LRRS KKEGFKTYKKNIYKNIPVDKWI TPREVFSGIVCKQNI
13455	43823	A	13535	283	406	HRTKISIVPEGIFKSFSPLAGIM TEQYFL*TLHRLRLIM
13456	43824	B	13536	1	1902	
13457	43825	A	13537	508	1041	LWREASKDIRQALKSFAGKEV VFYRPEEDAGDEKGYESFPW/C YQTIWHSPSRGLYSVHINPYLIP FFIGLQNRFTQFRLSETKEITNP YAMRLYESLCQYRKPDGSGIVS LKIDWIIERYQLPQSYQRPDPF RRRFLQVCVNEINSRTPMRLSYI EKKKGQRQITHIVFSFRDITSMIT
13458	43826	A	13538	1	1422	
13459	43827	B	13539	1	1002	

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13460	43828	A	13540	1	160	MVLIVAATV VVVVVVGLCWM AKSECRSAMRLSSLQVRIFTYLI GREAAFADNLKWMACANKES ALLDRFIFLILLCKEPWECHCL PLFKVAMP SKCDIPVICA HINIG FTLRQLRGFGPCNIGSFEAKDS KNPQVRVISQKHKALRCIWFIT CSICNPEFTEGALQGNKQRKRQ CLQWFRKALESNEPGFEFIQD KLLTQSLCFFPYTFLWLTGPHPS GSSYTDPCSSKADVTPSSAVQ EHSSALELKTIVSPITRQQHGF FTQISTLADVQENVMEYLHVLS RPKVIDQEHDVVWTEAYIDSTV CRVKRRQLLLQVPLTRKQQF LPAPYVDLDSARTRTNKQQQN PIIYTGSKQGSVILFHYGESWN LLRADQRLIFAKSWPRASRYQQ GHQDLFILRSDLPSQVFIRDKL MERRNRRTGRTEKARIWEVTD RTVRTWIGEAVAAAAADGVTF SVPVTPHTFRHSYAMHMLYAG IPLKVLQSLMGHKSISSTEYVTK VFALDVAARHRVQFAMPESDA VAMLKQL*QPQWWWSW*D CAGWRKVNAAPCVCLPFRFA SSHTSLDERLRLQTI
13461	43829	A	13541	48	668	
13462	43830	A	13542	1	1278	
13463	43831	A	13543	100	157	
13464	43832	A	13544	1	1122	
13465	43833	B	13545	1	1131	
13466	43834	A	13546	273	812	SHPFSTDWSTDTGVRKSIWC HRNCRWESPS*SC/WHLPKVILV FWLASWMMSRWLNYPDWVTII AQQLVMNVVSMQADC/KRIC WKYFCAG*CGKIFTYQ**TWN NTETSM SQPKCKMKRI/YSREE LAV*KMDHSDLSLW*KLEPL TCRSTSHFRQKLAQGFVPSTGT PGFIYS AK
13467	43835	B	13547	1	987	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
13468	43836	A	13548	246	2065	LVGWLGDGWLGDGWLIVLALPFM MIPWHSSIQPFTHPFNWNFG*M PELCPQINGMDSWLAGWM/CWL DGWLGDG*MAKLKRPVL*PD KEGNEIWDVMTVKPSGWTVR TFDKPRKRFIAFFIAGILFRAIKN HFLPRETLQCLPYILTGFRGQS EYFSIFSNDMLADTVMFILVAL PFMMIPWHSSIQPFTHPFNWNFG
13469	43837	A	13549	2	118	
13470	43838	A	13550	397	729	THGIRIGDFFCFTKRKLKRPVL* PDKEGNEIWDVMTVKPSGWT VRTFDKPRKRFIAFFIAGILFRAI KNHFLPRETLQCLPYILTGFRGQS QEYFSIFSNDMLADTVMFIL
13471	43839	A	13551	147	417	SSSWGRSSPQLVCGIFQTAGPQS LCKWNQ*VLAQTNKKTAGTSA DLVVPV*QL*RKAVVLPNTAP WRFWRTRQEWFSRGRSGYQS QET
13472	43840	A	13552	1	2418	
13473	43841	B	13553	1	1848	
13474	43842	A	13554	188	490	EWRNVCGVTGTEKVTPSAAAA ATASPIQVLTIVSVTSQIRAFSV LPVRRLLRRSMLSRINTCVNRF CNPICKGMRYGLICPL*SLLDGL CARLINQKGDS
13475	43843	A	13555	83	440	SLLFKCSGVIVLRRPLGYRQVM NVTTRCCLLRTHWMISLLFY*L VNRHRRSVEEYLVSYTLPMGV AVVKLLHLPKNFVSLITPRGRL EKERAFLFQHMRISITGLKIFV MHTSCPMVVC

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /-possible nucleotide deletion, \-possible nucleotide insertion)
13476	43844	A	13556	1337	2583	QQR*MCQNLMT*HQNRSGR SQNDF*RRRNISERSAVYR*R QLYIRRPQYAEPSVHVDEKGH KYLVEANTGTENGYQGEESLF NKAYYGGGTNFRKESQKLQ SAKKRDAELANGALGIELNND YTLKKVMKPLITSNTVFIRDKL MERRNRRTGRTEKARIWEVTD RTVRTWIGEAVAAAAADGVTF SVPVTPHTFRHSYAMHMLYAG IPLKVLQSLMGHKSISSTEYTK VFALDVAARJIRIKSDGTLQEH DGICEIHVAKYAEIFGLTSAEAS KDIRQALKSFAGKEVVFYRPEE DAGDEKGYESFPWFIKRAHSPS RGLYSVHINPYLIPFFIGLQNR TQFRLSEKTIINPYAMRVTNP CVSIVCVNEINSRTPMRLSYIEK KKGRQTTHIVFSFRDITSMITG
13477	43845	B	13557	1	696	
13478	43846	A	13558	326	1577	SGLLPIKVAFTKPQFLFILLRIW* AKYVHQARTL*DQR*ADHEA YRKTAVRRCSQTTQQAWEQSA HQQHHRH
13479	43847	B	13559	1	3822	
13480	43848	A	13560	848	1476	VNVTSFGSRPICSTSPVLSGL* GPVKEFDT*PSM*ISFELIPSVIF EPRESVNKYHLPILKTFARSISS VTTFEISGFITFFNV*SLFNSMI PRAPFANSASRFLALC*SFWLSL RKKFVPPP*YALLNKDSSPW/SS VFCSRVGFYKVFMAFVFNVV RVSQRMVVAGCIAFIDKLLNV LICFSVSVKNRFVIFHSVDFECV
13481	43849	A	13561	1	2196	
13482	43850	A	13562	326	3746	SGLLPIKVAFTKPQFLFILLRIW* AKYVHQARTL*DQRS*ADHEA YRKTAVRRCSQTTQQAWEQSA HQQHHRH*SCRYPS*ARCQ*LTG QIVHRGEKKEQLI
13483	43851	A	13563	3802	4075	IRCFYSPAPGYFPFRFRAVHKL NGDSLRFHMTSVYALQEA VRHTLVTLRQLVTLDPVDFQ RDDA*AIRAYDTDTGIRINAWH TDW
13484	43852	A	13564	1708	3198	
13485	43853	A	13565	1	1401	
13486	43854	A	13566	1214	1357	NKINMFIAALFTIAKT*WNQPK\ CPTMIDWIKRGSSRVASSSSPT RTR

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, * = Stop codon, / = possible nucleotide deletion, \ = possible nucleotide insertion)
13487	43855	A	13567	3363	3852	SHPFSTDWSSDTGVRSKSIWC HRNCRW/RVAVVKLLHLPKVII VFWLASWMMRSRWLHYPDWVT IIAQQVLMNVSVMQADCRMN LLEIFLRWLMRKIFHVRLLPAV STPPNCLNQLLFFLTPVNYLPG QGFAGFRNPPSNRIFACWGKPA WTACCNLSLRARR
13488	43856	B	13568	350	742	
13489	43857	A	13569	248	599	HRDSYKRMAYGLVISVVSLSR KLKRPVL*PDKEGNEIWVDMY TVKPSGWTVRTFDKPRKRFI FIAGILFRAIKNHFLPRETLQCLP YILTGFRRGQSEYFISFNMDLA DTVMFL
13490	43858	B	13570	1	2148	
13491	43859	A	13571	3064	5069	RSDPDENCC*TGH*STLFNWC WRNALSIWEPVCNEIFYRLIKPR WEIRWGKRAPVIPKHTLNTQPV EDTSLSTPAAPMVDSLIARVGV MARGNAITLPVCGRDVKFTLE VLRGDSVEKTSRVWSGNERDQ ELLTEDALDDLIPSLTGGQTP AFGRRVSGVIEIADGSRRRKAA ALTESDYRVLVGELDDQMAA LSRLGNDYRPTSA YERGQRYAS RLQNEFAGNISALADAENISRKI ITRCINTAKLPKSVVALFSHPRQ APCMKSNNALIVILGTVTLDAV GIGLVMPDLALKGLRVLLVEG NDPQGTASMYHGWWPDLHIHA EDTLLPFYLGEKDDVTYAIKPT CWPGLDIIPLSCLAHRIETELMG KFDEGKLPTDPLMLRLAIETV AHDYDVVIDSAPNLGIGTINVV CAAHALIVPTPAELFDYTSALQ FFDMLRDLLKNVDLKGFEVDV RILLTKYSNSNGSQSPWIEQIS DAWGSMLKNVHAIVTGDVAV GMDDIPQEARQYRHNQAYAYS IQGDGAEDDDERIVRFHTRVT DSDTLASDAARLTCRHGLGNQ RNGGVLIEDKFECFFSLTA VFA TRAYYAVYHLTGARHSDIVVA HGYAGCNVRFVALLGTNTTLE TYLSNQGSNGFSLHFGEVDVGQ

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *-Stop codon, /-possible nucleotide deletion, v=possible nucleotide insertion)
13492	43860	A	13572	1408	5578	CSHLIIQLANQNTHITFGKCSF TTATPIGNFYDTRYSSSTERRCLL TSQ*KRRDEIIQCVLKQLRAR SLPDPTRKVFSTLSRSTFRVNF TSRPHTGKVFVAFREPFLPPH RKPDITDTGYLYKRMAYGSVIS/ ICFTKPKLRKPVL*PDKEGNEIW VDMYTVKPSGWTVRTFDKPRK RFIAFFIAGILFRAIKNHFLPRET LQCLPYILTGFRGQSEYFSIFS NMDLADTVMFL
13493	43861	A	13573	2678	2884	SAPLQRNTARRFLFLKACSNR FCYRWRHMTAIPSYNRSKLREI KGGLYHMGIFRRFLASKETPTF CY
13494	43862	B	13574	1	7903	
13495	43863	A	13575	1	880	
13496	43864	A	13576	1	996	
13497	43865	A	13577	763	778	NRCEPPV*GTRFSQQLLLAKA TLLIEELYALTVHSWRPKW
13498	43866	A	13578	2	254	
13499	43867	A	13579	1	2358	
13500	43868	A	13580	206	382	
13501	43869	C	13581	1	1137	
13502	43870	A	13582	79	906	
13503	43871	A	13583	2	383	SPPEVVRLLGYHPPRHGHQ*HLF ASCRKGDVGRVRP*TRPDGSD LLPAQVPAGAARRGGTMPACV GTRSWYSTFWMEPAARPTPS MVSAASMGH*VTPSAGLYAITS RSRLPAGGGITMTTSCSGF
13504	43872	A	13584	1	1092	
13505	43873	A	13585	173	262	
13506	43874	A	13586	898	1391	QLGILRVNLLGIDLRV/GHQAA PPLHLLDLLQMH/SSPPCRPQ*A TSPPPSLRCRAPHR*SLAAP*A PPPRPFLSAGSPHRKGGPGPAPT GSWSSGNQAGLPCCLGWASVF LCPSHLPPPHLPQSSASLAFHRV KHLHLHNSVIDKMKYQLKFLC LLGEYLSV
13507	43875	A	13587	1	960	
13508	43876	A	13588	1318	1369	RDFHPK*HTGIQYIWQQLEINQ CDTSLSMVLPR*RDHFHPKSHLL PGAAQIQ
13509	43877	A	13589	212	385	
13510	43878	A	13590	377	505	
13511	43879	A	13591	69	193	CSLRSLAQMLPFYPRRSCLSCS L**PHCCLWLAALRSESK
13512	43880	A	13592	1	230	
13513	43881	A	13593	2	341	

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13514	43882	A	13594	1	2421	
13515	43883	A	13595	1	623	
13516	43884	A	13596	1	906	
13517	43885	A	13597	1	568	
13518	43886	A	13598	107	199	
13519	43887	A	13599	42	328	GGASGVCSF*CSE/LSSFWWVR GLAGSGVKLQTFATQEPSWLH PVDVPVGLQVELPASPAPCART PQPLGGRWDSAPWSRGRSSG AHGIDVALLP
13520	43888	A	13600	5	124	IWLWFFVSLT*RSRGSQ*VLQ LIKAPHVDLLVVTFGC
13521	43889	A	13601	827	973	HHQSALCI*LKFYTSLTHPVISLV VETLVVW*YLYKM*KKLWSWI RGRG
13522	43890	A	13602	2	503	
13523	43891	A	13603	56	792	
13524	43892	A	13604	1	411	
13525	43893	A	13605	1	1554	
13526	43894	A	13606	1	363	
13527	43895	A	13607	1	966	
13528	43896	A	13608	932	1189	
13529	43897	A	13609	146	323	
13530	43898	A	13610	1	1827	
13531	43899	A	13611	2	412	
13532	43900	A	13612	1	2238	
13533	43901	A	13613	2	411	GATDCVCYYTVGFNDTKTSAL HMVVGDSLAMDVSSVHIINSTL LRYSVTLGFGFYGDIIKDSDK KRRRLGLARYDFLCKTFFSHH* YEGTVTFLPAQHTVGSPRDRKP CRAGCFVCRQSKQQLLEEQKT ALYGLEL
13534	43902	A	13614	3	2185	
13535	43903	A	13615	206	1568	
13536	43904	A	13616	165	417	TWDYIRPNE*YM*MAKKKMP MD/VWCNGKNWRPAG.EFVDD GVTETHFSIGNHDCYIKAVSSGK RKEGIIHTLIVDNREIPEIAS
13537	43905	A	13617	463	837	
13538	43906	A	13618	1	765	
13539	43907	A	13619	3	510	AGVHKIEFEHGTSGKRVVVV DGKEEIRKEWMFKLVGKETFY VGAATKATINIDAIISGFAYEY TLEINGSLKKYMEDRSKTTNT WVLHMDGENFRJVLKEDAMD VWCHGKGIKRRPAGFVDDGTE TPLQYPGPMTCYIKAVSSGKR KEGIIHTLIVDNREIPEIAS
13540	43908	A	13620	342	585	
13541	43909	A	13621	1	1119	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13542	43910	B	13622	48	1104	
13543	43911	A	13623	656	916	GWRKYLQGAADMGIAEGGGS VWSSWASSSLISVPVR*LCES TSQ RSAPGWPLTGGSCSEVALWL CVNDFEFQMRLMPSRDSEPA
13544	43912	A	13624	179	682	
13545	43913	A	13625	1	7511	
13546	43914	A	13626	56	8669	
13547	43915	A	13627	42	8716	
13548	43916	A	13628	1	2457	
13549	43917	A	13629	3	571	
13550	43918	A	13630	1	867	
13551	43919	A	13631	1	2238	
13552	43920	A	13632	171	396	
13553	43921	A	13633	1	3940	
13554	43922	A	13634	554	619	
13555	43923	A	13635	1	1359	
13556	43924	C	13636	208	359	
13557	43925	A	13637	2	513	PSHDHSLKGLTRASGKVLHGEH AAVHGKVALAVSLNLRITFLRL QPHSNGKGDLSLPNIGIKRAW D VARLQSLDTSFL/RWTKEDLELI NKWAFQGERMIHGNPSGVDNA VSTWGGALRYHQKISSLRSP ALQILLTSTRG/PNRIRALVGGG RNRL/LEVPMGGPILLSW
13558	43926	A	13638	3	1331	RVDDFVGELLRLRRGGADVE AAAAAGFPAGMLSQVLLVSAP GKVLHGEHAVVHGKVALAVS LNLRTFLRLQPHSNGKVDLNL P NIGIMRAWDVARLHSLDTSFLG ECKEEKPEQGDVTTPTSEQVEK LKEVAGLPDDCAVTERLAVLA FLYLILSICKQALPSL/DIVV WSELPPGAGLGGSSAAVSVCLA AALLTVCEEIPNPKDGD/CVN R/WTKED/LEL/NK/WAF/QGER MIHGNP/SGV/DNAVQHLGEGA LRLPSRGRFSFL*RGSPVFQI/LG LTNTKVP/SAITRALVAGVRNRL LKFP/IVAPLLTSIDALS/ECERV LGEMGEAPAEQYL/VLEELIDM NQHHNLALGVGHASLDQLCQV TRARGLHSLKTGAGGGGCGITL LKPGLEQPEVEATKQALTSCGF DCL/ETSIGAPGVSIHSATSLDSR
13559	43927	A	13639	1	950	
13560	43928	A	13640	1	1653	
13561	43929	A	13641	1	2601	
13562	43930	A	13642	2	513	
13563	43931	A	13643	47	367	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13564	43932	A	13644	1	633	
13565	43933	B	13645	1	1110	
13566	43934	A	13646	172	1095	
13567	43935	A	13647	1	855	
13568	43936	A	13648	3	440	
13569	43937	A	13649	2	230	
13570	43938	A	13650	2	606	AEFDLCCSPCRRRLLGREEAGE EPTSPVTQYLQPRSPPECKMFA CAKLAICTP*SLJRAGSRVAYRPI SASVLSRPEASRTGEGSTVFNG A\QNGVVSQ/LIPKGSFKTSAISKK TLDTA\AKFIGAGAGNS*GVG WFLVAGIG\TVFWASLIHWVM ARKPFRWKQQLFSYA\ILGICL VLKAMGSPFVLMVAFILFAHV TEITA
13571	43939	A	13651	200	2320	
13572	43940	A	13652	224	640	
13573	43941	A	13653	1	357	
13574	43942	A	13654	43	183	
13575	43943	A	13655	3	478	SSAGREPDPSDLPRRLCFTHRLP AARRVWVQLCVHASPEPGGQGV CPGRSERMVRVFIASSGFVAI KKKQDQVVRFLANKIEFEEVD ITMSEEQRWMYKNVPPDKKP TQGNPLPPQIFNGDRYCGDYD RLFESKESNTVFSFLGLKPLAS KAEP
13576	43944	A	13656	2	428	CRDGKDVVSLVRATVWALSKR KLQPTR/ALTPPSAVNLIKQF LKDKPELVDVKVGVRTGCNG LSYTVETKTKGNSDEVIQDEA RVFIEKKAQLTPLGTEMDYVED KLSE/FMFNNPT*TCGCGAPGK LVETLGLTEIM
13577	43945	A	13657	1	1377	
13578	43946	A	13658	1	1215	
13579	43947	A	13659	1	452	REAEAADLRSEAPGRDGEDV GFLSSGQLSLGCKRKLQPTR ALTLPASAVNLIKQLLKE*P*AC R\LKVGVRTRGCNGLSYTLEYT KTKGDSDEVIQDGVVRVIEK\K AQLTLL*TEMDYVEDKLSKGV GVH\SPNIKGTCCGESFNI
13580	43948	A	13660	3	763	
13581	43949	A	13661	1	306	
13582	43950	A	13662	738	1022	GQHHPETKAWQRHNKKREF*T NILDEH*CKNP*NTGKPNPAT HQKAYPP*SSGLHPWDARLVQ HTKINKCNPAYKQNRQKPHD YLNRCRKGL

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13583	43951	A	13663	2	516	QKIDLPYQGEPEISIQKCQEA VRQVQGPVLVEDTCLCFNALG GLPGPYIKWFLKLPGLHQ FLAGVEGKSAAYALCTFALSTG DPSQPVRLFRGRTSGRIVAPRA CQDFGWD/PCFQPDGYEQTYAE MPKAEKNAVSHRFRA/LELQ EYFGKFGQLDFCKLEAGPFR
13584	43952	A	13664	7	227	
13585	43953	A	13665	1	415	
13586	43954	A	13666	234	510	
13587	43955	A	13667	2	402	
13588	43956	B	13668	530	1544	
13589	43957	A	13669	1	603	
13590	43958	B	13670	1	1527	
13591	43959	A	13671	1	1179	
13592	43960	A	13672	2	413	
13593	43961	A	13673	100	374	KHISPAKALELPFERNLI/PLQ LLKVRILKEGEM/LD/*HWFL** GMGTQVKGMPHKCYIIGKTGR VYNTQHAVGIVVNVKQV*VV
13594	43962	A	13674	1	1035	
13595	43963	A	13675	2	564	GPFGRRNRHLPVIRQNDGPQRGK RRGTPKYVF*/RPFRR/HGGGPL GPPYMRIVRKGDIVD/LKGMG/ TVQNGMPHKCYHGGKTGRVYN VTQHAVGIVVNVK/QVKGKILA KIRINVRIEHL/KHSKSPR*ASLK/ RVLKENDQEKERSPKKGTWG SNLKRHPAPPQKKHTL*RTNGK EPELLEPIPYEFHGHN
13596	43964	B	13676	68	391	
13597	43965	A	13677	1	404	PTRTWTRGRIPLSAPPSSRGAR GTMA DPRVRQIKIKTG/VKRL VKEGVLYEKEPKQ/QEEKIEKM RAEDGENYDIKKQAEIL/QESR MMIPDCQRRLEAA YLDLQRILE NEKDL/EAE EYK EARLVLDSV KLEA
13598	43966	A	13678	1	436	LLACRSMDCYLAIVHATRTLT QQRHLVKFICLGLRNLFLLLSL RILLFRRTFYPSNVSPVCYEDM GNNTANWMLRLILPQSGFIV PL/LIMLCFYRFTLHLTFKAHMG QKHWTMWWIFADVLIIILCWL PYNLLADTIMGT
13599	43967	A	13679	1	705	
13600	43968	A	13680	292	1489	
13601	43969	A	13681	434	1205	
13602	43970	A	13682	1	390	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13603	43971	A	13683	21	479	TYPEAWKLYYRSR*SRDLRKY HAHSVSP*QDQRYTS*KILKCD EHIKQLGSCITDPGNRETSNGT MHTVFHRDKTKDTHPESCCSSE KGGQPLPWFEHRKNVPQFAEP TETLFGPDSGKGAKSLVELLDE SECTSDIEIFISQDEIQSFMANN QSFYSNREQYRQHLKEKFNKY CRLNDHKRPICSGWVDNGWEA
13604	43972	B	13684	32	438	
13605	43973	A	13685	533	1226	
13606	43974	A	13686	1	1566	
13607	43975	A	13687	215	453	
13608	43976	A	13688	1	553	RRPARAAVIKQPPAPGASQHAA TPTQTPLCTPARPLPPMAHVQQ LEGRWRLVDS\KGF**NTMKE\I GVTIALRKMGRNAQAQICIT\TS DG*NPSPLKTESTLKT\TQFSC/T LWGEKFEETTA\DGQKKLTNCL STFPDGA\ALVQHQEWDERKS TVTKKN*KDGEISWLECVMMN\I VTCTPDSMKK
13609	43977	C	13689	11	106	
13610	43978	A	13690	3	155	LCELQKAIDLFTDAIKLNRLAI LYAKRASVFVKLQKPNAAIRD CDRAIEINPDSAQPYKWRGKAH R*ILAWPFCMPRGVSSSNYRS QMLPSETVTEPLK
13611	43979	A	13691	1	1732	
13612	43980	B	13692	95	1715	
13613	43981	A	13693	1	446	
13614	43982	A	13694	1	786	
13615	43983	A	13695	88	828	

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13616	43984	A	13696	157	1515	RREKMAELKYISGFGNECSSED PRCPGSLPEGQNNPQVCPYNLY AEQLSGSAFTCPRSTNKRSLWLY RILPSVSHKPFESIDEGHVTHNW DEVDPDPNQLRWKPFEPKASQ KKVDFVSGHLTLCCGAGDIKSN NGLAIHIFLCNTSMENRCFYNS DGDFLIVPQKGNLLIYTEFGKM LVQPNEICVIQGMRFSDIVFEE TRGYILEVYGVHFFELPDLP ANGLANPRDFLIPIAWYEDRQV PGGYTVINKYQGLFAAKQDV SPFNVVVAWHGNYTPYKYNLKA NFMVINSVAFDHADPSFTVL AKSVRPGVAIADFVIFPRWGV ADKTSGPPYYHRNCMKRFME LIRGQFEQKQGWFLPGGRG/SL HSTMTPHGPDADCFEAKSVK LALKRIADGTMAFMF*SSFNLA GPKWGLQAPRVLDKNYPKCW EPLKSPFVTPNSRNPAPEN
13617	43985	A	13697	1	156	
13618	43986	A	13698	8	306	
13619	43987	C	13699	1	1143	
13620	43988	A	13700	1	1551	MRKDSCASSMHQQVSRSKKRA GQKTPFEDQEGGQRLRSSHIR LGQFLLIEDCKTPSPSLGADAI AKQRKTSVSAASVSATIPIRR VQGPVTVGSGWARGVSAASGP RGTPGKKGKARSEKCSLSHGPO TNKPLVVQKGQKMEQANHPV GLVISVVYKDILKKIVQRETSH LIHVRYAEAITGRRTAPEDKGS LGRDMLAKAGAIYMNMGKGL PIWCHLLEEGIYLEVWALEGQF GRAKNACPQIRLKDPTTFPYQ RQYPLRPEAHKGLQDIVKHVK AQGLVKKCSGPCNTPILGVPKP NGQWSLVQDLRLISEAVIPLY VVPNPYTLSSQIPEAEWFPVL DLKDAFFCIPLHYDSHDSQFLF AFEDPTDHTSQLIWTVLPGQFR DSPHLFGQALAQDLGHFSPGT LVLYYVDDLLLTSSSEASCQQA TLDLLNFLANQGQYKASRSKAQ LCLQQVKYLGILARGTRTLGK ERIQPILAYPHPKTLKQLWGLF QIT/GFCQLWIPR*SKI
13621	43989	A	13701	188	688	

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13622	43990	A	13702	636	2628	SNDRTEDDCGKHPPMSSPP/TEP WVCLIEGQEIDFLDTGTTFVS LIPCLGRLSSRSVTIQGILGQPV RYFSLHLLSCNWETLLFSHAFLV MPESPPTLLGRDILAKAGAIISM KTGNKLPICCPLEGINPEVWA LEGQFGRAKNAHPLQIRLKDP SFPYQRQYPLRPEAHKGLQDIV KHLKAQDSVRKCSSPCNTPI LG VQKLNSQWRLVQDLRLINEAVI PLYPVVRNPYTLISQVPEEAEW FTVLDLKD
13623	43991	B	13703	302	619	
13624	43992	A	13704	1	5172	
13625	43993	A	13705	1	2091	
13626	43994	A	13706	1	1754	GPRGTGPGKARSEKGCSSLHG PQTNKPLVVQKGQKMEQANHP VGLVISVVYKDILKKIVQRETS HPLIHVRYAEAITGRRTAPEDK GSLGRDMLAKAGAIYMNMG N KLPIWCHLLEEGIYLEVWALEG QFGRAKNACPVQIRLKDP TTFP YQRQYPLRPEAHKGLQDIVKH VKAQGLVKKCSSPCNTPI LG VQ KPNQWWSLVQDLRLISEA VIPL YPVVPNPYTLISQIPEEAE WFP VLDLKDFAFFIPLHYD SHDSQF LFAFEDPTDHTS QLIWT VLPQ FRDSPHLFGQALAD LGHFSSP GTLVLQYVDDLLAT SSEASQ QATLDLLNFLANQGYKASRSK AQLCLQVKYLGIL LARGTRTL GKERIQPILAYPHPK TLKQLWG FLEITGFC*LWIPGY SKIARPLYT LIKETQRANTHLV EWESEETA FKTLKQALVQAPGL SLPTGQNF SLYVTERAGIALGV LTQTRGTT PQPVAHLKETD VVAKWPHC LRVVAAVLVSEAI KIQGKD LIVWTTHEVNGILG /AKGSLWL SDKRLFRYQALC LEGLVLIQRT SCGSHLAVTRLW ALYF
13627	43995	A	13707	2	887	

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13628	43996	A	13708	3	1750	GWAVPRPGPRGLTVATEAAAA AAAAAAAIISSRTRAPQAPEGR NRRLEKMADDIDIEAMLEAPY KKDENKLSSANGHEERSKKRK KSKSRSSHERKRSKSKERKRS RDRERKKSKSRERKRSRSEKRR RSRSRSDRRFRGRYRSPYSGP KFNSAIRGKIGLPHSIKLSRRRS RSKSPFRKDKSPVREPIDNLTPE ERDARTVFCMQLAARIRPRDLE EFFSTVGKVRDVRMISDRNSRR SGIAYVEFVDVSSVPLAIGLTG QRLVGVPIIVQASAEK\NRAA AMANNLQKGSAGPMRLYVGSS HFNITEDMLRGIFEPFGRIESQL MMDSETGRSKGYGITFSDSEC AKKALEQLNGFELAGRPMKVG HVTERTDASSASSFLDSDELER TGIDLTGTG\RLQLM\ARLAEG TGLQIPPAQQALQMSGSLAF GAVGRNLFCYRFKQDFSHQT ETSALSAAS\VOPLATQCFQLS NMFNPQTEKEVGWDTEIKDDV IEECNKHGGVHIHYVDKNSAQG NVYVKCPSIAEIAA\NALHGR WFAGKMITAAYVPLPTYHNL PDSMTATQLLVPSRR
13629	43997	A	13709	141	343	LHEGLLP*RGHALLSGALHG*C VGSCLFSTPRCLTSSACGYPS CTPGSCTAWCPSASRRRLSCWT
13630	43998	A	13710	5	426	
13631	43999	A	13711	1	1188	
13632	44000	A	13712	2	264	NKQPIWIPSRHLKPYHEPDAKE EIPGGS*GPTSCSHVETDAEDP NCHEQHLSNTATHLGTQDEAVI DGRRKPEESRTTSHICRCS
13633	44001	A	13713	1	700	
13634	44002	A	13714	3	483	
13635	44003	A	13715	2	361	RRFRAGAGYVVESTGVFTTME KAGAHLQGGAKRVIISAPSADT PMFVMGVNHEKYDNLKIIISNA SCTTNCLA/PPASTGAAKAVGK VPELNGKLTGMAFRVPTANVS VVDLTCRLEKPA
13636	44004	A	13716	2	249	SADAPMFDMGVNHEKYDNL NII\SVMKAGPVEKRP\AWHPMD TLP*LAPRSLFLCSNASCTTNCL EPLAKVIHDNFVIGLEGLMV

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13637	44005	A	13717	1	1079	GTRRQSAASSFASPAEPHRSDT MGKVKVG VNGFGRIGRLVTRA AFNSGKV DIVAINDPFIDLNYM VYMFQYDSTHGKFHGTVKAEN GKLVINGNPITIFQERYPSKIKW GDAGAEYFVESTGVFTTMEKA GAHLQGGAKRVIISAPADAPM FVMGVNHEKYDNSLKIISNA/S CTTNCLT/PLAKVIHDNFGIVEG LMTTVHAITATQKTVDPGSGKL WRDGRGALQNIIPASTGAACA VGKVIPELNGKLTGMAFRVPT ANVSVDLTCRLEKPAKYDDI KKVVQQA/SEGPKLGILGYTEH QVSSDFNSDTHSSTFDAGAGI ALNDHFVKLISWYDNEFGYSN RVVDLMAHMASKE
13638	44006	A	13718	3	483	
13639	44007	A	13719	2	361	RRFRAGAGYVVESTGVFTTME KAGAHQGGAKRVIISAPADT PMFVMGVNHEKYDNSLKIISNA SCTTNCLA/PASTGAACAVGK VIPELNGKLTGMAFRVPTANVS VVDLTCRLEKPA
13640	44008	A	13720	2	249	SADAPMDFMGVNHEKYDNSL NII/SVMKAGPVEKRP/WHPM D TLP*LAPRSLFLCSNASCTTNCL EPLAKVIHDNFGIVEGLMV
13641	44009	A	13721	1	1079	GTRRQSAASSFASPAEPHRSDT MGKVKVG VNGFGRIGRLVTRA AFNSGKV DIVAINDPFIDLNYM VYMFQYDSTHGKFHGTVKAEN GKLVINGNPITIFQERYPSKIKW GDAGAEYFVESTGVFTTMEKA GAHLQGGAKRVIISAPADAPM FVMGVNHEKYDNSLKIISNA/S CTTNCLT/PLAKVIHDNFGIVEG LMTTVHAITATQKTVDPGSGKL WRDGRGALQNIIPASTGAACA VGKVIPELNGKLTGMAFRVPT ANVSVDLTCRLEKPAKYDDI KKVVQQA/SEGPKLGILGYTEH QVSSDFNSDTHSSTFDAGAGI ALNDHFVKLISWYDNEFGYSN RVVDLMAHMASKE
13642	44010	C	13722	40	243	
13643	44011	A	13723	2	2972	
13644	44012	A	13724	1	602	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Met hod	SEQ ID NO: in USSN 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13645	44013	A	13725	1	325	MGRNQSRKAENTKNESASSPP KDRNSSPVREQSWTENEFDEL EVGFRKLVTITNFSELKEHVLTD HKEAKNLEKS\LEVVAAREISQE KEIKVFN*EKRKSNCPCLQMT
13646	44014	A	13726	1	981	
13647	44015	A	13727	1	739	MGRNQSRKAENSKNQSTSSPPK DCSSSPAREQNWTKNEFDELTE VGFRRLIANFSKLKECVLTHR KEAKNLEKSDRENGTKLENTL QDIIQENFPNLRQANIQIEIQ RIPQRYSLRRATPRHII\VRFTKV EMKEKMSRAAREKGRVTHKG KPIRLTADLSAENLQARREWGP VFNLK\NFQPRIPYPAKLSFISG GEIKSFDTKQMLRDFFTTRPAL QELLKEALNMERNNQYKPLQK HAKW
13648	44016	A	13728	1	1277	MKEQNGGGGREEDHKDKGIRQ LPSSLPSAGEAKSDKPEHHNRY RKEIASFEDEKRAMGVAKMAE QEQLQSAAPSMTNAEVTGAHG GRAEAGRGVDSGPKRKVLGDF PFLAKGSRDRLPGKAGHSLPKY YAFTKVLATGRQERNINISKK VIYTKTTSTGHQHPKIDKTT KMGRNQSRKAENSKNESTSSPP KGHSSSPATEQSGTENDFDEL EVGFRRSVTTNFYELKEDVQTH RKEAKNLEKRLDKWLTRINSV EKTLSDMELKTMARELRDTC SSFKSRFNQVEERVSVIEDPIYE LSREDKVRDKKVRNKQSLQEI WDYVVRPNLRVIGVPESDGEN GTKLENMLQDIIQENFPNLRQ ANIQIEIQRTQRYSSRRATPR HII\VRFTK\VEMKQKVLRAAREK GPVTHKGNSGSL
13649	44017	A	13729	1	1584	
13650	44018	A	13730	493	575	SHPMPNPANTRSQRNPTKKKQ KKNV\CDNIRELEQQMEDAYR GTRKRMPLSSSSMRSDGFDEE SQRYWRPKNEISGTLDDFLK AKSWNRKFYDYANMPDRWG\ QVAIKSYTLKNLQTVVISKILP TGRKHLPR*SHPMPNPANTRSQ RNPTKKKQKKNVCG
13651	44019	A	13731	1	655	
13652	44020	A	13732	2	1664	
13653	44021	A	13733	1	2364	
13654	44022	A	13734	1	224	

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13655	44023	A	13735	1033	7511	
13656	44024	A	13736	56	8669	
13657	44025	A	13737	42	8716	
13658	44026	A	13738	1	5046	
13659	44027	A	13739	1	2298	
13660	44028	A	13740	1	2362	
13661	44029	A	13741	1	2046	
13662	44030	A	13742	1	1503	
13663	44031	A	13743	1	813	
13664	44032	A	13744	185	735	
13665	44033	B	13745	317	910	
13666	44034	A	13746	1	867	
13667	44035	B	13747	1	2325	
13668	44036	A	13748	1	430	
13669	44037	A	13749	1	867	
13670	44038	A	13750	35	518	CLSRASPVLASMSGRGKTG GKARAKAKSRSSRAGLQFPVG RVHRLLRKGHYAERVGAGAPV VLAAWLEVAQPLRVLELAGN AA/RSNKKTRIIPRHLQLAIRND EEL*KLPGLP*RIAQGSRLVLPNI QA/VLLPKKTSATVGP/PAKPSG GKKATQASQEY
13671	44039	A	13751	1	937	
13672	44040	A	13752	1	1096	
13673	44041	A	13753	85	1512	
13674	44042	A	13754	3	2377	
13675	44043	A	13755	1	1134	
13676	44044	A	13756	49	408	
13677	44045	A	13757	47	2603	
13678	44046	A	13758	1	378	
13679	44047	A	13759	1	696	
13680	44048	A	13760	3	401	
13681	44049	A	13761	882	1106	KLHPYTTRQYCHFRI*TDVMAK RSRNAVKGSLALVWCALSDFA AGFTPDGCTRAFTFTGGWRK RDCRGAVAGG
13682	44050	A	13762	688	1100	
13683	44051	A	13763	476	552	
13684	44052	B	13764	178	1107	
13685	44053	A	13765	1	198	
13686	44054	B	13766	94	625	
13687	44055	A	13767	1	732	
13688	44056	A	13768	1	4443	
13689	44057	A	13769	216	575	PGAGDRYVGKPVSAVGTAVSC GVWSSMPDATLIASYQAYTSH VGRIRRSRRIR/TNTARADYPAL TALPFNNFRTHNRFGNAAASVL ASIGIGSSLICARISAHSGAEH KPPEPKAANIK

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
13690	44058	A	13770	1018	1489	KLPGQRRFVQTPSHVLHTLSYPTAPAQSSYPAPLSPSQDRAPTLAHQTT*FSASYTANAQWQRVAADHLKSVRETYAHVRQFSPALGNAPPDQLPLS*ASCVPKSGARYSSVIRQNRDRFFRATDHMYVTVPTRPKMWNPNVTQMNSFRA DTCE
13691	44059	A	13771	1013	1755	GSPGLRPGGAAGKALAPSGCTGNSHRAMP*PGAQAQTRPEKW A*QRP/HVSTGARGARVRALAA VAAAEAQRAAGAAVRAAALHTRAAVSAGAAARAVVQVVLAA RTREAGAAAAAQGVAQVQAES AIAAWLQAAPVHPLLTVGALE TGWAVADVGRVRCPTDPTQA AVEAGSICTCHPAHLTPQPVEPTRAGAFKGPGLTTAASIGTRVPVTGPRPRDKASGGSRGRAPGA EAAAGGDRDRAEGSSPAL
13692	44060	A	13772	1	1236	
13693	44061	A	13773	1	456	
13694	44062	A	13774	1	219	
13695	44063	A	13775	1707	1853	
13696	44064	A	13776	1	615	QLATFFFGGLPGGSAPWDPPGEACLWVLVRLPGRTVWVIQFVQLRSFFAPPFANHGRASSGRVS VHYGIAQTAEWAAEICGVGAR KIRELAAIFHQNTIMHFANGG/NPTRRS AVLSSMQGSLPGGCDAVDIHPVARIVEALENPGGAYQHNGMNRHFPDIRFIWWAGGANFTHHQDTRNLIRAWQNDYSYFRKGRIKAKMGPKLF
13697	44065	A	13777	407	661	ANWIKWRWIIRAMIHSSSSMWQTANSLASFISAPVTSSACRSTLPATRYWCI*WRSSAIWKWVILSGPVATRICTATIWIQLICN
13698	44066	A	13778	1	2448	
13699	44067	A	13779	3	1612	
13700	44068	A	13780	1	1626	
13701	44069	A	13781	3	118	
13702	44070	A	13782	1175	1396	
13703	44071	A	13783	197	933	
13704	44072	A	13784	2	64	IILLNSAPAWM*TFKLPGVDVNYMLHTQNK
13705	44073	A	13785	1	855	
13706	44074	B	13786	1	1605	
13707	44075	A	13787	1	588	
13708	44076	A	13788	1	2769	
13709	44077	A	13789	813	1341	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 09/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /possible nucleotide deletion, v=possible nucleotide insertion)
13710	44078	B	13790	1	999	
13711	44079	A	13791	1	281	
13712	44080	A	13792	1	1332	
13713	44081	A	13793	1	1384	MPITLRRSVEKEQLIEANTIMPF GKYKGRRLIDLPEEYLLWFARK DEFFPAEARYTHIDLHVPAPLLV MFTLDTRQSAACDRNP.HPIHVC SSWTSKCAPRLWTRALLPRTR TPPYATGTTIGSRASWFVTFPD ASFYRRKAPRQEFHTSLQGRSL YVRQRSTANPTEITRRTLHKM VEVNACLKQLDNKDIADYEHN QLMRRLRQLIAQSWHTDEIRKL RPSPEAIMTEQEKTSVVVEETR EAVDTSQPVAT
13714	44082	A	13794	1	2004	MTQQITLIKDKILSDNYFTLHNI TYDLTRKDGVEVIRHKREVVDR GNGATILLYNTKKKTVVLRQF RVATWVNGNESGQLIESCAGL LDNDEPEVCIRKEAIEETGYEV GEVRKLFELYMSPGGVTLEIHF FIAEYSDNQRANARGGVEDEDI EVLELVQCGGQIGVPTVLAVF ATGIGFLAMSVTKPRINAQPPY MPWRNL.AQLVEHINRTRIHRNL QFTDAFKRRLIDNICRKNNIIGT HTGQSKFSGQTQIFGEIPQVVP ASELAAMKQIKELQRLLGKK TMENELLKEAVEYGRAKKWIA HAPLLPGDGERTDDWMDGRRS RHTDDTDVLLRIHHVIGELPTY GYRRVWALLRRQAELDGMPIA NAKRVRIMRQNALLLERKPA VPPSKRAHTGRVAVKESNQRW CSDGFECFCDNGERLVRTFALD CCDRLSSRGRNAAAKRQRDDP LRWKFRLPSSGTTKLLMPLDQ APARFAPVFTCTLTILCTGHV VYTLPIHYDVAIKNNIRPERPM AASSIGAQMGHASPVSVAVVS VAMLGNVTFDGRHLEFLDLLAI TIPSTLIGILAIGIFSWFRGKDL KDEEFQKFISVPENREYVYGD ATLLDKKLPKSNWLA MWIFLG AIAVIALLGADSDLRSSF/GGKP

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 5,402,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, / =possible nucleotide deletion, \ =possible nucleotide insertion)
13715	44083	A	13795	3	918	DKTRKRRIRQ*IPNATSFYQNS PGLSE*LAAGTWTFAGNAPASS CGFRDRYLIVCSHQTPHVPQGI TVAAPDARAQAIRIVRQLQRF FHRFEGGHRQHRANKLLLEHP HIVLTQKNRRFEADALQPDPA WQQGTLSNGLQWQVLTTPQR SDRVEIRLLVNTGSLAESTQQS GYSHAIPRIALTQSGGLDAAQA RSLWQQGIDPKRPMPPVIVSYD TTLFNLISLPNNRNDLKEALSY LANATGKLTITPETINHALQSH DMVATLVFRYLKKGWWRYL KGSTLLSHDPAHPLKQVVEAK
13716	44084	A	13796	1	1368	MCPIEETASSFGGKPLSMVLVIQ MFMLLTGALIIILTKTNPASISK NEVFRSGMIAIVAYGIAWMA ETMFAPACYGYILPTYPSDLA AIQFDRSGTTHIGRFVINHSFILP GLIGVSVCVFGWIFAAIKRDA AAGRAKENVIFHHFPQSVKAD IATNPFKRPGGAFIRITQFRTV QTFRLSAYRLDFAGDRLRISTPR AKMRTAFKKDHLRQRRRCIRQ RAPPARHNLVGAVALPATVAG VNFTFSNPLDSSVLSLLTDFS TAVGSIVMLAVIMGLMLAFDM GGPVNKVAYAFMLICVAQGVY TVVAIAAVGICIPPLGMGLATLI GRKNFSAEERETGKAALVMGC VGVTGAIPFAAADPLR/PSFGG KPLSMVLVIQMFMLLTGALIIIL TKTNPASISKNEVFRSGMIAIVA VYGIWMAETMFAPACYGYI LPTYPSDLAAIQFDRSGTTHIGR FVINHSFILPGLIGVSVCVFGWI FAAIKRDAAAGRAKENVIFHHF PFQSVKADIATNPFKRPGGAFIR ITQFRTVQTFRLSAYRLDFAG DRLRISTPRAKMRTAFKKDHLR QRRRCIRQAPPARHNLVGAV ALPATVAGVNFTFSNPLDSSV LSLLTDFSTAVGSIVMLAVIM GLMLAFDMGGPVNKVAYAFM LICVAQGVYTVVAIAAVGICIPP LGMGLATLIGRKNFSAEERETG
13717	44085	A	13797	3	2185	
13718	44086	A	13798	1	920	

SEQ ID NO:	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in US 59/540,217	Nucleotide location of first codon for peptide sequence	Nucleotide location of last codon for last amino acid of peptide sequence	Amino acid sequence (X=Unknown, *=Stop codon, /=possible nucleotide deletion, v=possible nucleotide insertion)
13719	44087	A	13799	251	479	TQRVDWRSRSSISPGDGLHAFP AFGKEGGKMLDRLRERRDVKT LQQSGSAAAGAEFALAGAHPT GTTA*IQAINV
13720	44088	A	13800	1	939	
13721	44089	A	13801	1	386	
13722	44090	A	13802	3	524	
13723	44091	A	13803	1	548	
13724	44092	B	13804	67	1144	
13725	44093	A	13805	811	974	VSRRIKLDVTEEFARAGDNRKC ICQ*RHGLAERDIARLLVEIVVI WCDIGVIQA
13726	44094	A	13806	1164	1262	
13727	44095	A	13807	2	894	
13728	44096	A	13808	1	1587	MVKEGTFREDLFYRLNVIHLIL PPLDRRREDISLLANHFLQKFSS ENQRDIIDIPMAMSLTAWSW PGNIRELSNVIERAVVMNSGPPI FSEDLPPQIRQPVCNAGEVKTA PVGERNLKEEIKRVEKRIIMEVL EQQEGNRTRTALMLGISRRAL MYKLQEYDATGFFRDGMTIMV GGFMGIGTPSRLVEALLESQVR DLTLIANDTAFVDTGIGPLIVNG RVRKVIASHIGTNPETGRMRMSG EMDVVLVPQGTLEIQRGCGAG LGGFLNPTGVGTVEERQTSID TSTRKRPFELGRPSRNNDKGIRP VDQALDRKNIRE/ALHDSLKRRLQ TDYLDLYQVHWPLRPFCFGK LGYSWTDSPAPVSQDLTDLAL AEYQRAGKIRYIGVSNETAFGV MRYLHLADKHDLPRIVTIQNPY SLLNRSFEVGLAEVSQYEGVEL LAYSCLGFGTLTGKYLNGAKP AGARNTLFSRFTRYSGEQTKQA VAAYVDIARRHGLDPAQMALA FVRRQPFVASTLLGATTMDQL
13729	44097	A	13809	1	618	